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- (54) Title: SECRETED EXPRESSED SEQUENCE TAGS (SESTS)
- (57) Abstract

Secreted expressed sequence tags (sESTs) isolated from a variety of human tissue sources are provided.

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## SECRETED EXPRESSED SEQUENCE TAGS (SESTS)

### FIELD OF THE INVENTION

The present invention provides novel polynucleotides which are expressed sequence tags (ESTs) for secreted proteins.

# **BACKGROUND OF THE INVENTION**

Gargantuan efforts have been employed by various investigational projects to randomly sequence portions of naturally-occurring cDNAs. The rationale behind this approach to identification and sequencing genes is founded in two basic principles: (1) that transcribed cDNAs represent the product of the most important genes, namely those that are actually expressed *in vivo*, and (2) that efforts to sequence genes and other portions of the genome of target organisms which are not actually expressed wastes substantial effort on areas not likely to yield genetic information of therapeutic importance. Thus, the high-throughput sequencing efforts focus on only those portions of the genome which are expressed. The randomly produced cDNA sequences represent "expressed sequence tags" or "ESTs", which identify and can be used as probes for the longer, full-length cDNA or genomic sequence from which they were transcribed.

Although this "shortcut" approach to genomic sequencing presents savings of effort compared to sequencing of the complete genome, it still produced a vast array of ESTs which may not be directly useful as protein therapeutics. To date, the majority of protein-related drug discovery has focused on the use of secreted proteins to produce a desired therapeutic effect. Since the EST approach theoretically identifies all expressed proteins, it produces an EST library which contains a mixture of secreted proteins (such as hormones, cytokines and receptors) and non-secreted proteins (such as, for example, metabolic enzymes and cellular structural proteins), without identifying which ESTs correspond to proteins falling into either category. As a result, these methods are not optimally tailored to the needs of investigators searching for secreted proteins because they must separate the secreted "wheat" from the non-secreted "chaff", wasting effort and resources in the process.

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Co-assigned U.S. Patent No. 5,536,637, which is incorporated herein by reference, provides methods for focusing genomic sequencing efforts on sequences encoding the secreted proteins which are of most interest for identification of protein therapeutics. The '637 patent discloses a "signal sequence trap" which selectively identifies ESTs for secreted proteins, namely "secreted expressed sequence tags" or "sESTs". It is to these sESTs that the present invention is directed.

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### SUMMARY OF THE INVENTION

The present invention provides for sESTs isolated from a variety of human RNA/cDNA sources.

In preferred embodiments, the present invention provides an isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEO ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEO ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEO ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEO ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEO ID NO:55, SEO ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEO ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109. SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136. SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID 5

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NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145. SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172. SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEO ID NO:181. SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190. SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEO ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217. SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226. SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235. SEO ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, SEQ ID NO:242, SEQ ID NO:243, SEQ ID NO:244, SEQ ID NO:245, SEQ ID NO:246, SEQ ID NO:247, SEQ ID NO:248, SEQ ID NO:249, SEQ ID NO:250, SEQ ID NO:251, SEQ ID NO:252, SEQ ID NO:253, SEQ ID NO:254, SEQ ID NO:255, SEQ ID NO:256, SEQ ID NO:257, SEQ ID NO:258, SEQ ID NO:259, SEQ ID NO:260, SEQ ID NO:261, SEQ ID NO:262, SEQ ID NO:263, SEQ ID NO:264, SEQ ID NO:265, SEQ ID NO:266, SEQ ID NO:267, SEQ ID NO:268, SEQ ID NO:269, SEQ ID NO:270, SEQ ID NO:271, SEQ ID NO:272, SEQ ID NO:273, SEQ ID NO:274, SEQ ID NO:275, SEQ ID NO:276, SEQ ID NO:277, SEQ ID NO:278, SEQ ID NO:279, SEQ ID NO:280, SEQ ID NO:281, SEQ ID NO:282, SEQ ID NO:283, SEQ ID NO:284, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:287, SEQ ID NO:288, SEQ ID NO:289, SEQ ID NO:290, SEQ ID NO:291, SEQ ID NO:292, SEQ ID NO:293, SEQ ID

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or a complement of said sequence.

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In other embodiments, the present invention provides an isolated polynucleotide consisting of a nucleotide sequence selected from the group consisting of:

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or a complement of said sequence.

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In further embodiments, the present invention provides an isolated polynucleotide consisting essentially of a nucleotide sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:65, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:66, SEQ ID NO:66, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:6

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In yet other embodiments, the present invention provides an isolated polynucleotide comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of:

or a complement of said sequence.

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           NO:1473, SEQ ID NO:1474, SEQ ID NO:1475, SEQ ID NO:1476, SEQ ID
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           NO:1477, SEQ ID NO:1478, SEQ ID NO:1479, SEQ ID NO:1480, SEQ ID
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NO:1493, SEQ ID NO:1494, SEQ ID NO:1495, SEQ ID NO:1496, SEQ ID NO:1497, SEQ ID NO:1498, SEQ ID NO:1499, and SEQ ID NO:1500; or to a complement of said sequence.

The invention also provides for proteins encoded by the above-described 5 polynucleotides.

# **DETAILED DESCRIPTION**

The nucleotide sequences of the sESTs of the present invention are reported in the Sequence Listing below. Table 2 lists the "Clone ID Nos." assigned by applicants to each SEQ ID NO: in the Sequence Listing.

Table 2

Each pair of entries in this table consists of the SEQ ID NO (e.g., 1, 2, etc.) followed by the Clone ID No. for such sequence (e.g., B11, B18, etc.).

		•			•	1 - 3 - 7	,,	•
15	1	B11	21	C3	41	C639	61	D148
	2	B18	22	C32	42	C641	62	D154
	3	B21	23	C141	43	C642	63	D167
	4	B26	24	C143	44	C645	64	D179
	5	B40	25	C180	45	D4	65	D188
20	6	B115	26	C195	46	D7	66	D196
	7	B121	27	C293	47	D14	67	D200
	8	B124	28	C312	48	D15	68	D203
	9	B125	29	C539	49	D27	69	D233
	10	B142	30	C544	50	D68	70	D252
25	11	B196	31	C547	51	D69	71	D286
	12	B208	32	C571	52	D81	72	D303
	13	B224	33	C604	53	D100	73	D304
	14	B227	34	C607	54	D101	74	D305
	15	B232	35	C608	55	D104	75	D310
30	16	B236	36	C610	56	D105	76	D311
	17	B238	37	C617	57	D115	77	D318
	18	B255	38	C626	58	D121	78	D327
	19	C1	39	C627	59	D133	79	D329
	20	C2	40	C636	60	D143	80	El

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				•				
	81	E4	115	H291	149	J139	183	M141
	82	E5	116	H306	150	J143	184	M152
	83	EII	117	H383	151	J156	185	M194
	84	E12	118	H426	152	J168	186	M230
5	85	E14	119	H438	153	J297	187	M273
	86	E18	120	H541	154	J317	188	M292
	87	G1	121	H <b>54</b> 5	155	J322	189	M301
	88	G12	122	H657	156	J422	190	M313
	89	G16	123	H698	157	J435	191	M328
10	90	G20	124	H758	158	J509	192	M338
	91	G21	125	H770	159	J512	193	<b>O</b> 7
	92	G26	126	H849	160	J532	194	O47
	93	G31	127	H920	161	J546	195	O67
	94	G40	128	H978	162	J598	196	O75
15	<b>9</b> 5	G46	129	H999	163	J635	197	O99
	96	G53	130	H1004	164	J638	198	O135
	97	G55	131	H1010	165	J708	199	O139
	98	G58	132	H1045	166	J731	200	O268
	<b>9</b> 9	G68	133	H1052	167	M4	201	O276
20	100	G85	134	H1075	168	M6	202	O289
	101	G86	135	H1096	169	M43	203	O338
	102	G99	136	H1116	170	M60	204	O349
	103	G103	137	H1165	171	M68	205	O351
	104	G107	138	H1301	172	M71	206	O372
25	105	G108	139	H1408	173	M88	207	O386
	106	G112	140	H1413	174	M97	208	O417
	107	G114	141	H1456	175	M100	209	O418
	108	H45	142	I5	176	M114	210	O463
	109	H162	143	128	177	M120	211	S10
30	110	H165	144	I32	178	M121	212	S34
	111	H171	145	J5	179	M125	213	.S70
	112	H174	146	J54	180	M126	214	S169
	113	H225	147	J66	181	M128	215	S185
	114	H236	148	J135	182	M137	216	S195

	217	AA20	251	AJ6	285	AM72	319	AP137
	218	AA35	252	AJ8	286	AM93	320	AP76
	219	AB10	253	AJ52	287	AK679	321	AP87
	220	AA240	254	AJ53	288	AK684	322	AP90
5	221	AA244	255	AJ54	289	AK699	323	AP150
	222	AA246	256	AJ78	290	AM155	324	AP159
	223	AA287	257	AJ80	291	AM167	325	AP160
	224	AA299	258	AK368	292	AM207	326	AP162
	225	AA318	259	AJ127	293	AM217	327	AP168
10	226	AB45	260	AJ142	294	AM224	328	AP179
	227	AA36	261	AJ143	295	AM226	329	AP197
	228	AA363	262	AC339	296	AM235	330	AP215
	229	AA365	263	AC370	297	AM259	331	AP224
	230	AA351	264	AL14	298	AM266	332	AP226
15	231	AB290	265	AK401	299	AM267	333	AP242
	232	AC41	266	AK438	300	AM277	334	AP250
	233	AC18	267	AK583	301	AM279	335	AQ11
	234	AC175	268	AK585	302	AC387	336	AQ2
	235	AC114	269	AK598	303	AC395	337	AQ21
20	236	ACIII	270	AK604	304	AC410	338	AQ23
	237	AC100	271	AK609	305	AC412	339	AQ3
	238	AC222	272	AK620	306	AC423	340	AQ34
	239	AC325	273	AM10	307	AJ146	341	AQ5
	240	AI44	274	AM104	308	AJ147	342	AR15
25	241	AI6	275	AM123	309	AJ156	343	AR22
	242	A186	276	AM137	310	AJ168	344	AR28
	243	AJI	277	AM15	311	AJ169	345	AR3
	244	AJ10	278	AM16	312	AJ172	346	AR34
	245	AJ13	279	AM30	313	AJ173	347	AR42
30	246	A <b>J</b> 15	280	AM38	314	AJ174	348	AR54
	247	AJ20	281	AM39	315	AK528 .	349	AR61
	248	AJ21	282	AM42	316	AP116	350	AM282
	249	AJ26	283	AM46	317	AP120	351	AM307
	250	AJ27	284	AM66	318	AP135	352	AM349

	353	AM372	387	AR310	421	AM616	455	AM921
	354	AM392	388	AR323	422	AM622	456	AM931
	355	AM400	389	AR324	423	AM625	457	AM973
	356	AM430	390	AR325	424	AM666	458	AM996
5	357	AP11	391	AR349	425	AM686	459	AS56
	358	AP2	392	AR360	426	AM704	460	AS61
	359	AP56	393	AR364	427	AM726	461	<b>AS6</b> 3
	360	AP57	394	AR400	428	AM728	462	AS65
	361	AP58	395	AR415	429	AM735	463	AS83
10	362	AP60	396	AR417	430	AM741	464	AS85
	363	AP67	397	AM558	431	AM742	465	AS86
	364	AP7	398	AM566	432	AM754	466	AS88
	365	AQ53	399	AM600	433	AM781	467	AT107
	366	AQ54	400	AR420	434	AM795	468	AT111
15	367	AQ61	401	AR437	435	AM814	469	AT138
	368	AQ64	402	AR440	436	AM833	470	AT140
	369	AQ71	403	AR446	437	AM838	471	AT142
	370	AQ73	404	AR450	438	AT16	472	AT146
	371	AQ83	405	AR452	439	AT19	473	AT151
20	372	AM1075	406	AR455	440	AT20	474	AT157
	373	AM1076	407	AR463	441	AT4	475	AT181
	374	AM1083	408	AR464	442	AT53	476	AT97
	375	AR100	409	AR467	443	AT63	477	AS239
	376	AR69	410	AR474	444	AT64	478	AT226
25	377	AM1017	411	AR475	445	AT74	479	AT259
	378	AM1032	412	AS15	446	AT94	480	AT260
	379	AM1036	413	AS20	447	AT95	481	AT265
	380	AM1045	414	AS23	448	AM1000	482	AT280
	381	AM1060	415	AS31	449	AM856	483	AT340
30	382	AM1067	416	AS47	450	AM885	484	AT351
	383	AR253	417	AS48	451	AM889	485	AT352
	384	AK642	418	AS7	452	AM892	486	AT356
	385	AK647	419	AM610	453	AM910	487	AT359
	386	AK650	420	AM614	.454	AM918	488	AT361

	489	AS252	523	AU161	557	AW106	591	BE28
	490	AS263	524	AU164	558	AW107	592	BE3
	491	AS264	525	AZ285	559	AW109	593	BE34
-	492	AS268	526	AZ286	560	AW133	594	BE9
5	493	AS271	527	AZ287	561	AW140	595	AZ12
	494	AS294	528	AZ290	562	AW92	596	AZ22
	495	AS301	529	AZ188	563	AW95	597	AZ32
	496	AS330	530	AZ191	564	AW98	598	AZ45
	497	AS144	531	AZ204	565	BA185	599	AZ46
10	498	AS152	532	AZ219	566	BA204	600	BF143
	499	AS157	533	AW170	567	BA210	601	BF146
	500	AS162	534	AW176	568	BA226	602	BF157
	501	AS164	535	AW178	569	BG1	603	BF160
	502	AS167	536	AW179	570	BG13	604	BF169
15	503	AS180	537	AW182	571	BG3	605	BF171
	504	AS186	538	AW185	572	BG33	606	BF176
	505	AS187	539	AW189	573	BG36	607	BF178
	506	AU36	540	AW192	574	BG37	608	AS196
	507	AU39	541	AW194	<b>57</b> 5	BG40	609	AS202
20	508	AU43	542	AW199	576	BG43	610	AS209
	509	AU47	543	AW222	577	BG48	611	AS216
	510	AU50	544	AW231	578	BG58	612	AS230
	511	AU59	545	AZ261	579	BG72	613	AS232
	512	AU71	546	AZ264	580	BG73	614	AX101
25	513	AU101	547	AZ302	581	BF101	615	AX104
	514	AU102	548	AZ303	582	BF132	616	AX107
	515	AU105	549	AK649	583	AZ69	617	AX109
	516	AU106	550	AK663	584	BD51	618	AX122
	517	AU107	551	AR336	585	BD53	619	AX124
30	518	AU115	552	AR356	586	BD65	620	AX127
	519	AU118	553	AR398	587	BD66	621	AX128
	520	AU122	554	AR399	588	BD73	622	AX130
	521	AU138	555	AM1016	589	BD77	623	AX132
	522	AU139	556	AW105	590	BD80	624	AX136

	625	AX137	659	BG274	693	AW33	727	BG504
	626	AX143	660	BG276	694	AW36	728	BG510
	627	AX146	661	AX12	695	AW47	729	BG511
	628	AX51	662	AX17	696	AW49	730	BG513
5	629	AX55	663	AX256	697	AW52	731	BG516
	630	AX56	664	AX30	698	AW60	732	BG518
	631	AX60	665	AX32	699	AW66	733	BG526
	632	AX65	666	AX34	700	AW76	734	BG528
	633	AX78	667	AX49	701	AY241	735	BG552
10	634	AX80	668	AX6	702	AY259	736	BG553
	635	AX81	669	AX8	703	AY268	737	BG556
	636	AX92	670	AZ180	704	BA123	738	AX309
	637	AX97 `	671	BG191	705	BA134	739	AX315
	638	AX98	672	BG193	706	BA170	740	AX318
15	639	AX99	673	BG199	707	BA176	741	AY186
	640	AZ109	674	BG201	708	BA178	742	AY190
	641	AZ114	675	BG219	709	BA179	743	AY200
	642	BF286	676	BG220	710	BA216	744	AY208
	643	BF290	677	BG221	711	BA233	745	AY211
20	644	BF314	678	BG225	712	BD372	746	AY283
	645	BG236	679	BG228	713	BD375	747	AY289
	646	BG237	680	BG442	714	BD379	748	AY304
	647	BG240	681	BG449	715	BD380	749	AY307
	648	BG241	682	BG457	716	BD403	750	AY318
25	649	BG248	683	BG458	717	BD407	751	AY333
	650	BG249	684	BG461	718	BD409	752	AY334
	651	BG250	<b>68</b> 5	BG465	719	BD413	753	AY342
	652	BG251	686	BG467	720	BD414	754	AY358
	653	BG255	687	BG471	721	BG481	755	AY362
30	654	BG260	688	BG59	722	BG482	756	BF190
	655	BG267	689	AW12	723	BG492	757	BF191
	656	BG271	690	AW22	724	BG494	758	BF193
	657	BG272	691	AW24	725	BG495	759	BF197
	658	BG273	692	AW32	726	BG503	760	BF208

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	761	BF211	<b>79</b> 5	BG373	829	BD174	863	B117
	762	BF216	796	BG374	830	BD176	864	BI2
	763	BF221	797	BG379	831	BD177	865	B124
	764	BF227	798	BG386	832	BD178	866	BI25
5	765	BF228	799	BG388	833	BD183	867	BI3
	766	BF245	800	BG389	834	BE50	868	BI36
	767	BF250	801	BG391	835	BE64	869	BI37
	768	BF258	802	BG393	836	BE89	870	BI39
	769	BF259	803	BG396	837	BG490	871	B140
10	770	BF263	804	BG409	838	BG491	872	BI41
	771	BF270	805	BG411	839	BG501	873	BI46
	772	BF273	806	BG414	840	BG502	874	BM1
	773	BG280	807	BG420	841	BG512	875	BM17
	774	BG283	808	HW105	842	BG532	876	BM4
15	775	BG284	809	BB54	843	BK162	<b>87</b> 7	BM41
	776	BG288	810	BD101	844	BK165	878	BM46
	777	BG296	811	BD104	845	BK167	879	BM69
	778	BG305	812	BD107	846	BK171	880	BM88
	779	BG306	813	BD109	847	BK179	881	BM90
20	780	BG309	814	BD119	848	BK180	882	BA106
	<b>78</b> 1	BG324	815	BD121	849	BK183	883	BA12
	782	BG327	816	BD127	850	BK186	884	BA32
	<b>78</b> 3	BG329	817	BD128	851	BK194	885	BA38
	784	BG332	818	BD132	852	BK200	886	BA40
25	785	BG334	819	BD136	<b>8</b> 53	BK206	887	BA71
	<b>78</b> 6	BG335	820	BD137	854	BK216	888	BA79
	787	BG350	821	BD140	855	BK231	889	BA8
	788	BG356	822	BD144	856	BK232	890	BA88
	789	BG357	<b>82</b> 3	BD151	857	BK236	891	BA90
30	790	BG363	824	BD154	858	BK237	892	BA91
	791	BG365	825	BD164	859	BK241	893	BA98
	<b>79</b> 2	BG366	<b>8</b> 26	BD165	860	BK243	894	BK15
	793	BG368	827	BD169	861	BK246	895	BK17
	794	BG372	828	BD170	862	BK253	896	BK24

		897	BK257	931	AY428	965	BK146	999	BG139
		898	BK26	932	AY437	966	BK155	1000	BG140
		899	BK260	933	AY440	967	BK158	1001	BG141
		900	BK265	934	AY442	968	BK75	1002	BG142
	5	901	BK270	935	AY449	969	BK78	1003	BG145
		902	BK271	936	AY457	970	BK92	1004	BG148
		903	BK280	937	AY470	971	BK93	1005	BG151
		904	BK284	938	AY487	972	BK95	1006	BG156
		905	BK286	939	AY489	973	BK96	1007	BG158
	10	906	BK29	940	AY511	974	BM101	1008	BG160
		907	BK291	941	BE153	975	BM117	1009	BG168
		908	BK295	942	BF327	976	BM124	1010	BG170
		909	BK296	943	BI64	977	BM139	1011	BG171
		910	BK299	944	BI66	978	BM154	1012	BG172
	15	911	BK304	945	BI75	979	BM155	1013	BG173
		912	BK307	946	B180	980	BM158	1014	BG93
		913	BK308	947	BI81	981	BM94	1015	BG95
		914	BK339	948	BI82	982	AY102	1016	BI102
		915	BK34	949	B186	983	AY107	1017	BI103
:	20	916	BK343	950	BI87	984	AY122	1018	BI107
		917	BK40	951	BI88	985	AY131	1019	BI110
		918	BK41	952	BI91	986	AY137	1020	B1114
		919	BK48	953	B192	987	AY140	1021	B1117
		920	BK49	954	BK102	988	AY147	1022	B1120
;	25	921	BK57	955	BK105	989	AY157	1023	B1122
		922	BK59	956	BK107	990	AY160	1024	BI124
		923	BK61	957	BK112	<b>99</b> 1	AY183	1025	BI126
		924	BK68	958	BK114	992	AY93	1026	BI127
		925	BL341	959	BK115	993	BG102	1027	B1129
:	30	926	AY398	960	BK117	994	BG104	1028	BI133
		927	AY406	961	BK120	995	BG112	1029	BI139
		928	AY407	962	BK130	996	BG125	1030	BI 150
		929	AY408	963	BK134	997	BG132	1031	BI164
		930	AY421	964	BK142	998	BG137	1032	BI97

	1033	B198	1067	BQ58	1101	BO71	1135	BL209
	1034	B199	1068	BD189	1102	BO87	1136	BL210
	1035	BS1	1069	BD194	1103	BO9	1137	BL211
	1036	BS54	1070	BD199	1104	BD235	1138	BL219
5	1037	BS58	1071	BD200	1105	BD240	1139	BL220
	1038	BS81	1072	BD201	1106	BD241	1140	BL229
	1039	BS89	1073	BD208	1107	BD244	1141	BL230
	1040	BH100	1074	BD209	1108	BD247	1142	BL243
	1041	BH106	1075	BD213	1109	BD251	1143	BL247
10	1042	BHIII	1076	BD214	1110	BD257	1144	BL249
	1043	BH123	1077	BD222	1111	BD260	1145	BL255
	1044	BH131	1078	BH19	1112	BD262	1146	BL257
	1045	BH157	1079	BH195	1113	BD265	1147	BL271
	1046	BH297	1080	BH2	1114	BD268	1148	BL274
15	1047	BH306	1081	BH227	1115	BD522	1149	BL30
	1048	BH309	1082	BH272	1116	BD538	1150	BL67
	1049	BH316	1083	BH276	1117	BD544	1151	BL73
	1050	BH323	1084	BH281	1118	BD548	1152	BL89
	1051	BH339	1085	BH41	1119	BD561	1153	BD420
20	1052	BH365	1086	BH51	1120	BL147	1154	BD423
	1053	BH389	1087	BH66	1121	BL15	1155	BD426
	1054	BH392	1088	BH7	1122	BL152	1156	BD427
	1055	BJ54	1089	BH87	1123	BL156	1157	BD428
	1056	BJ62	1090	BH90	1124	BL160	1158	BD438
25	1057	BJ66	1091	BJ20	1125	BL178	1159	BD441
	1058	BJ67	1092	BJ27	1126	BL179	1160	BD445
	1059	BJ69	1093	BJ29	1127	BL183	1161	BD473
	1060	BJ70	1094	BJ38	1128	BL185	1162	BD486
	1061	BJ75	1095	BJ39	1129	BL186	1163	BD489
30	1062	BJ76	1096	BJ9	1130	BL187	1164	BD492
	1063	BJ78	1097	BOII	1131	BL194	1165	BD512
	1064	BJ87	1098	BO20	1132	BL196	1166	BL106
	1065	BQ20	1099	BO4	1133	BL201	1167	BL310
	1066	BQ3	1100	BO52	1134	BL205	1168	BNI

	1169	BN107	1203	BD351	1237	BN351	1271	BP22
	1170	BN12	1204	BN189	1238	BN354	1272	BP24
	1171	BN130	1205	BN201	1239	BN365	1273	BP25
	1172	BN132	1206	BN212	1240	BN422	1274	BT99
5	1173	BN133	1207	BN280	1241	BN425	1275	BP28
	1174	BN139	1208	BN284	1242	BN439	1276	BP3
	1175	BN141	1209	BN329	1243	BN460	1277	BP4
	1176	BN153	1210	BN331	1244	BN461	1278	BP43
	1177	BN156	1211	BN591	1245	BN463	1279	BP47
10	1178	BN171	1212	BO153	1246	BN472	1280	BP504
	1179	BN174	1213	BO157	1247	BN473	1281	BP506
	1180	BN180	1214	BO159	1248	BO100	1282	BP508
	1181	BN246	1215	BO166	1249	BO107	1283	BP521
	1182	BN267	1216	BO178	1250	BO114	1284	BP528
15	1183	BN268	1217	BO189	1251	BO121	1285	BP530
	1184	BN33	1218	BO194	1252	BO126	1286	BP532
	1185	BN40	1219	BO210-	1253	BO133	1287	BP537
	1186	BN48	1220	BO212	1254	BO137	1288	BP544
	1187	BN5	1221	BO213	1255	BO398	1289	BP545
20	1188	BN563	1222	BO218	1256	BO399	1290	BP55
	1189	BN65	1223	BO226	1257	BO401	1291	BP567
	1190	BN69	1224	BO279	1258	BO432	1292	BP569
	1191	BN81	1225	BO301	1259	BO528	1293	BP57
	1192	BN97	1226	BO323	1260	BO535	1294	BP590
25	1193	BN99	1227	BO358	1261	BO538	1295	BP61
	1194	BD286	1228	BO365	1262	BO549	1296	BP70
	1195	BD288	1229	BO385	1263	BO551	1297	BP71
	1196	BD297	1230	BO250	1264	BO93	1298	BP780
	1197	BD316	1231	BO254	1265	BP101	1299	BP783
30	1198	BD317	1232	BO256	1266	BP118	1300	BP784
	1199	BD321	1233	BO260	1267	BP121	1301	BP791
	1200	BD327	1234	BO261	1268	BP15	1302	BP797
	1201	BD335	1235	BO273	1269	BP19	1 <b>30</b> 3	BP806
	1202	BD339	1236	BN342	1270	BP21	1304	BP809

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1305	BP810	1339	BV243	1373	CC71	1407	BR572
1306	BP813	1340	BV248	1374	CC76	1408	BR559
1307	BP814	1341	BV250	1375	CC78	1409	BR538
1308	BP815	1342	BV259	1376	CC81	1410	BR537
1309	BP820	1343	BV273	1377	CC89	1411	BR533
1310	BP84	1344	BV275	1378	CD124	1412	BR500
1311	BP919	1345	BV49	1379	CD128	1413	BR48
1312	BP925	1346	BV51	1380	CD140	1414	BR475
1313	BQ115	1347	BV66	1381	CD145	1415	BR436
1314	BQ129	1348	BV70	1382	CD146	1416	BR434
1315	BS116	1349	BV71	1383	CD173	1417	BR4
1316	BT101	1350	BV72	1384	CD194	1418	BR346
1317	BT133	1351	BV73	1385	CD31	1419	BR342
1318	BT139	1352	BV88	1386	CD50	1420	BR338
1319	BT33	1353	BW345	1387	CF50	1421	BR333
1320	BT4	1354	CB25	1388	CF62	1422	BR332
1321	BW13	1355	CB3	1389	CF78	1423	BR212
1322	BW18	1356	CB30	1390	CF85	1424	BR195
1323	BW2	1357	CB37	1391	CF89	1425	BR194
1324	BW51	1358	CC144	1392	BR814	1426	BR19
1325	BW61	1359	CC145	1393	BR782	1427	BR141
1326	BW83	1360	CC149	1394	BR778	1428	BR122
1327	BV185	1361	CC153	1395	BR77	1429	BR107
1328	BV195	1362	CC162	1396	BR767	1430	BR1010
1329	BV200	1363	CC25	1397	BR758	1431	BR101
1330	BV202	1364	CC31	1398	BR733	1432	BR1008
1331	BV204	1365	CC322	1399	BR719	1433	BQ135
1332	BV206	1366	CC39	1400	BR711	1434	BP913
1333	BV210	1367	CC397	1401	BR71	1435	BP911
1334	BV212	1368	CC403	1402	BR63	1436	BP897
1335	BV227	1369	CC46	1403	BR616	1437	BP895
1336	BV238	1370	CC50	1404	BR610	1438	BP894
1337	BV239	1371	CC59	1405	BR607	1439	BP893
1338	BV241	1372	CC69	1406	BR595	1440	BP884
	1306 1307 1308 1310 1311 1312 1313 1314 1315 1316 1317 1318 5 1319 1320 1321 1322 1323 1324 1325 1326 1327 1328 5 1329 1330 1331 1332 1333 1334 1335 1336 1337	1306 BP813 1307 BP814 1308 BP815 5 1309 BP820 1310 BP84 1311 BP919 1312 BP925 1313 BQ115 0 1314 BQ129 1315 BS116 1316 BT101 1317 BT133 1318 BT139 5 1319 BT33 1320 BT4 1321 BW13 1322 BW18 1323 BW2 0 1324 BW51 1325 BW61 1326 BW83 1327 BV185 1328 BV195 5 1329 BV200 1330 BV202 1331 BV204 1332 BV206 1333 BV210 0 1334 BV212 1335 BV227 1336 BV238 1337 BV239	1306       BP813       1340         1307       BP814       1341         1308       BP815       1342         5       1309       BP820       1343         1310       BP84       1344         1311       BP919       1345         1312       BP925       1346         1313       BQ115       1347         1314       BQ129       1348         1315       BS116       1349         1316       BT101       1350         1317       BT133       1351         1318       BT139       1352         1319       BT33       1353         1320       BT4       1354         1321       BW13       1355         1322       BW18       1356         1323       BW2       1357         1324       BW51       1358         1325       BW61       1358         1326       BW83       1360         1327       BV185       1361         1328       BV195       1362         5       1329       BV200       1363         1331       BV204       1365	1306 BP813 1340 BV248 1307 BP814 1341 BV250 1308 BP815 1342 BV259 1309 BP820 1343 BV273 1310 BP84 1344 BV275 1311 BP919 1345 BV49 1312 BP925 1346 BV51 1313 BQ115 1347 BV66 1314 BQ129 1348 BV70 1315 BS116 1349 BV71 1316 BT101 1350 BV72 1317 BT133 1351 BV73 1318 BT139 1352 BV88 1319 BT33 1353 BW345 1320 BT4 1354 CB25 1321 BW13 1355 CB3 1322 BW18 1356 CB30 1323 BW2 1357 CB37 1324 BW51 1358 CC144 1325 BW61 1359 CC145 1326 BW83 1360 CC149 1327 BV185 1361 CC153 1328 BV195 1362 CC162 1329 BV200 1363 CC25 1330 BV202 1364 CC31 1331 BV204 1365 CC322 1332 BV206 1366 CC39 1333 BV210 1367 CC397 1334 BV212 1368 CC403 1335 BV227 1369 CC46 1336 BV238 1370 CC50 1337 BV239 1371 CC59	1306 BP813   1340 BV248   1374   1307 BP814   1341 BV250   1375   1308 BP815   1342 BV259   1376   1310 BP84   1344 BV275   1378   1311 BP919   1345 BV49   1379   1312 BP925   1346 BV51   1380   1313 BQ115   1347 BV66   1381   1315 BS116   1349 BV71   1383   1316 BT101   1350 BV72   1384   1318 BT139   1352 BV88   1386   1319 BT33   1353 BW345   1387   1320 BT4   1354 CB25   1388   1320 BT4   1354 CB25   1388   1322 BW18   1356 CB30   1390   1323 BW2   1357 CB37   1391   1325 BW81   1326 BW83   1360 CC149   1394   1327 BV185   1361 CC153   1395   1328 BV195   1362 CC162   1396   1329 BV200   1363 CC25   1397   1330 BV202   1364 CC31   1398   1332 BV204   1365 CC392   1399   1332 BV204   1365 CC397   1401   1334 BV212   1368 CC403   1402   1335 BV227   1368 CC403   1402   1335 BV227   1369 CC46   1403   1336 BV238   1370 CC50   1404   1337 BV239   1371 CC59   1405	1306 BP813   1340 BV248   1374 CC76   1307 BP814   1341 BV250   1375 CC78   1308 BP815   1342 BV259   1376 CC81   1309 BP820   1343 BV273   1377 CC89   1310 BP84   1344 BV275   1378 CD124   1311 BP919   1345 BV49   1379 CD128   1312 BP925   1346 BV51   1380 CD140   1313 BQ115   1347 BV66   1381 CD145   1314 BQ129   1348 BV70   1382 CD146   1315 BS116   1349 BV71   1383 CD173   1316 BT101   1350 BV72   1384 CD194   1317 BT133   1351 BV73   1385 CD31   1318 BT139   1352 BV88   1386 CD50   1319 BT33   1353 BW345   1387 CF50   1320 BT4   1354 CB25   1388 CF62   1321 BW13   1355 CB3   1389 CF78   1322 BW18   1356 CB30   1390 CF85   1323 BW2   1357 CB37   1391 CF89   1324 BW51   1358 CC144   1392 BR814   1325 BW61   1359 CC145   1393 BR782   1326 BW83   1360 CC149   1394 BR778   1327 BV185   1361 CC153   1395 BR77   1328 BV195   1362 CC162   1396 BR767   1329 BV200   1363 CC25   1397 BR758   1330 BV202   1364 CC31   1398 BR733   1331 BV204   1365 CC322   1399 BR719   1332 BV206   1366 CC39   1400 BR711   1333 BV210   1367 CC397   1401 BR71   1334 BV212   1368 CC403   1402 BR63   1335 BV237   1371 CC59   1405 BR607   1405 B	1306   BP813   1340   BV248   1374   CC76   1408   1307   BP814   1341   BV250   1375   CC78   1409   1308   BP815   1342   BV259   1376   CC81   1410   1309   BP820   1343   BV273   1377   CC89   1411   1310   BP84   1344   BV275   1378   CD124   1412   1311   BP919   1345   BV49   1379   CD128   1413   1312   BP925   1346   BV51   1380   CD140   1414   1313   BQ115   1347   BV66   1381   CD145   1415   1314   BQ129   1348   BV70   1382   CD146   1416   1315   BS116   1349   BV71   1383   CD173   1417   1316   BT101   1350   BV72   1384   CD194   1418   1317   BT133   1351   BV73   1385   CD31   1419   1318   BT139   1352   BV88   1386   CD50   1420   1320   BT4   1354   CB25   1388   CF62   1422   1321   BW13   1355   CB3   1389   CF78   1423   1322   BW18   1356   CB30   1390   CF85   1424   1323   BW2   1357   CB37   1391   CF89   1425   1326   BW83   1360   CC149   1394   BR782   1427   1326   BW83   1360   CC149   1394   BR778   1428   1327   BV185   1361   CC153   1395   BR77   1429   1328   BV195   1362   CC162   1396   BR767   1430   1330   BV202   1364   CC31   1398   BR783   1432   1331   BV204   1365   CC322   1399   BR719   1433   1333   BV206   1366   CC39   1400   BR711   1434   1333   BV210   1367   CC397   1401   BR71   1435   1336   BV227   1368   CC46   1403   BR616   1437   1336   BV238   1370   CC50   1404   BR610   1438   1337   BV239   1371   CC59   1405   BR607   1439   1439   1439   1430   1430   1430   1430   1430   1430   1430   1430   1430   1430   1430   1430   BV238   1370   CC50   1406   BR607   1439   1430   1430   1430   BV239   1371   CC59   1405   BR607   1439   1430   1430   1430   1430   1430   BV239   1371   CC59   1405   BR607   1439   1430   1430   1430   BV239   1371   CC59   1405   BR607   1439   1430   1430   1430   1430   BV239   1371   CC59   1405   BR607   1439   1430   1430   1430   1430   BV239   1371   CC59   1405   BR607   1439   1430   1430   1430   1430   1430   1430   1430   1430   1430   1430   1430   1430   1430   1430   1430   1430   1430   1430   1430

	1441	BP883	1475	BU65
	1442	BP875	1476	BU68
	1443	BP870	1477	BU76
	1444	BP859	1478	BV106
5	1445	BP837	1479	BV112
	1446	BP833	1480	BV123
	1447	BP499	1481	BV124
	1448	BP492	1482	BV126
	1449	BP488	1483	BV128
10	1450	BP484	1484	BV131
	1451	BP483	1485	BV133
	1452	BP481	1486	BV134
	1453	<b>BP47</b> 5	1487	BV135
	1454	BN418	1488	BV138
15	1455	BN415	1489	BV139
	1456	BN405	1490	BV140
	1457	BN394	1491	BV141
	1458	BN390	1492	BV145
	1459	BN387	1493	BV15
20	1460	BN379	1494	BV158
	1461	BN377	1495	BV160
	1462	BR84	1496	BV172
	1463	BR853	1497	BV180
	1464	BR854	1498	BV21
25	1465	BR884	1499	BV27
	1466	BT160	1500	BV29
	1467	BU165		
	1468	BU29		
	1469	BU44		
30	1470	BU45		
	1471	BU53		
	1472	BU57		
	1473	BU6		
	1474	BU60		

The "Clone ID No." for a particular clone consists of one or two letters followed by a number. The letters designate the tissue source from which the sEST was isolated. Table 3 below lists the various sources which were run through applicants' signal sequence trap. Thus, the tissue source for a particular sEST sequence can be identified in Table 3 by the one and two letter designations used in the relevant "Clone ID No.". For example, a clone designated as "BA312" would have been isolated from a human placenta (26 yrs.) library (i.e., selectin "BA") as indicated in Table 3.

As used herein, "polynucleotide" includes single- and double-stranded RNAs, DNAs and RNA:DNA hybrids.

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As used herein a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported across the membrane of the endoplpasmic reticulum.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H.U. Saragovi, et al., Bio/Technology 10, 773-778 (1992) and in R.S. McDowell, et al., J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites. For example, fragments of the protein may be fused through "linker" sequences to the Fc portion of an immunoglobulin. For a bivalent form of the protein, such a fusion could be to the Fc portion of an IgG molecule. Other immunoglobulin isotypes may also be used to generate such fusions. For example, a protein - IgM fusion would generate a decayalent form of the protein of the invention.

The present invention also provides both full-length and mature forms of the disclosed proteins. The full-length form of the such proteins is identified in the sequence listing by translation of the nucleotide sequence of each disclosed clone. The mature form of such protein may be obtained by expression of the disclosed full-length polynucleotide (preferably those deposited with ATCC) in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein may also be determinable from the amino acid sequence of the full-length form.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials.

Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms part or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information.

Species homologs of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

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The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides disclosed herein.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides capable of hybridizing, preferably under reduced stringency conditions, more preferably under stringent conditions, most preferably under highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in Table 1 below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

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Table 1

1		<del> </del>			
	Stringenc y Condition	Polynucleotide Hybrid	Hybrid Length (bp) <sup>‡</sup>	Hybridization Temperature and Buffer <sup>1</sup>	Wash Temperature and Buffer'
5	A	DNA:DNA	≥ 50	65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide	65°C; 0.3xSSC
	В	DNA:DNA	< 50	T <sub>B</sub> *; 1xSSC	T <sub>B</sub> *; 1xSSC
	С	DNA:RNA	≥ 50	67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide	67°C; 0.3xSSC
	D	DNA:RNA	< 50	T <sub>D</sub> *; 1xSSC	T <sub>D</sub> *: lxSSC
	E	RNA:RNA	≥ 50	70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide	70°C; 0.3xSSC
10	F	RNA:RNA	< 50	T <sub>F</sub> *; 1xSSC	T <sub>F</sub> *; 1xSSC
	G	DNA:DNA	≥ 50	65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide	65°C; 1xSSC
	н	DNA:DNA	< 50	T <sub>H</sub> *; 4xSSC	T <sub>H</sub> *; 4xSSC
	I	DNA:RNA	≥ 50	67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide	67°C; 1xSSC
	j	DNA:RNA	< 50	T <sub>J</sub> *; 4xSSC	T <sub>j</sub> *; 4xSSC
15	К	RNA:RNA	≥ 50	70°C; 4xSSC -or- 50°C; 4xSSC, 50% formamide	67°C; 1xSSC
	L	RNA:RNA	< 50	T <sub>L</sub> *; 2xSSC	T <sub>L</sub> *; 2xSSC
	М	DNA:DNA	≥ 50	50°C; 4xSSC -or- 40°C; 6xSSC, 50% formamide	50°C; 2xSSC
	N	DNA:DNA	< 50	T <sub>N</sub> *; 6xSSC	T <sub>N</sub> *; 6xSSC
	О	DNA:RNA	≥ 50	55°C; 4xSSC -or- 42°C; 6xSSC, 50% formamide	55°C; 2xSSC
20	Р	DNA:RNA	< 50	T <sub>P</sub> *; 6xSSC	T <sub>P</sub> *; 6xSSC
	Q	RNA:RNA	≥ 50	60°C; 4xSSC -or- 45°C; 6xSSC, 50% formamide	60°C; 2xSSC
	R	RNA:RNA	< 50	T <sub>R</sub> *; 4xSSC	T <sub>R</sub> *; 4xSSC

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sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from in vitro culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include Saccharomyces cerevisiae, Schizosaccharomyces pombe, Kluyveromyces strains, Candida, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include Escherichia coli, Bacillus subtilis, Salmonella typhimurium, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, California, U.S.A. (the MaxBac®kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl® or Cibacrom blue 3GA

Sepharose<sup>®</sup>; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, MA), Pharmacia (Piscataway, NJ) and InVitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from Kodak (New Haven, CT).

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Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The protein may also be produced by known conventional chemical synthesis.

Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequences can be made by those skilled in the art using known techniques. Modifications

of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Patent No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and may thus be useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are believed to be encompassed by the present invention.

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## **USES AND BIOLOGICAL ACTIVITY**

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA).

#### Research Uses and Utilities

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The polynucleotides provided by the present invention can be used by the research community for various purposes. The primary use of polynucleotides of the invention which are sESTs is as porbes for the identification and isolation of full-length cDNAs and genomic DNA molecules which correspond (i.e., is a longer polynucleotide sequence of which substantially the entire sEST is a fragment in the case of a full-length cDNA, or which encodes the sEST in the case of a genomic DNA molecule) to such sESTs. Techniques for use of such sequences as probes for larger cDNAs or genomic molecules are well known in the art.

The polynucleotides can also be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise antiprotein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

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Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., J. Immunol. 149:3778-3783, 1992; Bowman et al., J. Immunol. 152: 1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon γ, Schreiber, R.D. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6 - Nordan, R. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley

and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

## Immune Stimulating or Suppressing Activity

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A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre

syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

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Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (e.g., B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the 30 molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-

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blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor: ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral

infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigenpulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

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In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected ex vivo with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection in vivo.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I  $\alpha$  chain protein and  $\beta_2$  microglobulin protein or an MHC class II  $\alpha$  chain protein and an MHC class II  $\beta$  chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I

or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured 10 by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowmanet al., J. Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

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Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: *In vitro* antibody production, Mond, J.J. and Brunswick, M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-

3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

## 25 Hematopoiesis Regulating Activity

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A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for

example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

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Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland,

H.J. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

## Tissue Growth Activity

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A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-liketissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-liketissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic

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plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

### 15 Activin/Inhibin Activity

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A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin  $\alpha$  family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- $\beta$  group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale

et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

#### Chemotactic/Chemokinetic Activity

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A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W.Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

#### Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

## 15 Receptor/Ligand Activity

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A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in:Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W.Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med.

169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

## Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusioninjury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

## 20 <u>Tumor Inhibition Activity</u>

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

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## Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting

(suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or caricadic cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate. vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

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#### **ADMINISTRATION AND DOSING**

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A protein of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources) may be used in a pharmaceutical composition when combined with a pharmaceutically acceptable carrier. composition may also contain (in addition to protein and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin stem cell factor, and erythropoietin. The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or compliment its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein of the invention, or to minimize side effects. Conversely, protein of the present invention may be included in formulations of the particular cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent.

A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that

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can directly signal T cells. Alternatively antibodies able to bind surface immunolgobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithin, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent No. 4,235,871; U.S. Patent No. 4,501,728; U.S. Patent No. 4,837,028; and U.S. Patent No. 4,737,323, all of which are incorporated herein by reference.

As used herein, the term "therapeutically effective amount" means the total amount of each active component of the pharmaceutical composition or method that is sufficient to show a meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, the term refers to that ingredient alone. When applied to a combination, the term refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein of the present invention is administered to a mammal having a condition to be treated. Protein of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

Administration of protein of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

When a therapeutically effective amount of protein of the present invention is administered orally, protein of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein of the present invention, and preferably from about 25 to 90% protein of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein of the present invention, and preferably from about 1 to 50% protein of the present invention.

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When a therapeutically effective amount of protein of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skiil in the art.

The amount of protein of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein of the present invention with

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which to treat each individual patient. Initially, the attending physician will administer low doses of protein of the present invention and observe the patient's response. Larger doses of protein of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about  $0.01~\mu g$  to about 100~mg (preferably about 0.1~ng to about 10~mg, more preferably about  $0.1~\mu g$  to about 1~mg) of protein of the present invention per kg body weight.

The duration of intravenous therapy using the pharmaceutical composition of the present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is contemplated that the duration of each application of the protein of the present invention will be in the range of 12 to 24 hours of continuous intravenous administration. Ultimately the attending physician will decide on the appropriate duration of intravenous therapy using the pharmaceutical composition of the present invention.

Protein of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R.P. Merrifield, J. Amer.Chem. Soc. 85, 2149-2154 (1963); J.L. Krstenansky, et al., FEBS Lett. 211, 10 (1987). Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein.

For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a

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pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalciumphosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses(including hydroxyalkylcelluloses),including methylcellulose, ethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate,

poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt%, preferably 1-10 wt% based on total formulation weight, which represents the amount necessary to prevent desorbtion of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells.

In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- $\alpha$  and TGF- $\beta$ ), and insulin-like growth factor (IGF).

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The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins of the present invention.

The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA).

Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in rder to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

Patent and literature references cited herein are incorporated by reference as if fully set forth.

# Table 3

Sel.	Species	Tissue	Cell Type
AA	Human	Kidney	19-23wks., M/F pool of 5
AB	Human	Fetal Lung	Fetal Lung
AC	Human	Placenta	26yrs., 1 specimen
AD	Murine	Embryo	Fetal ES cells
ΑE	Murine	Spleen	Adult spleen
AF	Murine	Fetal Brain	Fetal Brain
AG	Murine	Fetal Brain	Fetal Brain
AH	Murine	Fetal Thymus	Fetal Thymus
ΑI	Human	Blood	Adult PBMC/TH1or2
AJ	Human	Testes	10-61yrs., pool of 11
AK	Human	Kidney	19-23wks., M/F pool of 5
AL	Human	Neural	Adult Glioblastoma line TG-1
AM	Human	Kidney	19-23wks., M/F pool of 5
AN	Murine	Bone Marrow	Adult Stromal cell line FCM-4
AO	Murine	Thymus	Adult Subtr. Adult Thymus
AP	Human	Placenta	26yrs., 1 specimen
AQ	Human	Ovary	PA-1 Teratocarcinoma
AR	Human	Retina	16-75yrs., pool of 76
AS	Human	Brain	19-23wks., M/F pool of 5
AT	Human	Blood	Adult lymphocytes+dend. cells
AU	Human	Testes	10-61yrs., pool of 11
ΑV	Murine	Spleen	Adult spleen
AW	Human	Ovary	PA-1 Teratocarcinoma
AX	Human	Testes	10-61yrs., pool of 11
ΑY	Human	Retina	16-75yrs., pool of 76
ΑZ	Human	Colon	Caco-2 Adenocarcinoma
В	Human	Blood	PeripheralBloodMononuclearCell
BA	Human	Placenta	26yrs., 1 specimen
BB	Human	Blood	Adult PBMC/TH1or2
BC	Murine	Embryo	Fetal ES cells
BD	Human	Kidney	19-23wks., M/F pool of 5
BE	Human	Blood	Adult PBMC/TH1or2
BF	Human	Brain	19-23wks., M/F pool of 5
BG	Human	Brain	N/A
BH	Human	Ovary	PA-1 Teratocarcinoma
BI	Human	Kidney	19-23wks., M/F pool of 5
BJ	Human	Ovary	PA-1 Teratocarcinoma
BK	Human	Retina	16-75yrs., pool of 76
BL	Human	Testes	10-61yrs., pool of 11
BM	Human	Muscle	N/A
BN	Human	Placenta	26yrs., 1 specimen
BO	Human	Retina	16-75yrs., pool of 76
BP	Human	Kidney	19-23wks., M/F pool of 5
BQ	Human	Colon	Caco-2 Adenocarcinoma Caco2

BR	Human	Kidney	19-23wks., M/F pool of 5
BS	Human	Pituitary	Adult Pituitary
BT	Human	Blood	Adult PBMC
BU	Human	Placenta	26yrs., 1 specimen
BV	Human	Brain	N/A
BW	Human	Blood	Adult PBMC
вх	Human	Ovary	PA-1 Teratocarcinoma
BY	Human	Blood	Adult PBMC/TH1or2
BZ	Human	Kidney	19-23wks., M/F pool of 5
C	Human	Blood	PeripheralBloodMononuclearCell
CA	Murine	Embryo	Fetal ES cell embryoid bodies
CB	Human	Brain	19-23wks., M/F pool of 5
CC	Human	Brain	N/A
		Brain	
CD	Human		19-23wks., M/F pool of 5
CE	Human	Blood	Adult lymphocytes+dend. cells
CF	Human	Placenta	26yrs., 1 specimen
CG	Human	Testes	10-61yrs., pool of 11
CH	Human	Kidney	19-23wks., M/F pool of 5
CI	Human	Brain	N/A
CJ	Human	Brain	19-23wks., M/F pool of 5
CK	Human	Testes	10-61утs., pool of 11
CL	Human	Retina	16-75yrs., pool of 76
CM	Human	Adult Lung	Adult Lung
CN	Human	Brain	19-23wks., M/F pool of 5
CO	Human	Brain	N/A
CP	Human	SalivaryGland	N/A
CQ	Human	Heart	13-73yrs., pool of 3
CR	Human	Testes	10-61yrs., pool of 11
CS	Human	Brain	19-23wks., M/F pool of 5
CT	Human	Brain	N/A
CU	Human	Pineal Gland	N/A
CV	Human	Mammary	Adult Human Mammary
CW	Human	Brain	19-23wks., M/F pool of 5
CY	Human	Pineal Gland	N/A
CZ	Human	Testes	10-61yrs., pool of 11
D	Human	Blood	PeripheralBloodMononuclearCell
DA	Human	Placenta	26yrs., 1 specimen
DB	Human	Prostate	Adult Prostate
DC	Human	Pineal Gland	Adult Pineal Gland
DD			
	Human	Testes	10-61yrs:, pool of 11
DE	Human	Testes	Adult NCCIT TeratoCA
DF	Human	Brain	N/A
DG	Human	Placenta	26yrs., 1 specimen
DH	Human	Brain	19-23wks., M/F pool of 5
DI	Human	Testes	10-61yrs., pool of 11
DJ	Human	Placenta	26yrs., 1 specimen
DK	Human	Fetal Kidney2	Fetal Kidney

DI	II	Dunin	NT/A
DL	Human	Brain Brain	N/A
DM DN	Human	Brain Basin	N/A
DN	Human	Brain	19-23wks., M/F pool of 5
DO	Human	Testes	10-61yrs., pool of 11
DP	Murine	Embryo	Fetal ES cell embryoid bodies
DQ	Human	Placenta	26yrs., 1 specimen
DR	Human	SalivaryGland	N/A
DT	Human	Brain	N/A
DU	Human	Brain	19-23wks., M/F pool of 5
DV	Human	Pineal Gland	Adult Pineal Gland
DW	Human	Brain	N/A
DX	Human	Testes	10-61yrs., pool of 11
DY	Human	Brain	N/A
DZ	Human	Testes	Adult NCCIT TeratoCA
E	Human	Blood	PeripheralBloodMononuclearCell
EA	Human	Brain	19-23wks., M/F pool of 5
EB	Human	Melanoma	Adult Melanoma
EC	Human	Brain	N/A
ED	Human	Placenta	26yrs., 1 specimen
EE	Human	Testes	10-61yrs., pool of 11
EF	Human	Liver	Adult Liver
EG	Human	Pancreas	Adult HPC-3 Ductal AdenoCA
EH	Human	Blood	Peripheral Blood Mononuclear Cell
EI.	Human	Brain	19-23wks., M/F pool of 5
EJ	Human	Placenta	<del>-</del>
EK	Human	Brain	26yrs., 1 specimen
EL	Human	Testes	19-23wks., M/F pool of 5
EM	Human		10-61yrs., pool of 11
EN		Fetal Kidney2	Fetal Kidney
EO	Human	Brain	19-23wks., M/F pool of 5
EP	Human	Adrenal Gland	Adult Adrenal Gland
	Human	Placenta	26yrs., 1 specimen
EQ	Human	Testes	10-61yrs., pool of 11
ER	Human	Brain	19-23wks., M/F pool of 5
ES	Human	Placenta	26yrs., 1 specimen
ET	Human	Testes	10-61yrs., pool of 11
EU	Human	Kidney	Adult Kidney
EV	Human	Stomach	Adult Stomach
EW	Human	Placenta	26yrs., 1 specimen
EX	Human	Testes	10-61yrs., pool of 11
EY	Human	Brain	19-23wks., M/F pool of 5
EZ	Human	Fetal Kidney2	Fetal Kidney
FA	Human	Brain	19-23wks., M/F pool of 5
FB	Human	Placenta	26yrs., 1 specimen
FC	Human	Testes	10-61yrs., pool of 11
FD	Human	SalivaryGland	N/A
FE	Human	Brain	N/A
FF	Human	Testes	Adult NCCIT TeratoCA
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FG	Human	Brain	N/A
FH	Human	Brain	19-23wks., M/F pool of 5
FI	Human	Small Intest	Adult Small Intestine
FJ	Human	Lung CA	Adult Lung CA
FK	Human	Kidney	Adult Kidney
FM	Human	Brain	N/A
FN	Human	Brain	19-23wks., M/F pool of 5
FO	Human	Brain	N/A
FP	Human	Placenta	26yrs., 1 specimen
FQ	Human	Testes	10-61yrs., pool of 11
FR	Human	Placenta	26yrs., 1 specimen
FS	Human	Testes	10-61yrs., pool of 11
FT	Chicken	Fetal Lung	Fetal Lung
FU	Chicken	Limb Bud	Fetal St. 23 Limb Bud
FV	Human	Testes	Adult NCCIT TeratoCA
FW	Human	Testes	Adult NCCIT TeratoCA
FX	Human	Brain	19-23wks., M/F pool of 5
FY	Human	Placenta	26yrs., 1 specimen
FZ	Human-	Placenta	26yrs., 1 specimen
G	Human	Blood	PeripheralBloodMononuclearCell
GA	Human	Testes	10-61 yrs., pool of 11
GB	Human	Placenta	26yrs., 1 specimen
GC	Human	Testes	10-61 yrs., pool of 11
GD	Human	Placenta	26yrs., 1 specimen
GE	Human	Brain	N/A
GF	Human	Brain	19-23wks., M/F pool of 5
GG	Human	Fetal Kidney2	Fetal Kidney
GH	Human	Placenta	26yrs., 1 specimen
GI	Human	Retinoblastoma	Adult Retinoblastoma Y79
GJ	Murine	Spleen	Adult Spleen
GK	Human	Fetal Kidney2	Fetal Kidney
GL	Murine	Lymph Node	Adult Lymph Node
GM	Human	Uterus	N/A
GN	Human	Blood	PeripheralBloodMononuclearCell
GO	Human	Adrenal Gland	Adult Adrenal Gland
GP	Human	Ovary	PA-1 Teratocarcinoma
GQ	Human	Pineal Gland	N/A
GR	Human	Pancreas	Adult HPC-3 Ductal AdenoCA
GS	Human	Retina	16-75yrs., pool of 76
GT	Human	Brain	N/A
GU	Human	Fetal Kidney2	Fetal Kidney
GV	Rat	Retina	Newborn Retina
GW	Chicken	Limb Bud	Fetal St.26 Limb Bud
GX	Human	Brain	N/A
GY	Human	Testes	10-61yrs., pool of 11
GZ	Human	Brain	19-23wks., M/F pool of 5
H	Human	Blood	PeripheralBloodMononuclearCell

77.4	**	<b></b>	
HA	Human	Testes	Adult NCCIT TeratoCA
HB	Human	Fetal Kidney2	Fetal Kidney
HC	Human	Brain	19-23wks., M/F pool of 5
HD	Human	Brain	N/A
HE	Human	Testes	10-61yrs., pool of 11
HF	Human	Brain	19-23wks., M/F pool of 5
HG	Human	Fetal Kidney2	Fetal Kidney
HH	Human	Brain	N/A
HI	Human	Testes	10-61yrs., pool of 11
·HJ	Human	Brain	N/A
HK	Human	Brain	19-23wks., M/F pool of 5
HL	Human	Fetal Kidney2	Fetal Kidney
HM	Human	Testes	Adult NCCIT TeratoCA
HN	Human	Fetal Kidney2	Fetal Kidney
НО	Human	Brain	N/A
HP	Human	Brain	19-23wks., M/F pool of 5
HQ	Human	Testes	<del>-</del>
HR	Human	Brain	10-61 yrs., pool of 11 N/A
HS	Human	Brain	
HT	Human	Brain	N/A
HU			19-23wks., M/F pool of 5
HV	Human	Fetal Kidney2	Fetal Kidney
	Human	Testes	10-61 yrs., pool of 11
HW	Human	Brain	N/A
HX	Human	Brain Hippoca	Adult Brain Hippocampus
HY	Human	Trachea	Adult Trachea
HZ	Human	Brain Thalamus	Adult Brain Thalamus
I	Human	Blood	PeripheralBloodMononuclearCell
IA	Human	Thyroid	Adult Thyroid
IB	Human	Embryonal CA	Fetal NT2-D1
IC	Human	WER1-Rb1 line	Adult Retinoblastoma
ID	Human	Muscle	N/A
Œ	Human	Brain	19-23wks., M/F pool of 5
IF	Human	Uterus	N/A
IG	Human	Testes	10-61 yrs., pool of 11
IH	Human	Muscle	N/A
n	Human	Brain	N/A
IJ	Human	Blood	PeripheralBloodMononuclearCell
IK	Human	Retinoblastoma	Adult Retinoblastoma Y79
IL.	Human	Retina	16-75yrs., pool of 76
IM	Human	Various	Various
IN	Human	Prostate	Adult Prostate
IO	Human	Brain	19-23wks., M/F pool of 5
IP	Human	Fetal Kidney2	Fetal Kidney
IQ	Human	Prostate	Adult Prostate
IR	Human		
IS		Brain Hippoca	Adult Brain Hippocampus
IT .	Human	Trachea	Adult Trachea
11	Human	Brain Thalamu	Adult Brain Thalamus

#### SEQUENCE LISTING

(i) APPLICANT: Jacobs, Kenneth McCoy, John LaVallie, Edward Racie, Lisa Merberg, David Treacy, Maurice Spaulding, Vikki Agostino, Michael

- (ii) TITLE OF INVENTION: SECRETED, EXPRESSED SEQUENCE TAGS
- (iii) NUMBER OF SEQUENCES: 1500
- (iv) CORRESPONDENCE ADDRESS
  - (A) ADDRESSE: Genetics Institute, Inc.
  - (B) STREET: 87 CambridgePark Drive
  - (C) CITY: Cambridge
  - (D) STATE: Massachusetts
  - (E) COUNTRY: U.S.A
  - (F) ZIP: 02140
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy Disk
  - (B) COMPUTER: IBM PC Compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Brown, Scott A.
  - (B) REGISTRATION NUMBER: 32,724
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (617) 498-8224
  - (B) TELEFAX: (617) 876-5851
- (2) INFORMATION FOR SEQ ID NO:1:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 335 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTCGACCCCA	TCCCATCCAA	TAGTCCCCAT	CTCTTCTCAG	CTCTCTCTGT	AGTITCICIT	61
CCTCCGCCTG	CCTTTTAAGT	TAGTGTTTCC	CAGGACAGAG	GTGACTCAGT	TGTATCCAGA	120
CCGCTCTGTG	ACTGAACACC	CACTTTCTTT	TCCTTTTCCA	ATAAATATAT	GTAACATACA	18
TGTCAACTAG	GAACAAAACA	GTATCTCAGG	AATCCACCAT	CCAGTTAAAA	ATGGACCCTT	24

ACCCTTACCG TGCCCCTGCA GAGACCCCAA TACAGCGCAT TTCCCTCATT CTTTTGCTTT TCTCAAGTTT TACCACGGCC TCTTTGGCCC TCGAG	300 335
(2) INFORMATION FOR SEQ ID NO:2:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 514 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	•
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
GAATTCGGCC AAAGAGGCCG TTGACCATTG ATAGAACACA GGCATACACA GGAAGATACA	60
TTCACAGAAG AGCTTCCTGC ACAAAGTAAG CCACCAGCGC AACATGACAG TGAAGACCCT	120
GCATGGCCCA GCCATGGTCA AGTACTTGCT GCTGTCGATA TTGGGGCTTG CCTTTCTGAG	180
TGAGGCGGCA GCTCGGAAAA TCCCCAAAGT AGGACATACT TTTTTCCAAA AGCCTGAGAG TTGCCCGCCT GTGCCAGGAG GTAGTATGAA GCTTGACATT GGCATCATCA ATGAAAACCA	240
GCGCGTTTCC ATGTCACGTA ACATCGAGAG CCGCTCCACC TCCCCCTGGA ATTACACTGT	300 360
CACTTGGGAC CCCAACCGGT ACCCCTCGGA AGTTGTACAG GCCCAGTGTA GGAACTTGGG	420
CTGCATCAAT GCTCAAGGAA AGGAAGACAT CTCCATGAAT TCCGTTCCCA TCCAGCAAGA	480
GACCCTGTCG ACGGCCTCTT TGGCCCTCGA GACA	514
(2) INFORMATION FOR SEQ ID NO:3:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 393 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
GTCGACCCTC CACCTGCAAA TCCACTGTCC ATACCCTTGG ATTGGTTGAA GAGCCTTTGG TCATACTGAA CTTCATTGGA AGTCCGAGGA TTAGGAACAC CGAGAGCAAT AACTTCACTG	60 120
ATATCCCGAT TTTCATTTCT CTGAAGTTTC GACCTCTTAT CAGGAGCTGC CCTGGAAAGA	180
TTCCGGTCAT GCTGTCTCTC TTTTCGCCTG TCATGCCGGA TTTCATCCCT CTCACGTGCC	240
TCCCCATCCT CTTTTTCCAC ATGAGTTTTG ATCCCAGCTC TTCTCTCCCT GGCTTTCTGG	300
GCCATTTCTC TAAGTTTCTC TNCANGTNTN NCCTTTTCTT TCTGAGCCAT TTTTCTCTCT	360
ACTTGGGCGT CGACGGCCTC TGGGGCCCTC GAG	393
(2) INFORMATION FOR SEQ ID NO:4:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 564 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
GTCGACCAGG CATACACAGG AAGATACATT. CACAGAAAGA GCTTCCTGCA CAAAGTAAGC	. 60
CACCAGCGCA ACATGACAGT GARGACCCTG CATGGCCCAG CCATGGTCAA GTACTTGCTG	120

```
CTGTCGATAT TGGGGCTTGC CTTTCTGAGT GAGGCGGCAG CTCGGAAAAT CCCCAAAGTA
                                                                      180
GGACATACTT TTTTCCAAAA GCCTGAGAGT TGCCCGCCTG TGCCAGGAGG TAGTATGAAG
                                                                      240
CTTGACATTG GCATCATCAA TGAAAACCAG CGCGTTTCCA TGTCACGTAA CATCGAGAGC
                                                                      300
CGCTCCACCT CCCCCTGGAA TTACACTGTC ACTTGGGACC CCAACCGGTA CCCCTCGGAA
                                                                      360
GTTGTACAGG CCCAGTGTAG GAACTTGGGC TGCATCAATG CTCAAGGAAA GGAAGACATC
                                                                      420
TCCATGAATT CCGTTCCCAT CCAGCAAGAG ACCCTGGTCG TCCGGAGGAA GCACCAAGGC
                                                                      480
TGCTCTGTTT CTTTCCAGTT GGAGAAGGTG CTGGTGACTG TTGGCTGCAC CTGCGTCACG
                                                                      540
TCAACGGCCT CTTTGGCCCT CGAG
                                                                      564
```

- (2) INFORMATION FOR SEQ ID NO:5:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 356 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTCGACCTTC	AGTTGCCTCA	GACCCCAGTA	ATACAACGGT	CACCACCATG	AAACCTACAG	60
CGGCATCTAA	TACAACAACA	CCAGGGATGG	TCTCAACAAA	TATGACTTCT	ACCACCTTAA	120
AGTCTACACC	CAAAACAACA	AGTGTTTCAC	AGAACACATC	TCAGATATCA	ACATCCACAA	180
TGACCGTAAC	CCACAATAGT	TCAGTGACAT	CTGCTGCTTC	ATCAGTAACA	ATCACAACAA	240
CTATGCATTC	TGAAGCAAAG	AAAGGATCAA	AATTTGATAC	TGGGAGCTTT	GTTGGTGGTA	300
TTGTATTAAC	GCTGGGAGTT	TTATCTATTC	TGTCAACGGC	CTCTTTGGCC	CTCGAG	356

- (2) INFORMATION FOR SEQ ID NO:6:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 520 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTACTGCTGC	ACGGACTCTG	GAACCATGAA	CATATTTGAT	CGAAAGATCA	ACTTTGATGC	60
GCTTTTAAAA	TTTTCTCATA	TAACCCCGTC	AACGCAGCAG	CACCTGAAGA	AGGTCTATGC	120
AAGTTTTGCC	CTTTGTATGT	TTGCGGCGGC	TGCAGGGGCC	TATGTCCATA	TGGTCACTCA	180
TTTCATTCAG	GCTGGCCTGC	TGTCTGCCTT	GGGCTCCCTG	ATATTGATGA	TTTGGCTGAT	240
GGCAACACCT	CATAGCCATG	AAACTGAACA	GAAAAGACTG	GGACTTCTTG	CTGGATTTGC	300
ATTCCTTACA	GGAGTTGGCC	TGGGCCCTGC	CCTGGAGTTT	TGTATTGCTG	TCAACCCCAG	360
CATCCTTCCC	ACTGCTTTCA	TGGGCACGGC	AATGATCTTT	ACCTGCTTCA	CCCTCAGTGC	420
ACTCTATGCC	AGGCGCCGCG	GCTACCTCTT	TCTGGGAGGT	ATCTTGATGT	CAGCCCTGAG	480
CTTGTTGCTT	TTGTCGACGG	CCTCTTTGGC	CCTCGAGACA			520

- (2) INFORMATION FOR SEQ ID NO:7:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 526 base pairs
    - (3) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
GTCGACGTAC CACCAGCAAC CATCAATCCC GTCTCCTCCT GCCTCCTCTC CTGCAATCCA
                                                                      60
CCCCGCCACG ACTATCGCCA TGGCAGCCCT GATCGCAGAG AACTTCCGCT TCCTGTCACT
                                                                      120
TTTCTTCAAG AGCAAGGATG TGATGATTTT CAACGGCCTG GTGGCACTGG GCACGGTGGG
                                                                      180
CAGCCAGGAG CTGTCCTCTG TGGTGGCCTT CCACTGCCCC TGCTCGCCGG CCCGGAACTA
                                                                      240
CCTGTACGGG CTGGCGGCCA TCGGCGTGCC CGCCCTGGTG CTCTTCATCA TTGGCATCAT
CCTCAACAC CACACCTGGA ACCTCGTGGG CGAGTGCCAG CACCGGAGGA CCAAGAACTG
                                                                      360
CTCCGCCGCC CCCACCTTCC TCCTTCTAAG CTCCATCCTG GGACGTGCGG CTGTGGCCCC
                                                                      420
TGTCACCTGG TCTGTCATCT CCCTGCTGCG TGGTGAGGCT TATGTCTGTG CTCTCAGTGA
                                                                      480
GTTCGTGGAC CCTTCCTCAC TCACGGCCTC TTTGGCCCTC GAGACA
                                                                      526
```

- (2) INFORMATION FOR SEQ ID NO:8:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 438 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTCAMCTGTG	CAGCGGAGTT	TGACTTTATG	GAAAAAGAGA	CTCCACTGAG	ATACACAAAG	60
ACATTATTGC	TTCCAGTTGT	TCTTGTAGTG	TTTGTTGCTA	TTGTTAGAAA	GATTATTAGT	120
GATATGTGGG	GTGTCTTAGC	TAAACAACAG	ACACATGTAA	GAAAACACCA	GTTTGATCAT	180
GGAGAGCTGG	TTTACCATGC	ATTGCAATTG	TTAGCATATA	CAGCCCTTGG	TATTTTAATT	240
ATGAGACTAA	AACTCTTCTT	GACACCATAC	ATGTGTGTTA	TGGCATCACT	GATCTGCTCA	300
AGACAGCTAT	TTGGATGGCT	CTTTTGCAAA	GTACATCCTG	GTGCTATTGT	GTTTGTTATA	360
TTAGCAGCAA	TGTCAATACA	AGGTTCAGCA	AATCTGCAAA	CCCAGTGGAA	GTCGACGGCC	420
TCTTTGGCCC	TCGAGACA					438

- (2) INFORMATION FOR SEQ ID NO:9:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 395 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
GTCGACCCTA CACCATGTTC TTCTCCACGT TCTACCACGC CTGCGACCAG CCCGGGGAGG 60
CGGTGCTGTG CATCCTCAGC TACGACACGC TGCAGTACTG CGACTTCTTG GGCTCCGGGG 120
CGGCCATCTG GGTCACCATC CTGTGCATGG CACGGCTCAA GACAGCCCTG AAATACGTGC 180
TGTTTCTTCT GGGTACACTG GTCATCGCCA TGTCCTTGCA GCTGGACCGC AGGGGCATGT 240
GGAACATGCT GGGGCCCTGC CTCTTTGCCT TCGTGATCAT GGCCTCCATG TGGGCTTACC 300
GCTGCGGGGCA CCGGCGCAG TGCTACCCCA CCTCGTGGCA GCGCTGGGCC TTCTACCTCC 360
TGCCCGGCGT CTCTACGGCC TCTTTGGCCC TCGAG 395
```

- (2) INFORMATION FOR SEQ ID NO:10:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 321 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTCGACAGAM WNCAACCCTC	AGACGCCACA	TCCCCTKACA	AGCTGMCAGG	CAGGTTCTCT	60
TCCTCTCACA TACTGACCCA	CGGKTCCACC	CTCTCTCCCC	TGGAAAGGAC	ACCATGAGCA	120
CTGAAAGCAT GATCCGGRAC	GTGGAGCTGK	CCGAGGAGGN	GYTCCCCAAG	AAGACAGGGG	180
GGRCCCAGGG CTCCAGGCGG	GGGTTTGTTC	CTCAGWCTCT	TCTCCTTCCT	GATCGNGGGA	240
GGGGGCACCA CGCTCTTCTG	TCTGCTGGAC	TŢTGGAGTGA	TCGGNCCCCA	GAGGGAAGGA	300
GTTCCCCAGG GGAACCTCTC	T				321

- (2) INFORMATION FOR SEQ ID NO:11:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 532 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: CDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTCGACGGCC	GAGAWGGACA	TGAAGCAATA	TCAAGGCTCC	GGCGGCGTCG	CCATGGATGT	60
GGNACGGAGT	CGCTTCCCCT	ACTGCGTGGT	GTGGACGCCC	ATCCCGGTGN	TCACGTGGTT	120
TTTCCCCATC	ATCGGCCACA	TGGGCATCTG	CACATCCACA	GGAGTCATTC	GGGACTTCGC	180
GGGCCCCTAC	TTTGTCTCAG	AGGACAACAT	GGCCTTTGGA	AAGCCTGCCA	AGTACTGGAA	240
GTTGGACCCT	GCTCAGGTCT	ATGCTAGCGG	GCCCAACGCA	TGGGACACGG	CTGTGCACGA	300
CGCCTCTGAG	GAGWACAAGC	ACCGCATGCA	CAATCTCTGC	TGTGACAACT	GCCACTCGCA	360
CGTGGCATCG	GCCCTGAATC	TGATGCGCTA	CAACAACAGC	ACCAACTGGA	ATATGGTGAC	420
GCTCTGCTTC	TTCTGCCTGC	TCTACGGGAA	GTACGTCAGC	GTTGGGGCCT	TCGTGAAGAC	480
CTGGCTGCCC	TTCATCCTTC	TCCTGTCGAC	GGCCTCTTTG	GCCCTCGAGA	CA	532

- (2) INFORMATION FOR SEQ ID NO:12:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 580 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
GTGTACACCA AGATGATGAC CAAGAAGCCG GGCATGTTCT TCAACCCCGA GGAGTCGGAG
CTGGACCTGA CCTACGGNAA CAGATACAAN AACGTGAAGC TCCCTGACGN CTACGAGCGC
                                                                      120
CTCATCCTGG ACGTCTTCTT TGGGAGGCAG ATGNACTTCG TGCGCAGGGA CGANCTCCNT
                                                                      180
GAGGNCTGGC GTATTTTCA CCCCACTGNT GTACCANATT GAGCTNGAGA AGGCCAAGCC
                                                                      240
TCCAGGAACA CATGTGGGGT CATTACCAAA CAGGGTCCAT CCACATGATG GTGAACATCA
                                                                      300
ANCTTTGGGC GGACAANGAT TGCTGGGAAT GGGAATCCTG TTCACTGGGG AGCTCTGGGA
                                                                      360
GTTCTTGAGC TTTGCTGAAA GGTACCCTGC CATCATCTAT AACATCCTGC TCTTTGGGCT
                                                                      420
GACCAGTGCC CTGGGTCAGA GCWTCATCTT TATGACGATT GTGTATCTTG GTCCCCTGAC
                                                                      480
CTGCTCCATC ATCACTACAA CTCGAAAGTT CTTCACAAAW KTGCCCGCTG TGATCCTCTT
                                                                      540
CGCCAATCCC ATGTCGACGG CCTCTTTGGC CCTCGAGACA
```

. (2) INFORMATION FOR SEQ ID NO:13:

<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 434 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:	
GTCGACACTA CTTATGCGGC TACTTTGTCC AGGGCACAAA ATGCCGTGGC AGTATCTAAC TAAACCCCCA CAAAACTGCT TAATAACAGT TTKGRATGTG AGAAATTTAG ATAATTTAAA TATAAGGTGC AGGTTTTAAT TTCTGAGATT CTTCTTTTCT ATTTTTATTA AAAAGAAAAT AATTTTCAGA TTTAATTGAA TTGGAAAAAA CAATACTTCC CACCAGAATT ATATATCCTG AAAATTGTAT TTTTGTTATA TAAACAACTT TTAAGAAAGA TCATTATCCT TTTCTCTACC TAAATATGAG GAGTCTTAGC ATAATGACAA ATATTTATAA TTTTTCAATT AATGGTACTT GCTGGATCCA CACTAACATC TTTGCTAATA ATCTCATTGT TTCTTCGTCA ACGGCCTCTT TGGCCCTCGA GACA	60 120 180 240 300 360 420 434
(2) INFORMATION FOR SEQ ID NO:14:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 523 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:	
GTGGACGTTT TTTTTTTTTT TTTCTTTTTT TTAAGAAAAA CCCATTTTT TCCTTAAGGA CTTACTAGC AAAATTTCTT AAACTTCGAG GACTCTACTA GCCATGGCCG AGCATTCTT GTCAGAATAT CAACACCAGC CTCAAACTAG CAACTGTACA GGTGCTGGTG CTGTCCAGGA AGAGCTGAAC CCTGAGCGCC CCCCAGGCGC GGAGGAGGGG GTGCCCGAGG AGGACAGTAG GTGGCAATCG AGAGCGTTCC CCCAGTTGGG TGGCCGTCCG GGGCCGGAGG GGAAGGGAG CCTGGAATCC CAACCACCTC CCTTGCAGAC CCAGGCCTGT CCAGAATCTA GCTGCCTGAG AGAGGGCGAG AAGGGCCAGA ATGGGGACGA CTCGTCCGCT GGCGGCGACT TYCCGCCGCC GGCAGAAGTG GAACCGACGC CCGAGGCCGA GCTGCTCGCC CAGCCTTGTC ATGACTCCGA GGCCAGTAAG ATGGGGTCGA CGGCCTCTTT GGCCCTCGAG ACA  (2) INFORMATION FOR SEQ ID NO:15:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 142 base pairs (B) TYPE: nucleic acid	60 120 180 240 300 360 420 480 523
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:	
GTCGACCCTC ANTGTTCTGG AACTGGTCTT GGAAGGGATN GTTTATNCTG AGTACACCTG GGAAGTATTT GGGTACTGTC ANGAGCTGGA GTTGNCCTNG NATTACCNTC TTCTGCCCNA TCTGGTGGTA GGGGTAAACC NG  (2) INFORMATION FOR SEQ ID NO:16:	60 120 142
97	

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 534 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GTCCACCCGG	GCCGCCCCTC	GCCGCCCGGG	CTCTTCGCGG	GCTGCTCTTT	GTCTCCCCGA	60
CCTCGATCCC	TGCGTCTCCG	GCGGCGTGCG	GGCTCGTCTG	AGGCTTCCCG	CATCTCCCCG	120
CTGGAACTCC	TGCCTCCCGG	GGGTTAGAGG	AGGGTTCGTT	CGAGGGCTGG	AAGCGGGAAA	180
GCGGGGCGGA	AGGACTGGGC	TCATCGCCTC	CTGATTAACT	CGTTGTCTTT	ACTTAAAATG	240
ACTTTTCCCC	CACTTTGTCA	AACTTGAGAA	CTGTSTTGTG	TGTGTGTGTT	TCCTTGAGTC	300
TCTAGCTTCA	AAATTAAGAG	TAGGCGCTAC	CGCTGCGATT	GTGGGCAGTT	GTGTGGTTGG	360
CGGCTGCGTT	TGGAGCTCTG	AGTTGAAAAG	ATGTACGTGA	ATGTATGGTT	TAGATTTTGT	420
TCTTTTTTTT	GCGATTGTCT	GATTGGGAGT	ACTTTTCCTT	TGCGAAATGG	GCGAATTTGG	480
TTTTCTTTTT	GTTCATTGAG	AACTGGGTCG	ACGGCCTCTT	TGGCCCTCGA	GACA	534

- (2) INFORMATION FOR SEQ ID NO:17:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 558 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTCGMCGAAG GG	GAAGAAGAA (	GATGAACAAG	AACAATGCCA	AGGCTCTGAG	CACCTTGCGT	60
CAGAAGATCC GA	AAAATACAA (	CCGTGATTTC	GAGTCCCATA	TCACAAGCTA	CAAGCAGAAC	120
CCCGAGCAGT CT	rgcggatga A	AGATGCTGAG	AAAAGTGAGG	AGGATTCAGA	AGGCTCTTCA	180
GATGTGGATG AG	GGATGAGGA (	CGGAGTCAGT	GCTGCAACTT	TCTTGAAGAA	GAAATCAGAA	240
GCTCCTTCTG GG	GGAGAGTCG (	CAAGTTCCTC	MAAAAGATGG	ATGATGAAGA	TGAGGACTCA	300
GAAGATTCCG TA	AGATGATGA	AGACTGGGAC	WCAGGTTCCA	CATCTTCCGA	CTCCGACTCA	360
GAGGAGGAAG AA	AGGGAAACA	AACCGCGCTG	GCCTCAAGAT	TTCTTAAAAA	GGCACCCACC	420
ACAGATGAGG AC	CAAGAAGGC	AGCCGAGAAG	AAACGGGAGG	ACAAAGCTAA	GAAGAAGCAC	480
GACAGGAAAT CO	CAAGCGCCT (	GGATGAGGAG	GAGGAGGACA	ATGAAGGCGG	GGTCACGGCC	540
TCTTTGGCCC TC	CGAGACA					558

- (2) INFORMATION FOR SEQ ID NO:18:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 465 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GTTGACGGCC	AGCTTGCTGT	CTAACTTTTC	ACATCGGAGA	AGCTCCTTGG	CCTGGGAGGA	60
CTTCTCCGTG	CCTTCCCCCT	TCCCAGAGAT	GCCCCTGTCG	AGGGAGTGGC	AGAGACCATC	120
CTGGAGGGTG	CCAGGAGCGG	GGGCCCGTCT	GAAGTCCCCG	CCACCCTGGC	GGTGCTCCGC	180
AGGCACCGGG	CCATCCGACA	TCGCACCCTC	GCTGGCGCGC	ACGCTGGCCT	GCTTGTGAAG	240

ACCATCCTTC	AGCAGGCTGC	CCAGCGGTCC	CCCCTCCTCC	ATAGACGCTT	TOTTOTO A A A	200
						300
AGTACTTGAC	CTTTCCACAG	CCTTCGGATA	GACTTTCTTC	TCTCTCTCTT	CCAGCTTAAA	360
CAGAGCAAAG	TTTTCCAAAT	CACTCCCGGG	TCCATGGGAT	TTCTGGTGGG	ATTCCTGTTT	420
CTCTGGGAAG	CCGTCTGGTC	GACGGCCTCT	TTGGCCCTCG	AGACA		465
					•	
(2) INFORM	TION FOR CE	O TO NO.10				

- (2) INFORMATION FOR SEQ ID NO:19:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 694 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GNNNTCGTTG	TTCCAGAACT	TGATGAGGGG	ATCTCGGAAC	AACACNGAAA	CTTTTCCCTC	60
CCTCANTNAC	GCACCNCGAC	TCTCTATTGA	GCCAACGGNA	ANNCGGCCCT	TCCCTCCAAG	120
TAACTTTGNA	TTTGAAAATA	AAAAAAAAAG	NTTGCTGTCC	TTGCTATCCA	AGAATAAATA	180
GACCTNCAAN	TATTAATCTT	TTGTTTCCCT	CGTCATTGTT	CTCGTTCCCT	TTCTNCCTTG	240
TTTCTTTTTC	TGCACAATAT	ATCAAGCNAT	ACCAAGCATA	CAATCAAACT	CCAAGCTCGG	300
AATTCGGCCA	NAGAGACCGT	CGACGGAAGA	AATTGNCTGG	AAACTTGTTC	ATGGTGATAT	360
ATACCGTCCN	CCAAGAAAAG	GGATGCTGCT	ATCAGTCTTT	CTAGGATCCG	GGACACAGAT	420
ATTAATTATG	ACCTTTGTGA	CTCTATTTTT	CGCTTGCCTG	GGAGTTTTGT	CACCTGCCAN	480
CCGAGGAGCG	CTGATGACGT	GTGCTGTGGT	CCTGTGGGTG	CTGCTGGGCA	CCCCTGCAGG	540
CTATGTTGCT	GCCAGATTCT	ATAAGTCCTT	TGGAGGTGAG	AAGTGGAAAA	CAAATGTTTT	600
ATTAACATCA	TTTCTTTGTC	CTGGGATTGT	ATTTGCTGAC	TTCTTTATAA	TGAATCTGAT	660
CCTCTGGTCA	ACGGCCTCTT	TGGCCCTCGA	GACA			694

- (2) INFORMATION FOR SEQ ID NO:20:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 473 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```
AGACTCGTCT CAGACCAGTT GCAGCCTTCT CAACCCAAAC GCCGACCAAG GAAAAACTCA
                                                                       60
CTACCATGAG AATTGCAGTG ANTTGCTTTT GCCTCCTAGG CATCACCTGT GCCATACCAG
                                                                      120
NTAAACAGGC TGATTCTGGA AGTTCTGAGG AAAAGCAGCT TTACAACAAA TACCCAGATG
                                                                      180
CTGTGNCCAC ATGGCTAAAC CCTGACCCAT CTCAGAAACA GAATCTCCTA GCCCCACAGA
                                                                      240
CCCTTCCAAG TAAGTCCANC GAAAGCCATG ACCACATGGA TGATATGGAT GATGAAGATG
                                                                      300
ATGATGACCA TGTGGACAGC CAGGACTCCA TTGACTCGAG CGACTCTGAT GATGTAGATG
                                                                      360
ACACTGATGA TTCTCACCAG TCTGATGAGC CTCACCATTC TGATGAATCT GATGAACTGG
                                                                      420
TCACTGATTT TCCCACGGAC CTGCCGTCGA CGGCCTCTTT GGCCCTCGAG ACA
                                                                      473
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- (2) INFORMATION FOR SEO ID NO:21:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 204 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AGAAGCTGTG	ATCTTCAAGA	CCATTGTGTC	CAAGGAGATC	TGTCTGATCC	CAAGCAGAAG	60
TGGGTTCAGG	ATTCCATGGA	CCACCTGGAC	AAGCAACCCA	AAACTCCGAA	GACGTGAACA	120
CTCACTCCAC	AACCCAAGAA	TCTGCAGCTA	ACTTATTTTC	CCCTAGCTTT	CCCCAGACGT	180
CGACGCCTCT	TTGCCCTCGA	GACA				204

- (2) INFORMATION FOR SEQ ID NO:22:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 472 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GTCCACACAC	GCCGACCACG	GAAAACTCAC	TACCATGAGA	ATTGCAGTGA	TTTGCTTTTG	60
CCTCCTAGGC	ATCACCTGTG	CCATACCAGT	TAAACAGGCT	GATTCTGGAA	GTTCTGAGGA	120
AAAGCAGCTT	TACAACAAAT	ACCCAGATGC	TGTGGCCACA	TGGCTAAACC	CTGACCCATC	180
TCAGAAGCAG	AATCTCCTAG	CCCCACAGAA	TGCTGTGTCC	TCTGAAGAAA	CCAATGACTT	240
TAAACAAGAG	ACCCTTCCAA	GTAAGTCCAA	CGAAAGCCAT	GACCACATGG	ATGATATGGA	300
TGATGAAGAT	GATGACGACC	ATGTGGACAG	CCAGGACTCC	ATTGACTCGA	ACGACTCTGA	360
TGATGTAGAT	GACACTGATG	ATTCTCACCA	GTCTGATGAG	TCTCACCATT	CTGATGAATC	420
TGATGAACTG	GTCACTGATT	TTCCGTCGAC	GGCCTCTTTG	GCCCTCGAGA	CA	472

- (2) INFORMATION FOR SEQ ID NO:23:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 340 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTCGACTGAA	AATTAACCCT	CAGACGCCAC	ATCCCCTGAC	AAGATGCCAG	GCAGGTTCTC	60
TTCCTCTCAC	ATACTGACCC	ACGGGTCCAC	CCTCTCTCCC	CTGGAAAGGA	CACCATGAGC	120
ACTGAAAGCA	TGATCCGGGA	CGTGGAGCTG	GCCGAGGAGG	NNTTNNCCAA	GAAGACAGGG	180
GGGGCCCAGG	GGTCCAGGNG	GNGCTTGTTC	CTCAGACTCT	TCTCCTTCCT	GATCGTGGGA	240
GGNGNCACCA	CGCTCTTCTG	NCTGNTGNAC	TTTGGAGTGG	ATCCGGGCCC	CAGAGGGAAG	300
AGTTCCCCCA	GGGGACTCTT	CTCTAATCNA	GNCCTCTTGG			340

- (2) INFORMATION FOR SEQ ID NO:24:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 496 base pairs(B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
    - (D) TOPOLOGI: Timea.
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTCGACGCGC	GCCGGTAAAA	ATGGCGAAAT	GGGGGTAGGC	GGCGCTGGAC	CTGAAGAGAT	60
GGGGCGCGCA	GGTGGGGCGG	TTGTCAGAGC	CCCCTGACGT	GGGCGCCGG	CTTTTATCGG	120
CGATTTGATC	TGGCGACCTC	GGGCCGGCGC	CTAAGAGGTC	AGACTGCGGA	GCCTGCGGGT	180
CGCCAGCGGC	CCCGCCGAGT	GCCGGAGGCA	ATGGATGAAC	AGAGCGTGGA	GCGCTGKCTG	240
WCAGAGCAGA	GAGCTCAATG	TCCTCATTCC	CGTGCTCCAC	TCCAGCTACG	AGAACTAGTA	300
AATTGTCGTT	GGGCAGAAGA	AGTAACACAA	CAGCTTGATA	CTCTTCAACT	CTGCAGTCTC	360
ACCAAACATG	AAGAAAATGA	AAAGGACAAA	TGTGAAAATC	ACCATGAAAA	ACTTAGTGTA	420
TTTTGCTGGA	CTTGTAAGAA	GTGTATCTAC	CATCAGTGTG	CACTTTGGGT	CGACGGCCTC	480
TTTGGCCCTC	GAGACA					496

- (2) INFORMATION FOR SEQ ID NO:25:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 267 base pairs(B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGATCTGNAC AAGAAGGAGA CCTCTGTCAT CTGGAGGAGA NTGNCCAACC CTTTTCC	TTT 120
GAGNETCAGG GNGGGETGTE TAACATTGET ATANTGAACA ACAACNTGAA TACETTG	ATC 180
CAGCGTTCCA ACCACACTCA GNCCACCAAC GATCCCCCTG AGGTGACCGT GTTTCCC	AAG 240
GTCACGGCCT CTTTGGCCCT CGAGACA	267

- (2) INFORMATION FOR SEQ ID NO:26:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 451 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (11) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTCGACCTTG	AAGATGTTTT	CTAAAGAATC	AAAAATGCTA	CAAAGAAGTA	TATCATTTTC	60
AAATATGGCT	TTATCGTCTT	GTTTACTTTT	ACCAGGAGAT	GCCACTGTCA	TAACTTCTTC	120
ATGGGATAAT	AATGTCTATT	TTTATTCCAT	AGCATTTGGA	AGACGCCAGG	ACACGTTAAT	180
GGGACATGAT	GATGCTGTTA	GTAAGATCTG	TTGGCATGAC	AACAGGCTAT	ATTCTGCATC	240
GTGGGACTCT	ACAGTGAAGG	TGTGGTCTGG	TGTTCCTGCA	GAGATGCCAG	GCACCAAAAG	300
ACACCACTTT	GACTTGCTGG	CCGAGCTGGA	ACATGATGTC	AGTGTAGATA	CAATCAGTTT	360
AAATGCTGCA	AGCACACTGT	TAGTTTCCGG	CACCAAAGAA	GGCACAGTGA	ATATTTGGGA	420
CCTCACAACG	GCCTCTTTGG	CCCTCGAGAC	A			451

- (2) INFORMATION FOR SEQ ID NO:27:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 456 base pairs(B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GTTGACGCAA	GTTGCTGGGC	TGGTGGGGGC	CTGTCAAGTG	AGGCCTGGTG	GAGAAAGGTT	60
GAATTTGGAG	GGCCAGGAAC	AAGCTGGGAT	GCAGGGGAGG	CTTTCTAAAC	TCTACAGTGC	120
TTCTAGAGAT	GACGAGGAGG	TAGGGAGTAG	AAGAGAGCCG	GACAGATTAG	GGAGCTCCCA	180
GGGTGAGCTT	GTGGGCAGSC	CTSCAGAGGA	GAAGAGGCTC	TTCCCTAGGA	GCTCAGAGGG	240
ACTTGTTCTG	GAAGACTGAT	GGGAGATGTA	TGCAGCTGTT	TAGAGGCTGC	TTTGGAGAAC	300
AAATGAACAT	GGTTCTGGTT	GTGCAAGCAG	TTACTGTGGT	TCTTTTTGCT	CATATATCTT	360
CCAATAAAGA	CATTGAGCGA	GGAGAGTTGA	TACCGTCATG	TTTTTGGAGC	TTAAGCACAG	420
ACTGGCAGGT	CGACGGCCTC	TTTGGCCCTC	GAGACA			456

- (2) INFORMATION FOR SEQ ID NO:28:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 395 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GTCGACAGAA	TTCACAACAT	CCCAAGATTC	CACCTCNCAA	GATGTTTTCT	AAAGNAATCA	60
AAAATGCTAC	AAAGAAGTAT	ATCATTTTCA	AATATGGCTT	TATCGTCTTG	TTTACTTTTA	120
CCAGGAGATG	CCACTGTCAT	AACTTCTTCA	TGGGATAATA	ATGTCTATTT	TTATTCCATA	180
GCATTTGGAA	GACGCCAGGA	CACGTTAATG	GGACATGATG	ATGCTGTTAG	TAAGGATCTG	240
TTGGCATGAC	AACAGGCTAT	ATTCTGCATC	GTGGGACTCT	ACAGTGAAGG	TGCGGTCTGG	300
TGTTCCCTGC	AGAGATGCCA	GGCACCAAAA	GACACCACTT	TGGCTTGNTG	GCCGAGCTGG	360
ACATGATGTC	AGNGTNGGTA	CAATCAAGNT	TANNA			395

- (2) INFORMATION FOR SEQ ID NO:29:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 471 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTGGNCCGAG	ATAGAGGAGG	CTTCCCTCCA	AGAGGACCCC	GGNGTTCCCG	AGGGAACCCC	60
TCTNGAGGAG	GAAACGTCCA	GCACCGAGCT	GGAGACTGGC	AGTGTCCCAA	TCCGGGTTGT	120
GGAAACCAGA	ACTTCCCCTG	GAGAACAGAG	TGCAACCAGT	GTAAGGCCCC	AAAGMCTGAA	180
GGCTTCCTCC	CGCCACCCTT	TCCGCCCCCG	GGTGGTGATC	GTGRCAGAGR	TGGCCCTGST	240
GGCATACGGG	GAGGAAGAGR	TGGCCTCATG	GATCGTGGTG	GTCCCGGTGG	AATGTTCAGA	300
GRTGGYCGTK	GTGGAGACAG	AGRTGKCTTC	CGTKGTGGCC	GGGGCATGGA	CCGAGGTGKC	. 360
TTTGGTGGAG	GAAGACNAGG	TGTCCCTGGG	GGCCCCCCTG	NTCCTTTGAT	GGAACAGATG	420
GGAGGAAGAA	GAGGAGGACG	TGGGTCGACG	NCCTCTTTGT	CCCTCGAGAC	A	471

- (2) INFORMATION FOR SEQ ID NO:30:
  - (i) SEQUENCE CHARACTERISTICS:
    - (λ) LENGTH: 406 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GTCGACCGTC	TACGCCTACA	CCATGTTCTT	CTCCACGTTC	TACCACGCCT	GCGACCAGCC	60
CGGGGAGGCG	GTGCTGTGCA	TCCTCAGCTA	CGACACGCTG	CAGTACTGCG	ACTTCTTGGG	120
CTCCGGGGCG	GCCATCTGGG	TCACCATCCT	GTGCATGGCA	CGGCTCAAGA	CAGTCCTGAA	180
ATACGTGCTG	TTTCTTCTGG	GTACACTGGT	CATCGCCATG	TCCTTGCAGC	TGGACCGCAG	240
GGGCATGTGG	AACATGCTGG	GGCCCTGCCT	CTTTGCCTTC	GTGATCATGG	CCTCCATGTG	300
GGCTTACCGC	TGCGGGCACC	GGCGCCAGTG	CTACCCCACC	TCGTGGCAGC	GCTGGGCCTT	360
CTACCTCCTG	CCCGGCGTCT	CTACGGCCTC	TTTGGCCCTC	GAGACA		406

- (2) INFORMATION FOR SEQ ID NO:31:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 448 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTCGCCCAGC AAGTGAGCA	ATCCTCCGAG	GCACCAGGGN	ACTCCAGCCC	ATGCCATGGC	60
GGATTCTGAG CGCCTCTCG	G CTCCTGGCTG	CTGGGCCGCC	TGCACCAACT	TCTCGCGCAC	120
TCGAAAGGGA ATCCTCCTG	TTGNTGAGAT	TATATTATGC	CTGGTGATCC	TGATCTGCTT	180
CAGTGNCTCC ACACCAGGC	T ACTCCTCCCT	GTCGGTGAYT	GAGATGATCC	YTSCTCSCTA	240
TCTTTCCTYT GTTGTCTAC	A TGTGTGACCT	GCACCACCAA	GATACCATTC	ATCAACTGSS	300
CCTGGAGTGA TTTCTTCCG	A ACCCTCATAG	GGGSAATCCT	CTACCTGATC	AMCTCCATTG	360
TKGTCCTKGT TGAGAGAGG	A AACCACCCCN	TNAATCGTTC	GTAGGGGTAC	TGGGCCTAAT	420
CGCTACGGCC TCTTTGGCC	C TCGAGACA				448

- (2) INFORMATION FOR SEQ ID NO:32:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 397 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TTNCAATCNC CGA	ATCCCCAT CACGAATGGG	GGGCACCGGG	TTACCCCCCC	CCTCCCGCCG	60
TAGGGTAGGC ACA	ACNOTGAG CCAGTCAGTG	TATCGCGCGT	GCATCCCCGG	ACATCTAAGG	120
GCATCACAGA CCT	GTTNTTG NTCAATCTCG	GGTGGNTGNN	CGCCACTTGT	CNCTCTAAGA	180
ANATGGGGGA CGC	CCGNCCGC TCGGGGGTNC	CGTAACTAGN	TAGNATNCCA	GAGTCTCGTT	240
CGTTATCGGA AGT	TAACCAGA CANATCGCTO	CNCCAACTAA	GANNGGCCAT	NCACCACCAC	300
CCACGGAATC GAG	SANAGAGC TATCAATCT	TTGTAGGACA	TAACCCGGCT	TCTTGGTCAT	360
CATCHTGGTG TAC	CNCGNCCT CTTTGNCCCT	CGAGACA			397

- (2) INFORMATION FOR SEQ ID NO:33:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 365 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TCCTGCCTGC	TGGGCCGCCT	TNCACCCAAC	TTCTCGCGCA	CTCGAAAGGG	AATCCTCCTG	60
TTTGCTGAGA	TAAATANTAT	NCCTGGTGAT	CCTGATCTGC	TTCAGTGCCT	CCACACCAGA	120
CNACTCCTCC	CTGTCGGTGA	TTGAGATGAT	CCTTGCTGCT	ATTTTCTTTG	TTGTCTACAT	180
GTGTGACCTG	CACACCAAGA	TACCATTCAT	CAACTGGCCC	TGGAGTGATT	TCTTCCGAAC	240
CCTCATAGCG	GCAATCCTCT	ACCTGATCAC	CNCCGTTGTT	GTCCTTGTTG	AGAGAGGAAA	300
CCACTCCTAC	AATCGTCGCA	GGGGTACTGG	GCCTAATCGC	TACGGCCTCT	TTGGCCCTCG	360
AGACA						365

- (2) INFORMATION FOR SEQ ID NO:34:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 455 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GTCGACGACA	CGCTGTCTTC	ACTACCTGAT	TGCCCAGAAG	ATCCACACTG	TCTACACTAC	60
CTGCCTGGCC	AGTAGATCCA	CGGTATCTAC	ACTACCTCCC	TGGCCAGCAG	ATTCACCCAG	120
TCTACACTAA	CCGCTTGTCC	AGCAGGTCCA	CCCTGTCTAC	ACTACGTGCC	TGCCAGCAGA	180
TCCAAGCTGT	CTACACTCCC	TGCCTGGCCA	GTAGATCCAT	GCTATCTCCA	CTACCTGCCT	240
ATCCAACTGA	TCCACCCTCT	CTTTACTACC	TTCCTGTCCG	GCAGATTGAC	CCTCTCTACT	300
CTACCTGCCT	GGCCAGCAGA	TCCACGCTAT	CTACACTACC	TGACTTACCA	GATCCACCCT	360
GTCTACACTA	CATGCTTGTC	CAGCAGGTCC	ACCCTGTCTA	CACTACCTGC	CTCTCCAGAA	420
GATCCACGTC	AACGGCCTCT	TTGGCCCTCG	AGACA			455

- (2) INFORMATION FOR SEQ ID NO:35:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 506 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGGANTTNGG	CCCAAAGAGC	CCGTTTGAGT	NAACCNAAGA	AGTCAAGATT	GGCCCNAAGT	60
TCCAGANATG	TTTTGAAGAC	CTGGAGAACT	GTTACAGTGN	AAATGAAGAA	GACAGTTCCT	120
CCATTGATCA	TCTGTCTCTG	AATCAGAAAT	CCTTCTATCA	TGTAAGCTAT	GGCCCACTCC	180
ATGAAGGCTG	CATGGATCAA	TCTGTGTCTC	TGAGNATCTC	TGAAACCTCT	AAAACATCCA	240
AGCTTACCTT						300
GACGGTTGAG	TTTAANCCAA	TCCATCACTG	ATGATGACCT	GGAGGCCATC	GCCAATGACT	360
	AATCATCAAG					420
ACAACTTTAT	GAGGATCATC	AAATACGAAT	TCATCCTGAA	TGACGCCCTC	AATCAAAGGT	480
CGACGGCCTC	TTTGGCCCTC	GAGACA				506

- (2) INFORMATION FOR SEQ ID NO:36:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 475 base pairs

(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CGGTAACGCN	GTTNTCCTNA	GGCGAGCTCA	GGGAGNACAA	GAAACCCTCC	CGTGGAGCAA	60
GAANGCCACA	AGCTCNCTTG	ATCTTGATTA	TCAGGACGAA	AACAGACCGT	GAAAGCGGGG	120
CCTCACGATC	CTTCTGACCT	NNTGGGTNTT	AAGCAGGAGG	TGTCAGAAAA	GTTNCCACAG	180
GGATAACTGN	CTTGTGNCGN	CCAAGCGNTC	ATAGCGACGT	CGCTTTTTGA	TCCTTCGATG	240
TCGGCTCTTC	CTATCATTGT	GAAGCAGAAT	TCACCAAGCG	TTGGATTGTT	CACCCACTAA	300
TAGGGAACGT	GAGCTGGGTT	TAGACCGTCG	TGAGACAGGT	TAGTTTTACC	CTACTGATGA	360
TGTGTTGTTG	CCATGGTAAT	CCTGCTCAGT	ACGAGAGGAA	CCGCAGGTTC	AGACATTTGG	420
TGTATGTGCT	TGGCTGAGGA	GCCAATGGTC	GACGGCCTCT	TTGGCCCTCG	AGACA	475

- (2) INFORMATION FOR SEQ ID NO:37:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 460 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GTTGACCCGA	TGGAGGAGGA	GGAGGTTGAG	ACGTTCGCCT	TTCAGGCAGA	AATTGCCCAG	60
TTGATGTCAT	TGATNCATCA	ATACTTTCTA	CTCGANCAAA	GAGATCTTTC	TGAGAGAGCT	120
CATTTCAAAT	TCATCAGATG	CATTGGACNC	AATCCGGTAT	GAAAGCTTGA	CAGATCCCAG	180
TAAATTAGAC	TCTGGGAAAG	AGCTGCATAT	TAACCTTATA	CCGAACAAAN	AAGANCGAAC	240
TCTCACTATT	GTGGATACTG	GAATTGGAAT	GACCAAGGCT	GACTTGATCA	ATAACCTTGG	300
TACTATCGCC	AAGTCTGGAC	CAAAGCGTTC	ATGGAAGCTT	TGCAGGCTGG	TGCAGATATC	360
TCTATGATTG	GCCAGTTCGG	TGTTGGTTTT	TATTCTGCTT	ATTTGGGTGC	TGAGAAAGTA	420
ACTGTGATCA	CCGTCGACGG	CCTCTTTGGC	CNGCGAGACA			460

- (2) INFORMATION FOR SEQ ID NO:38:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 435 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TCAAGCAATA	CCCAAGCAAA	CAATCNACTC	CAANCTCGGA	ANTCGNCCNA	AGAGACCGTC	60
GACCCCGTGT	TCACNATGGT	AGNNACGCCG	NCTACCATCG	ANAGTTGATA	GGGCAGACGT	120
TCGNGTGGGT	CGTCTCCCCC	CCGGGGGGCG	TGCGATCGCC	CCGAGGTTAT	CTAGAGTCAC	180
CACACCCGCC	GGCGCCCNCC	CCCCGNCCGN	NAAAAAAAGA	GGGGCTGTCN	GGGNTGGTTT	240
TGNTNTGATA	AATANACGCA	TCCCCCCCC	GNNGGGGGNN	AGCGCCCGTC	GGCATGTATT	300
ANCTCTAGAA	TTACCACAGT	TATCCAAGTA	GGAGAGGAGC	GAGCGNCCAN	AGGANCCATA	360
NCTGATTTAA	TGAGCCATTC	NCAGTTTCNC	TGTTCCGNCC	GTGCGTACGN	AACGACCTCT	420
TTGTNCNTAA	AGNCG					435

- (2) INFORMATION FOR SEQ ID NO:39:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 490 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GTCGACCACA	CTGCTGCTCA	CGCTCAGCAA	CCTCATGTTC	CTGGCCCCCA	TCGCCGTCTC	60
AGTGCGGCGA	TTCTTCCTGG	TGGAGGCCTC	CGTCTACGCC	TACACCATGT	TCTTCTCCAC	120
GTTCTACCAC	GCCTGCGACC	AGCCCGGGGA	GGCGGTGCTG	TGCATCCTCA	GCTACGACAC	180
GCTGCAGTAC	TGCGACTTCT	TGGGCTCCGG	GGCGGCCATC	TGGGTCACCA	TCCTGTGCAT	240
GGCACGGCTC	AAGACAGTCC	TGAAATACGT	GCTGTTTCTT	CTGGGTACAC	TGGTCATCGC	300
CATGTCCTTG	CAGCTGGACL	GCAGGGGCAT	GTGGAACTTG	CTGGGGCCCT	GCCTCTTTGC	360
CTTCGTGATG	ATGGCCTCCA	TGTGGGCTTA	CCGCTGCGGG	CACCGGCGCC	AGTGCTACCC	420
CACCTCGTGG	CAGCGCTGGG	CCTTCTACCT	CCTGCCCGGC	GTCTCTACGG	CCTCTTTGGC	480
CCTCGAGACA		•				490

- (2) INFORMATION FOR SEQ ID NO:40:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 516 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CGTCTCAGGC CAGTTNCANC	CTTCTCANNC	AGAACGGCGN	CCCAAGGAAA	ANCTCACTAC	60
CATGAAGAAT TGCAGTGATT	TGCNTTTGCC	TCCTAGGCAT	CACCTGTGCC	ATACCAGNTA	120
AANCAGGCTG ATTCTGGAAG	TTNCTGAGGG	AAAAAGCAGC	TTTACAACAA	ATACCCAGAT	180
GCTGTGGCCA CATGGCTAAA	CCCTGANCCA	TCTCAGAAGC	AGAATCTCCT	AGCCCCACAG	240
AATGCTGTGT CCTCTGAAGA	AACCAATGAC	TTTAAACAAG	AGACCCAAAC	AAGTNAGTCC	300
NACGAAAGCC ATGACCACAT	GGATGATATG	GATGATGAAG	ATGATGATGA	CCATGTGGAC	360
AGCCAGGACT CCATTGACTC	GNNCGACTCT	GATGATGTAG	ATGACACTGA	TGATTCTCAC	420
CAGTCTGACG AGTCTCACCA	TTCTGATGAA	TCTGATGAAC	TGGTCACTGA	TTTTCCCACG	480
GACCTGCCGT CGACGGCCTC	TTTGACCCTC	GAGACA			516

- (2) INFORMATION FOR SEQ ID NO:41:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 521 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GCCAAGACTC	GTCTCAGNCC	AGTTGCAGCC	TTCTCANCCA	AACNCCGACC	CAAGGANAAC	60
TCCCCTACCA	TGAGAATTGC	AGTGATTTGC	TTTTGCCTCC	TAGGCATCAC	CTGTGCCATA	120
CCAGTTAAAC	AGGCTGATTC	CTGGAAGTTC	CTGAGGAAAA	GCAGCTTTAC	AACAAATACC	180

CAGATGCTGT	GTCCACATGG	CTAAACCCTG	ACCCATCTCA	GAAGCAGAAT	CTCCTAGCCC	240
CACAGAATGC	TGTGTCCTCT	GAAGAAACCA	<b>NTGACTTTAA</b>	ACAAGAGANN	CANCCAAGTA	300
AGTCCANCGA	AAGCCATGAC	CACATGGATG	ATATGGATGA	TGAAGATGAT	GATGACCATG	360
TGGACAGCCA	GGACTCCATT	GACTCGANCG	ACTCTGATGA	TGTAGATGAC	ACTGATGATT	420
CTCACCAGTC	TGACGAGTCT	CACCATTCTG	ATGAATCTGA	TGAACTGGTC	ACTGÄTTTTC	480
CCACGGACCT	GCCGTCGACG	GCCTCAATGN	CCCTCGAGAC	G		521

- (2) INFORMATION FOR SEQ ID NO:42:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 516 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GCAAGCAANC	AATCCAACCC	AAGNTNGGGA	NTCGNCCNAA	GAGNCCGTTG	ANCAGAAGCC	60
ANTNATGGAT	GANCAGCGCG	ACCTTATCTC	CAACAATGAG	CAACTGNCCA	TNCTGGGNCC	120
GGNCGCCCTG	GGGCNCCGGA	GAGCAAGTGC	ANCCGCGGAG	CCCTGTACAC	AGGCTTTTCC	180
ATCCTGGTGA	CTCTGCTCCT	CGCTGGCCAG	GCCACCACCG	CCTACTTCCT	GTACCAGCAG	240
CAGGNCCGGC	TGGACAAACT	GACAGTCACC	TCCCAGAACC	TGCAGCTGGA	GAACCTGCGC	300
ATGAAGCTTC	CCAAGCCTCC	CAAGCCTGTG	AGCAAGATGC	GCATGNCCAC	CCCGCTGCTG	360
ATGCAGGCGC	TGCCCATGGG	AGCCCTGCCC	CAGGGGCCCA	TGCAGAATGC	CACCAAGTAT	420
GGCAACATGA	CAGAGGACCA	TGTGATGCAC	CTGCTCCAGA	ATGCTGACCC	CCTGAAGGTG	480
TACCCGCCGT	CGACGGCCTC	TTTGGCCCTC	GAGACA			516

- (2) INFORMATION FOR SEQ ID NO:43:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 494 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```
TGCTATCCNA GNATAAAATA AGACCCTGCA ANTATTAATC TTNTTTGTTT CCTCGTCATT
                                                                      60
GTTCTCGTTC CCTNTCTTCG TTGTTTCTNN TTCTGCACAA TATNTTCAAG CTATACCGAG
                                                                      120
CATACAATCA AACTCCAAGC TCGGAATTCG NCCAAAGAGG CCGTCGAGCC GAATTCTCCA
                                                                      180
CNAGAATAGC ATTTCTGCTC ATCTGCATGG TCGCAGTCAC GAGCCAGATG NCCTGNTTTN
                                                                      240
CCACAGTTGT AGCAGCATTG CTCTCGCTCT CTCTTGGGCT CCTTGCAGTC CTTGGCAATG
                                                                      300
TGGCCGCCTC TACCGCAGTT ATAGCAGGCA TCCTCCTGAA GATCACAATC CTTGGCAAGA
                                                                      360
TGACCAGACT CACCACAGCG ATAACAAATA TCTGGAAGAG ACGAGGAAAC AAACTGGAAA
                                                                      420
CCTCTATCCG AGGTAAAACC ACCTCTGCCA CGGCTTCTCA TTCCACGACC ACGGCCTCTT
                                                                      480
TGGCCCTCGA GACA
                                                                      494
```

- (2) INFORMATION FOR SEQ ID NO:44:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 654 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```
CCTCCANATN ANCTITNTTC CTCTCATTGT NTCGTCCCTC CTCCTTGTTC TTTNCTGCCC
AAAATCCANC AAANCCAACA ACCATCCNCN CCACCTGGAA GTNGCCCAAA GAGGCCGNAC
                                                                      120
CAAGAAGTGT CGATTCCTTT GTNTGNAGGA GCGACCAGGA ACATCTACGG TTGAGAAGAA
                                                                      180
AGAAAGANTG CCTTCGTCGA TGTCTTCCTG TGTGAANTTT CCAGACATAG CCCAGTCGAC
                                                                      240
CAGCCTTCCC CACNAGACTG GAGCGTCTCT ATTGTATNTG GGTCCCTGTA AGAGTAGAAG
                                                                      300
GGTGAAAATC CCANTGTGTC TGAGTNTTGC GCCNCCACCA TAAACACCGC CTTTTTCTCG
AATTTCTGTA TNCAAGAAAN TGTCAGTCAT CACACGTGCA AGGATNTTAA GACTGNCATG
                                                                      420
ATCTGGGNCC GTGTAGGGGN CAGNTCGGAT NCATTCACCC ACGTAATTCA CCGGGANGGG
CATCAGGAAG TGAGTCTTCA TCTCCCAGGG CGTGNAGGTG GGTNCCATGA CCAGCTTCCT
                                                                      540
AATGACCTGG GAGCCATGGG GAACGTGGGC ATCTCCACCA GAGCTACTGG GCACAGGTTT
                                                                      600
CTCGACCGTG TGTGGNCGCA CAGACCGTCG ACGGCCTCTT TGNCCCTCGA GACA
                                                                      654
```

- (2) INFORMATION FOR SEQ ID NO:45:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 500 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GTCGACCTGA	GAATCTGGAA	AAATTGGAGA	AGTTGGGTAT	GAGCTCAGAC	CTGGTGAGCA	60
GGCTGCCTAC	CATTTATAGA	AATGCACATG	ACATCAAGAA	TAAGAGCTCT	GCCCCCAGCA	120
GAGTGCCTCC	TCTTTTTGTC	CCACAGGGGA	CTTCTGAAAG	AAAAGACAGT	TCAGGTTCTG	180
TGTCCCCAMA	CACTCTTAGC	CAGGAGGAGG	GTGATCAGAT	CTGTTTGTKC	CATATCCGGA	240
AAAGTTGTAG	CTTTCAAGAT	AAGTGCCATA	GAGTTCATTT	CCATTTGCCG	YATCGATGGC	300
AATTCTTGGA	TAGAGGCAAA	TGGGAGGATT	TGGACNACAT	GGAACNTATT	GTAGAGNCAT	360
ATTGCAATCC	CCCCATAGAA	AGGATCCTGT	GCTCTGAGTC	AGCCAGTACC	TTTCACTCTC	420
ATTGTCTGAA	CTNTAACGCC	ATGACTTACG	GTGCTACCCA	GGCTCGCCGC	CTCTCCACGG	480
CCTCTTTGGC	CCTCGAGACA					500

- (2) INFORMATION FOR SEQ ID NO:46:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 466 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

```
GTCGACACAA ATGTTTCCTT GGATAATCCA GCTTTACATG GTGAGAACCA TGCTAGAGTC
CCTCATTGCA GACAAAAGTG GTTCCAAGAA AACCTTGAGA AGTAGCCTTG AGGGGCCCAC
CATATTGGAC ATAGAAAAAT TTCATCGAGA GTCATTCTTC TACACTCACT TGATAAATTT
L80
CAGTGAAACG CTGCAGCAGT GCTGTGACCT TTCGCAGCTG TGGTTCCGAG AGTTCTTCCT
GGAGCTGACC ATGGGCAGGA GGATCCAGTT CCCCATTGAG ATGTCGATGC CCTGGATCCT
GACGGACCAC ATCCTGGAGA CCAAGGAGGC ATCGATGATG GAGTACGTGC TCTACTCCCT
GGACCTGTAC AATGACAGCG CCCACTACGC GCTCACCAGG TTCAACAAGC AGTTCCTCTA
420
CGACGAAATT GAGGCCGAGG TCACGGCCTC TTTGGCCCTC GAGACA
466
```

(2) INFORMATION FOR SEQ ID NO:47:

```
(i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 384 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:
GTCGACGGAA GTTGATTTTT AATGATAAAG TACAATGAAG GGAGGGCAGA GGGGCTAAGC
                                                                       60
CTAGCTGTCT GGGGTGCTGT GGTGGTGGTA GACTGGCTAC ACAAACTGTT GCTGCTGCTG
                                                                      120
CTGCTTCTTG GTGGCCGCCT TGCTGGCGAG GTCCTTGGCC TTCTCTGTAG CTGCCAGTGC
                                                                      180
CGTCTCCTTT GCCTTCTCT TGGCTTCCTT GGCTGTCTCA ACAAGTGTTT TGGAAGGGGC
                                                                      240
CTCGCCTTGC AGCTTAGCCA AGATATATTC AAAACCCTTC ATAGTCTTGG TCACGTTGCT
                                                                      300
TTTGAACCGG GCAAGACCAA ATTCCTGGAC AGCTCTGGCT ACACAAACTG TTGCTGGTCA
                                                                      360
ACGGCCTCTT TGGCCCTCGA GACA
                                                                      384
(2) INFORMATION FOR SEQ ID NO:48:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 546 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:
GTGACGGGAC AAAAATCTAG GGAGGCACCA ATCCTGAAAG AGTTTAAGGA AGAAGGGGAA
GAGATACCTA GAGTAAAACC AGAGGAGATG ATGGATGAGA GACCCAAAAC AAGATCCCAG
                                                                      120
GAACAGGAGG TGTTAGAGAG AGGAGGGAGA TTTACAAGAT CCCAGGAAGA GGCTAGAAAA
AGTCATCTGG CCAGACAGCA GCAGGAGAAG GAAATGAAAA CAACATCTCC CCTTGAGGAG
                                                                      240
GAAGAAAGAG AAATAAAATC TTCACAAGGC TTAAAGGAAA AATCGAAGTC TCCTTCCCCT
CCTCGACTGA CTGAAGATCG AAAGAAGGCC CCACTTGTAG CGCTGCCAGA GCAAACTGCC
                                                                      360
AGCGAGGAGG AGACTCCTCC ACCTTTACTA ACAAAGGAAG CATCTTCTCC ACCACCTCAT
                                                                      420
CCACAGCTCC ATAGCGAAGA AGAAATAGAG CCCATGGAAG GCCCAGCCCC CCCTGTCCTC
                                                                      480
ATTCAGTTAT CTCCTCCTAA TACAGATGCT GACACCAGGT CGACGGCCTC TTTGGCCCTC
                                                                      540
GAGACA
                                                                      546
(2) INFORMATION FOR SEQ ID NO:49:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 520 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:
GTCGACGTCG GTGGTGCGAG CGGCGGCGGC GGCGGTTCCA GCATGAAGAG GAGAGCTGGC
                                                                        60
CTGGGGGGCA GCATGAGGTC AGTGGTGGGC TTCTTGTCCC AGCGGGGCTC GCATGGGGAC
                                                                       120
CCCCTGCTCA CTCAGGACTT TCAGAGGAGA CRCCTGCGGG GCTGCAGAAA CCTCTACAAG
                                                                       180
AAGGACCTCC TCGGCCACTT CGGCTGTGTC AATGCCATTG AATTCTCCAA CAATGGAGGC
CAGTGGCTGG TCTCAGGAGG AGATGACCGC CGGGTTCTGC TATGGCACAT GGAACAAGCC
                                                                       300
ATCCACTCCA GGGTCAAGCC CATACAGCTG AAAGGAGAGC ACCATTCCAA CATTTTTTGC
```

CTGGCTTTCA ACAGTGGGTA CACTAAAGTG TTCTCTGGAG GCAATGATGA GCAAGTTATC	420
CTCCATGATG TTGNAAGCAG TGAGACATTG GACGTGTTTG CTCATGAAGA TGCAGTATAT	480
GACTTGTCTG TGGTCNGCGC CCTCTTTGGC CCTCGAGACA	520
(2) INFORMATION FOR SEQ ID NO:50:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 475 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GTCGACTCCA	GACACACCCC	CCAGTCGAGC	CCTGCAGCCA	AACAGAGCCT	TCACAACCAG	60
CCACACAGAG	CCTGCCTCAG	CTGCTCGCAC	AGATTACTTC	AGGGCTGGAA	AAGTCACACA	120
GACACACAAA	ATGTCACAAT	CCTGTCCCTC	ACTCAACACA	AACCCCAAAG	CACAGAGAGC	180
CTGCCTCAGT	ACACTCAAAC	AACCTCAAAG	CTGCATCATC	ACACAATCAC	ACACAAGCAC	240
AGCCCTGACA	ACCCACACAC	CCCAAGGCAC	GCACCCACAG	CCAGCCTCAG	GGCCCACAGG	300
GGCACTGTCA	ACACAGGGGT	GTGCCCAGAG	GCCTACACAG	AAGCAGCGTC	AGTACCCTCA	360
GGATCTGAGG	TCCCAACACG	TGCTCGCTCA	CACACACGGC	CTGTTAGAAT	TCACCTGTGT	420
ATCTCACGCA	TATGCACACG	CACAGCCCTC	AACGGCCTCT	TTGGCCCTCG	AGACA	475

- (2) INFORMATION FOR SEQ ID NO:51:
  - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 456 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CCTGCCACAA	TAATNTCCNA	AGCCTAAAAC	CCGAGCAATA	CAANCNAACC	CAAGCTCGGA	60
AATCGGGCCA	AAGAGACCGT	TCTTAGNTGG	TGGAGCGATT	TGTCTGGTTN	ATTCCGATAA	120
ACGAACGAGA	CTCTGGCATG	CTAACTAGTT	ACGCGACCCC	CGAGCGGTCG	GCGTCCCCCA	180
ACTTCTTAGA	GGGACAAGTG.	NCGTTCANCC	CACCCGAGAT	TGAGCAATAA	CAGGTCTGTG	240
ATGCCCTTAG	ATGTCCGGGG	CTGCACGCGC	GCTACACTGA	CTGGCTCAGC	GTGTGCCTAC	300
CCTACGCCGG	CAGGCGCGGG	TAACCCGTTG	AACCCCATTC	GTGATGGGGA	TCGGGGATTG	360
CAATTATTCC	CCATGAACGA	GGAATTCCCA	GTAAGTGCGG	GTCATAAGCT	TGCGTTGATT	420
AAGTCCCTGT	CGACGGCCTC	TTTGGCCCTC	GAGACA			456

- (2) INFORMATION FOR SEQ ID NO:52:
  - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 501 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

```
GGCTGSGGGC TGWCGACTAT GAACAGRTCG AGAAMGTGKN CGATTACTAC CCGGAGTACA
                                                                      120
AGCTRCTCTY CGAGGGTGCA GGTAGGCAAC CCTGGAGACA TGACKCTGGA GGGMCGATTA
                                                                      180
CTTTGAGYAC GAGGTAAARC TGAACAAGTT GTSCTTCCTG ANACAGTWCC ACCTTGGTGT
                                                                      240
CTTCTATRCC TTCGTGAAGC TCAAGGAGCA GGAGTGTCKC AACATCGTGT GGATCGCTGA
                                                                      300
ATGTATCTRC CAACGCMMSS GCRMMYCSMA MSWCAWCCWY ATTCTSTRTC CTKSYAASGT
                                                                      360
CWCAMTGAAN CWAGCCCTCT CAATTGCACT GCACTGTGTG TGTGTGTGTG TGTGTTGTGC
                                                                      420
GTGTGTGTTG CGTGTGTGT TATGTGGTCT GTGACAAGCC TGTGGCTCAC CTGGTCGACG
                                                                      480
GCCTCTTTGG CCCTCGAGAC A
                                                                      501
```

#### (2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 579 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CCNCCGTTTG	TTGTNNTGCA	CCAAANANCC	NCNAATTGNC	CANANAAAAT	TGATGGGAAG	60
ACCACTTAAA	GGGGGGGNAN	TTAGGCGGGN	CAAAGACAAG	GCACCCNACA	AGATGTCGTT	120
TGTTCCAGAG	CTGATTGAGG	GGTATCTCGG	AAGNAACACN	GAAACTTTTT	TCCTTCCTTC	180
AATTCAACGC	ACACTACTCT	CTAATGAGCN	NCGGAATACG	GCCTTCCTTC	CAGTTACTTG	240
AATNTGAAAT	AAAAAAAAGT	TTGCTGTCTT	GCTATCCAAG	TATAAATAGA	CCTGCAATTA	300
TTAATCTTTT	GTTTCCTCGT	CATTGTTCTC	GTTCCCTTTC	TTCCTTGTTT	CTTTTTCTGC	360
ACAATATTTC	AAGCTATACC	AAGCATACAA	TCAACTCCAA	GCTCGGAATT	CGGCCAAAGA	420
GGCCGTCGAC	GAACCACCGG	CTGAAAATTG	GCTTCTTCAA	CCAGCAGTAT	GCAGAGCAGC	480
TGCGCATGGA	GGAGACGCCC	ACTGAGTACC	TGCAGCGGGG	CTTCAACCTG	CCCTACCAGG	540
ATGCCCGCAA	GTGCCTGGGC	CGCTTTGGCC	CTCGAGACA			579

- (2) INFORMATION FOR SEQ ID NO:54:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 549 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CCTGCNCCAA	NANTTCCNAA	CCNAATAACC	CAANAANACC	AATCCNNNCT	CCANCTGGGG	€	0
AATTCGGNCC	NAAGAGACCG	TTGTNTTGAT	GACAAGTCGA	AGCCAANAAT	ACCATNCAAC	12	<u> 0</u>
CTGCTCCCAA	TCATGCAGGN	TNCNGCCACT	GCTGCCCTTG	CCGTCCCTCC	TCTGCACCAT	16	30
GGCTNCTCCT	GCAACCAGGT	CCTCTCTGCA	CCACTTGCTG	CTGANACGCC	GACCGCCTGC	24	10
TGCTTCAGCT	ACACCTCCCG	ACAGATTCCA	CAGAATTTCA	TAGCTGACTA	CTTTGAGACG	3 0	00
AGCAGCCAGT	ACTCCAAGCC	CAGTGTCATC	TTCCTAACCA	AGAGAGGCCG	GCAGGTCTGT	3 6	50
NNTGACCCCA	GTGAGGAGTG	GGTCCAGAAA	TACGTCAGTG	ACCTGGAGCT	GAGTGCCAGA	42	20
GGGGTCCAGA	AGCTTCGAGG	CCCAGCGACC	TCAGTGGGCC	CAGTGGGGAG	GAGCAGGAGC	4.8	30
CTGANCCTTG	GGAACATGCG	TGTGACCTCT	ACAGCTACCT	CGTCGACGGC	CTCTTTGGCC	54	40
CTCGAGACA						´ 54	49

- (2) INFORMATION FOR SEQ ID NO:55:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 461 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GTCGACCTCC	CAGGTCATTA	GGAAGCTGGT	CATGGAACCC	ACCTTCAAGC	CCTGGCAGAT	60
GAAGACTCAC	TTCCTGATGC	CCTTCCCGGT	GAATTACGTG	GGTGAATGCA	TCCGAACTGT	120
CCCCTACACG	GACCCAGATC	ATGCCAGTCT	TAAAATCCTT	GCACGTTTGA	TGACTGCCAA	180
ATTCTTGCAT	ACAGAAATTC	GTGAAAAAGG	CGGTGCTTAT	GGTGGAGGCG	CAAAACTCAG	240
CCACAATGGG	ATTTTCACCC	TTTACTCTTA	CAGGGACCCA	AATACAATAG	AGACGCTCCA	300
GTCTTTTGGG	AAGGCTGTCG	ACTGGGCTAA	GTCTGGAAAA	TTCACACAGC	AAGACATCGA	360
CGAAGCCAAA	CTTTCTGTCT	TCTCAACCGT	AGATGCTCCT	GTCGCTCCTT	CAGACAAAGG	420
AATGGACCAC	TTCTTGTACG	GCCTCTTTGG	CCCTCGAGAC	A		461

- (2) INFORMATION FOR SEQ ID NO:56:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 511 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GTCGACAATA	ATTCCACCTC	ACCAGGATAA	TACCCATCCT	TCAGCACCAA	TGCCTCCACC	60
TTCTGTTGTG	ATACTGAATT	CAACTCTAAT	ACACAGCAAC	AGAAAATCAA	AACCTGAGTG	120
GTCACGTGAT	AGTCATAACC	CTAGCACTGT	ACTGGCAAGC	CAGGCCAGTG	GTCAGCCAAA	180
CAAGATGCAG	ACTTTGACAC	AGGACCAGTC	TCAAGCCAAA	CTGGAAGACT	TCTTTGTCTA	240
CCCAGCTGAA	CAGCCCCAGA	TTGGAGAAGT	TGAAGAGTCA	AACCCATCTG	CAAAGGAAGA	300
CAGTAACCCT	AATTCTAGTG	GAGAAGATGC	TTTCAAAGAA	ATCTTTCAAT	CCAATTCACC	360
GGAAGAATCT	GAATTCGCCG	TGCAAGCGCC	TGGGTCTCCC	CTAGTGGCTT	CCTCTTTATT	420
AGCTCCTAGC	AGTGGCCTTT	CAGTTCAAAC	TTCCCACCAG	GGCTTTACTG	CAAAACAAGC	480
ACGGTCAACG	GCCTCTTTGG	CCCTCGAGAC	Α			511

- (2) INFORMATION FOR SEQ ID NO:57:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 483 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GTCGACAGTC	CAAAGTCTCA	AGACAGTTAT	CCTGTTAGTC	CTCGACCTTT	TAGTAGTCCA	60
AGTATGAGCC	CCAGCCATGG	AATGAATATC	CACAATTTAG	CATCAGGCAA	AGGAAGCACC	120
GCACATTTTT	CAGGTTTTGA	AAGTTGTAGT	AATGGTGTAA	TATCAAATAA	AGCACATCAA	180
TCATATTGCC	ATAGTAATAA	ACACCAGTCA	TCCAACTTGA	ATGTACCAGA	ACTAAACAGT	240
ATAAATATGT	CAAGATCACA	GCAAGTTAAT	AACTTCACCA	GTAATGATGT	AGACATGGAA	300
ACAGATCACT	ACTCCAATGG	AGTTGGAGAA	ACTTCATCCA	ATGGTTTCCT	AAATGGTAGC	360
TCTAAACATG	ACCACGAAAT	GGAAGATTGT	GACACCGAAA	TGGAAGTTGA	TTCAAGTCAG	420
TTGAGACGCC	AGTTGTGTGG	AGGAAGTCAG	GCCGCGTCTA	CGGCCTCTTT	GGCCCTCGAG	480
ACA						483

### (2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 522 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GTCGACGAGG TGGTG	ATCAT GGAAGACGCC	CCTGACTATT	ATGCAGTGGA	AGACATTTTC	60
AGCGAGATCT CAGAC	ATTGA TGAGACAATT	CATGACATCA	AGATCTCTGA	CTTCATGGAG	120
ACCACCGACT ACTTC	GAGAC CACTGACAAT	GAGATAACTG	ACATCAATGA	GAACATCTGC	180
GACAGCGAGA ATCCT	GACCA CAATGAGGTC	CCCAACAACG	AGACCACTGA	TAACAACGAG	240
AGTGCTGATG ACCAC	GAAAC CACTGACAAC	AATGAGAGTG	CAGATGACAA	CAACGAGAAT	300
CCTGAAGACA ATAAC	AAGAA CACTGATGAC	AACGAAGAGA	ACCCTAACAA	CAACGAGAAC	360
ACTTACGGCA ACAAC	TTCTT CAAAGGTGGC	TTCTGGGGCA	GCCATGGCAA	CAACCAGGAC	420
AGCAGCGACA GTGAC	AATGA AGCAGATGAG	GCCAGTGATG	ATGAAGATAA	TGATGGCAAC	480
GAAGGTGACA ATGAG	GTCAC GGCCTCTTTG	GCCCTCGAGA	CA		522

- (2) INFORMATION FOR SEQ ID NO:59:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 533 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GTCGACAGAT	CATGTTGGAA	GAGCCCCCAG	TAGCAAAAGT	GTTAGAGCCT	TCAGAAACCC	60
TTGTGGTATC	ATCAGAGACA	CCTACTGAGG	TGTACCCTGA	GCCAAGCACA	TCAACAACAA	120
TGGATTTTCC	AGAGTCATCT	GCAATTGAAG	CGCTAAGATT	GCCAGAGCAG	CCTGTAGACG	180
TACCATCGGA	GATTGCAGAT	TCATCCATGA	CAAGACCGCA	GGAGTTGCCG	GAGCTGCCTA	240
AGACCACAGC	GTTGGAGCTG	CAGGAGTCGT	CGGTGGCCTC	AGCGATGGAG	TTGCCGGGGC	300
CACCTGCGAC	CTCCATGCCG	GAGTTGCAGG	GGCCCCCTGT	GACTCCAGTG	CTGGAGTTAC	360
CTGGGCCCTC	TGCTACCCCG	GTGCCAGAGT	TGCCAGGGCC	CCTTTCTACC	CCAGTGCCTG	420
AGTTGCCAGG	GCCCCCTGCG	ACAGCAGTGC	CTGAGTTGCC	AGGGCCCTCT	GTGACACCAG	480
TGCCACAGTT	GTCGCAGGAA	TTGCCGTCAA	CGGCCTCTTT	GGCCCTCGAG	ACA	533

- (2) INFORMATION FOR SEQ ID NO:60:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 515 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CCACCAGACA TAAAGTAG	TG ACATGATCAG	AGGAATCATC	AGCAACTGCA	TNTCCATTGC	60
TAAGCCAGTA ATCACGAT	rgc aaatccagtt	AAAGAGGAGC	ATGAATAAAT	AGTCTGCTGG	120
CCTCCCATCA AAAGCTC	TTCAAGTCG	CGTAGAATAC	TGATATAAGA	AATATANATT	180

GACCAAATAA AGAAATCCAG TTCCTGGACC CACAGGGAAA TAAAAGGTGG CAGTGATTGN CCTCCAAATC TGAAAGCGAT ANAGGAAGGC TTCGGGCCAG AGGAAGAGGT AGGCCGGGCT GATGAGGCCG AGTTTGCCGA CCAAGGGCAC GGNGACGGTG GCGGCGAACC AATAGCGCGT GATCGCCGGG ATGCTCCTGA ACCAGTCTCC GATGTCCGAC ATCTTCGACC CACAGGTAGC CAAGATGCAC AAGACCGCC GACTCCCCGC GCCGACCCCC TCACGACGCG GCCGGCTCCG CGACTGTTAG GTGTCTAGGT GGAAGCCGCC TCGAC	240 300 360 420 480 515
(2) INFORMATION FOR SEQ ID NO:61:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 357 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:	
ATNCNGGAGN CCCAGATGCT GTGGGCCATG ATCGCANNTT GNNTGAGAGA ATTGGCAGAA NCAGANTACT CCTAGCNAGA NCAGTATTNT GTGTNACTCT GGAGAATTNC AGTGATGNAA AAAAANAGAC CNGTNCAAGT AAGTCCAGCG AAAAGCATGC CCACATGGAT GAANTGGATG NTGNTGTAGA TGANGCTGGT NAAGCNNANC AGTCTGNTGA GNCTCCTCGA GTCTGATGGA TCTNATGAGC AGANCGNTGA TTCGTCNGCC GCCGTNCTCC TTNGAGCCCN CNAGACA	60 120 180 240 300 357
(2) INFORMATION FOR SEQ ID NO:62:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 396 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:	
CTTGTAGATG GAGCGGGGAG NCAGACTNCT GGGNGCTGCG TGANTGCTGA CGTGAGATGG ATTAATTAAT GGCNAGCAAG NATGGNGNCT NCGAGCCCCT CCCTGNNCGT NCCTNCCAGN NGTGGCAATN GCGTACGTGG NCAGACTTCA GGNAGAAAAA AAAAAAANGG GNCNCGTAAG CTGCTGCGGG NNCAGCAGCT TGAGACTGNC AAGTGACTCA GATGCAGAGT CAGACTNTCG	60 120 180 240
CTGCTGCGGG NNCAGCAGCI TGAGACIGNC AAGIGACICA GAIGCAGAGI CAGACITICO	300

- (2) INFORMATION FOR SEQ ID NO:63:
  - (i) SEQUENCE CHARACTERISTICS:

ACTNCCGTCG NCGGCCTCNT TGGCCTTTNG AGGCGA

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GTCTTTGACC AGCAGCCTCT ATCGGAACCA CAGTACCAGC TTCAGTCTTT CAAACCTCAC

360 396

CGCTGGGGGA	GGGAAGGGTC	AAGTCGAGGG	AAGGTGAAAC	CAAAAGGCAC	TGAGCATGCG	120
TGGTGGGGCA	GGGAAGGACA	CCATCACTCC	AGAGACAGTA	TGGTAACAAA	GGGACAGGAA	180
TGGTCCAGGC	CAGCTTCAGG	CTCTTCAGAA	GCCAGAGAGA	TGTCCAAGTC	TACCAAACCG	240
AGTTCTCCAA	GGCTTTTCAA	GAAATGGGAT	TTGCTTGCAA	GATGAATGAG	GGAGGAGGTC	300
CCATGGCTTC	TAAGAGATCA	ACCCAAGTCT	TCCAATACTC	ACTGCTAAGT	CCCACCTGGG	360
TCCCCCAGAG	CCAGGAAGCT	CCCTGGTGGC	AGGTCCCCCT	CTTGCCCTCA	CGGCCTCTTT	420
GGCCCTCGAG	ACA					433

- (2) INFORMATION FOR SEQ ID NO:64:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 452 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

	GTCGACAAAA	TAGTTCTGTT	AAAGAATACC	GAATGGAAGT	TCCATCTTCG	TTTTCAGAAG	60
	ACATGTCAAA	TATCAGGTCA	CAGCATGCAG	AAGAACAGTC	CAACAATGGT	AGATATGACG	120
	ATTGTAAAGA	ATTTAAAGAC	CTCCACTGTT	CCAAGGATTC	TACCCTAGCT	GAGGAAGAAT	180
	CTGGGTTCCC	TTCTACTTCT	ATCTCTGCAG	TTCTGTCTGA	CTTAGCTGAC	TTGAGAAGCT	240
	GTGATGGCCA	AGCTTTGCCC	TCCCAGGACC	CTGAGGTTGC	TTTATCTCTC	AGTTGTGGCC	300
•	GTTCCAGAGG	ACTCTTTAGT	CATATGCAGC	<b>AACATGACAT</b>	TTTAGATACC	CTGTGTAGGA	360
	CCATTGAATC	TACAATCCAT	GTCGTCACAA	GGATATCTGG	CAAAGGAAAC	CAAGCTGCTT	420
	CTTGGTCAAC	GGCCTCTTTG	GCCCTCGAGA	CA			452

- (2) INFORMATION FOR SEQ ID NO:65:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 401 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CTNAAANTTA	CCATCACAGT	TNCTACAATC	GGCTCTTTCC	AATTTGGCNA	CAACNCTGGG	60
TCATCAATGC	TCCTGAGAAG	ATCATAAAGG	AATTTATCAA	TAAAACTTTG	TCGGACAAGG	120
GAAATNCCCC	ACCCTCTGAG	GTGCTGCTCA	CGTCTCTCTG	GTCCTTGTCT	GTGACCATAT	180
TTTCCGTCGG	GGGNATGATC	GGCTCCTTTT	CCGTCGGACT	CTTCGTCAAC	CGCTTTGGCA	240
GGCGCAANNC	AATGCTGATT	GTCAACCTGT	TGGCTGTCAC	TGGTGGCTGC	TTTATGGGAC	300
TGTGTAAAGT	AGCTAAGTCG	GTTGAAATGC	TGATCCTGGG	TCGCTTGGTT	ATTGGCCTCT	360
TCTGCGGACT	CTGGTCGACG	GCCTCTTTGG	CCCTCGAGAC	A		401

- (2) INFORMATION FOR SEQ ID NO:66:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 558 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```
GTTGAGAGCA GCATGTTTTN NCCACTGAAA CTCATCCTGC TGCCAGTGTT ACTGGATTAT
                                                                       60
TCCTTGGGCC TGAATGACTT GAATGTTTCC CCGCCTGAGC TAACAGTCCA TGTGGGTGAT
                                                                      120
TCAACTCTGA TGGGATGTGT TTTCCAGAGC ACAGAAGACA AATGTATATT CAAGATAGAC
TGGACTCTGT CACCAGGAGA GCACGCCAAG GACGAATATG TGCTATACTA TTACTCCAAT
                                                                      240
CTCAGTGTGC CTATTGGGCG CTTCCAGAAC CGCGTACACT TGATGGGGGA CATCTTATGC
                                                                      300
AATGATGGCT CTCTCCTGCT CCAAGATGTG CAAGAGGCTG ACCAGGGAAC CTATATCTGT
                                                                      360
GAAATCCGCC TCAAAGGGGA GAGCCAGGTG TTCAAGAAGG CGGTGGTACC GCATGTGCTT
                                                                      420
CCAGAGGAGC CCAAAGAGCT CATGGTCCAT GTGGGTGGAT TGATTCAGAT GGGATGTGTT
                                                                      480
TTCCAGAGCA CAGAAGTGAA ACACGTGACC AAGGTAGAAT GGATATTTTC GTCGACGGCC
                                                                      540
TCTTTGGCCC TCGAGACA
                                                                      558
```

### (2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 539 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GTGGAGAAAA	TTGCTGCTGA	GAAGGACATT	TTGAAGGTTT	TGTTGGCTGA	AAAAGCTGTT	60
TCTGGAATCA	CCCCTAGATC	TTTCTTGAAG	ACTTGAATTA	GATTACAGCG	ATGGGGACAC	120
AGAAGGTCAC	CCCAGCTCTG	ATATTTGCCA	TCACAGTTGC	TACAATCGGC	TCTTTCCAAT	180
TTGGCTACAA	CACTGGGGTC	ATCAATGCTC	CTGAGAAGAT	CATAAAGGAA	TTTATCAATA	240
AAACTTTGAC	GGACAAGGGA	AATGCCCCAC	CCTCTGAGGT	GCTGCTCACG	TCTCTCTGGT	300
CCTTGTCTGT	GGCCATATTT	TCCGTCGGGG	GTATGATCGG	CTCCTTTTCC	GTCGGACTCT	360
TCGTCAACCG	CTTTGGCAGG	CGCAANTCAA	TGCTGATTGT	CAACCTGTTG	GCTGTCACTG	420
GTGACTGCTT	TATGGGACTG	TGTAAAGTAG	CTAAGTCGGT	TGAAATGCTG	ATCCTGGGTC	480
GCTTGGTTAT	TGGCCTCTTC	TGCGGACTCT	GGTCGACGGC	CTCTTTGGCC	CTCGAGACA	539

#### (2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 365 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GTTGACCCCA	TTTTCCACCA	CCAAGCAAGC	AGAGCCTGTT	GTTTTGTCCA	AAATCAAAAC	60
TGCACATCCA	CAGAGCAGAG	ATCTCAAAGA	TTATGCGAGA	ATGTCAGGAA	GAAAGTTTCT	120
GGAAGAGAGC	TCTGCCTTTT	TCTCTTGTAA	GCATGCTTGT	CACCCAGGGA	CTAGTCTACC	180
AAGGTTATTT	GGCAGCTAAT	TCTAGATTTG	GACCATTGCC	CAAAGTTGCA	CTTGCTGGTC	240
TCTTGGGATT	TGGCCTTGGA	<b>AAGGTATCAT</b>	ACATAGGAGT	ATGCCAGAGT	AAATTCCATT	300
TTTTTGAAGA	TCAGCTCCGT	GGGGCTGGTT	TTGGTCCGTC	GACGGCCTCT	TTGGCCCTCG	360
AGACA						365

- (2) INFORMATION FOR SEQ ID NO:69:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 497 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GTCGACCTCG	GTAAATGCCT	CAGTTCCCCT	CCCAGATGGA	GGCATCGTTG	TGAGAGTCTG	60
ATTGGGAGGG	GAATATGAAA	ATGTTTTCGG	AAGATAAAAG	TACTACACAG	ATGTGAGGTG	120
GTTTTGCCTT	GGAAGAAAGT	GCTCCTTAGA	TGTGTCTGGA	TGTTATGCAG	AGTGATCGTG	180
GCGTGTCAAT	CTTTCTTTTG	GGTGTTTTGC	AGCCTGAGAC	ATAAGGTAAT	TGTCAGAAAA	240
GGGAGACGTA	GAAGTGTGGA	TCTGTGGAAG	CTCACTCTTA	ACAAGAATTC	TAAGATGCAC	300
ATTTAAGTAC	TTGCCATGAC	GTGAGGTGTT	GTCACACGTC	AACCCTGAGA	TGCTGTCAGT	360
GTCCCAGGGG	ACTTGACATT	TATGTTACCC	AGGAATGACT	GTGTAAATGT	GCAGGTGCAG	420
GCCGGGCGCC	GTGGCTCAGT	GCCTGTAATC	CCAGCACTTT	GGGAGCCCCG	TCGACGGCCT	480
CTTTGGCCCT	CGAGACA					497

- (2) INFORMATION FOR SEQ ID NO:70:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 437 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GTAGACANCA	NTAGAAAAAC	AAAAATCTCA	TAATGCAAAA	GCATCAAGTG	TTTGACTCTG	60
AGAAGCGCCT	TGTATGCCCA	GTTACTCTCG	TTCTCCCTCA	GCTCTTGCTT	GTGCTTCTCC	120
ACCTGCCATT	CCACTTTGGC	CTGGTACTGC	CTGTAGTCTT	CCTGGCAGGC	CCCAGCTCCA	180
GTTCTTTGGA	GCAGCTGGGC	ATCCAAGAAG	AGGTCATTGC	TGTGGAAGGA	GCCCTCTCGC	240
TCCCTCCCCA	GCCTCTCAAT	CACAGCCAGG	AGCTCTGCCT	GCTGCTGCCT	CTGCTCCTCC	300
ACAGAGCCCC	AGTTGTTGAA	GGCACAGTAC	CTTCTCTCAC	ACTCCCGCGC	CAGGTCTTTC	360
AGGCTGCAGT	TGTCCGTGTT	TGCTACATAG	TCATCCAGGG	CCTGGCCCCG	TCGACGGCCT	420
CTTTGGCCCT	CGAGACA					437

- (2) INFORMATION FOR SEQ ID NO:71:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 518 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CCTGCNCNAA	ANNANTCCAA	GCNAANNCCC	AAACAATCCC	AATNCCNACC	CCAAGCTNGG	60
GAGTTCGGCC	CAAAAGAGGC	CCNNCGAACG	TAGATTNCAG	TGAGCCAAGA	TCGTNCCACT	120
GCACNCCAAG	CCNGGGCANC	CAAGAGCGAA	ACTCCGTCNC	CNCNNNANAA	AGAGAAAATT	180
AGCCGGGCGT	GGTGGCGTTA	ATCCCANCTA	CTTGTGAGGN	TAAGGGAGGA	GAATTGCTTG	240
AACCCAGGAG	GCAGAGGTTG	CAGTGAGCTG	AGATCACGCC	ATTGCACTCC	AGCCTGGGCC	300
ACAAGAGCAA	GACTCCATCT	CCCAAAAAAA	AAAAAAATAG	CGTCAGAAAA	ATGTCCTTGT	360
ATGCCATTTT	CTCCATTTTA	TTGACATTTT	GCCCGACTTT	TGTCTTTGTT	TCAGGGAAAT	420
CGTGGAACAC	ATGGTCCAGC	ACTTTAAAAC	ACAGATCTTT	GGGGATCGGA	AGCCCGTGTT	480
TGACGGCAGG	GTCAACGGCC	TCTTTGNCCC	TCGAGACA			518

- (2) INFORMATION FOR SEQ ID NO:72:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 481 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

AAACCAAAAC	TCATGTTGCT	TGNCCCCCCA	TCGTCGTCTC	AAGTGNGGGC	GANNACTTTC	60
CTGGTTGGAG	CCCTCCGTCC	NAACNNCTAA	CACAATGTTC	TTTCNCAAAC	GTTCTACNAA	120
CGCCTGCGAC	NAGNCCAGGG	AGGGGGTGCT	GTGNATCCTC	AGCNACGACA	CGCTGCAGTA	180
CTGCGACTTC	TTGGGCTCCG	GGGCGGCCAT	CTGGGTCACC	ATNCTGTGNA	TGGCACGGCT	240
CAAGACAGTC	CTGAAATACG	TGCTGTTTCT	TCTGGGTACA	CTGGTCATCT	CCATGTCCTT	300
GCAGCTGGAC	CGCAGGGGCA	TGTGGAACAT	NCTGGGGCCC	TCCCTCTTTG	CCTTCGTGAT	360
CATGGCCTCC	ATGTGGGCTT	ACCGCTGCGG	GCACCGGCGC	CAGTGCTACC	CCACCTCGTG	420
GCAGCGCTGG	GCCTTCTACC	TCCTGCCCGG	CGTCTCTACG	GCCTCTTTGN	CCCTCGAGAC	480
A						481

- (2) INFORMATION FOR SEQ ID NO:73:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 513 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GACCCTCCAN	TAATAANCCT	TTTGTTTCCC	TCGTCNNTGT	TNGTCCGTTC	CCCTTTCCTN	60
CCCTTGTTTC	NNTNTCCTGC	ACCAATATTT	CCAANCTAAT	ACCCAAGCAA	NACAATCCNA	120
ACTCCAAGCT	CGGGAATTCG	GCCCAAAGAG	ACCGTAGGCC	GAAACCCACC	GGANGGAACC	180
				CTCTCTTGGC		240
				GTGCTAAAGA		300
				TTATCAAAGA		360
				TAAAGCTTTC		420
				TTGTGGAGAA		480
		GGCCCTCGAG				513

- (2) INFORMATION FOR SEQ ID NO:74:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 519 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

CAANTAATAA ANCTTTTGT	TCCCTCGNCA	TTGTNNTCGT	TCCCCTGTCC	NGCCTTGTTT	60
CCNNNGTCCT GCACCAATAT	TTCCAAACCN	AATACCCAAG	CATACAATCC	NNACTCCAAG	120
CTNGGAATTC GCCCANAGAC					180

GATATATACC	GTCCTCCAAG	AAANGGGATG	CTGCTATCAG	TCTTTCTAGG	AGCCGGGANA	240
CAGATATTAA	TTATGACCTT	TGTGACTCTA	TTTTTCGCTT	GCCTGGGAGT	TTTGTCACCT	300
CCCANCCGAG	GAGCGCTGAT	GACGTGTGCT	GTGGTCCTGT	GGGTGCTGCT	GGGCACCCCT	360
GCAGGCTATG	TTNCTGCCAG	ATTCTATAAG	TCCTTTGGAG	GTGAGAAGTG	GAAAACAAAT	420
GTTTTATTAA	CATCATTTCT	TTGTCCTGGG	ATTGTATTTG	CTGACTTCTT	TATAATGAAT	480
CTGATCCTCT	GGTCAACGGC	CTCTTTGGCC	CTCGAGACA			519

- (2) INFORMATION FOR SEQ ID NO:75:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 506 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CGGGCCCAAA	GACANGCANN	CCNACAAGAT	GTCGTTGTTC	CAAGAAGCTG	ATNGAGGGGT	60
ATCTCGGAAG	CACACGGAAA	CTTTTTCCTT	CCTTCAATTC	NACGCACACT	AACTCTCTAA	120
TGAGCAANCG	GTATACGGCC	TTCCTTCCAG	TTACTTGNAT	GTGAAATAAA	AAAAAGTTTG	180
CTGTCTTGCT	ATCAAGTATA	AATAGACCTN	CAATTATTAA	TCTTTTGTTT	CCTCGTCATT	240
GTTCTCGTTC	CCTTTCTTCC	TTGTTTCTTT	TTCTGCACAA	TATNTCAAGC	TATACCAAGC	300
ATACAATCAA	CTCCAAGCTC	GGAATTCGGC	CNAAGAGGCC	GTCGACCGTT	CGTTATCGGA	360
ATTAACCAGA	CAAATCGCTC	CACCAACTAA	GAGCGNCCAT	GCACCACCAC	CCACGGAATC	420
GAGAAAGAGC	TATCAATCTG	TTGAAGAACA	TGCCCGGCTT	CTTGGTCATC	ATCATGGTGT	480
ACACGNCCTC	TTTGNCCCTC	GAGACA				506

- (2) INFORMATION FOR SEQ ID NO:76:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 500 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

TTCCTTGTTT	CCTTTTTCCT	NCCCCAATAT	TTCCAAGCTA	ATACCCAAGC	AATACAATCC	60
NACTCCAANC	TCGGGAATTC	GGCCCACAGA	GACCGNTGAC	CNTGTAAATG	AGTGAGGCAG	120
GAGTCCCGNG	GAGGTTAGTT	GTGTCAATAA	AAATGATTAA	GGATACTAGT	ATAAGAGATC	180
AGGNTCGTCC	TNTAGTGTTG	TGTATGGNTA	TCATTTGTTT	TGAGGNTAGT	TTGATTAGTC	240
ATTGTTGGGT	GGTGATTAGT	CGGTTGTTGA	TGAGATATNT	GGAGGTGGGG	ATCAATAGAG	300
GGGGANATAG	AATGATCAGT	ACTCCGNCAG	GTAGGCCTAG	GATTGTGGGG	GCAATGAATG	360
AAGCGAACAG	ATTTTCGTTC	ATTTTGGTTC	TCAGGGTTTG	TTATAATTTT	TTATTTTTAT	420
GGNCTTTGGT	GAGGGAGGTA	GGTGGTAGTT	TGTGTTTAAT	ACAAAAAGTT	GGGTCGACGN	480
CCTCTTTGNC	CCTCGAGACA					500

- (2) INFORMATION FOR SEQ ID NO:77:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 581 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
    - (5, 10102001, ====0
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

```
AACCGGATTC GGNCCNAAAG AGACCGGTTG CCCAAAACTT TCTGCTGAGA AGGACATTTT
GGAGGGGNTT TGTTGGGCTG AAAAAAAGCT GTTTCCTGGG AATNNAACCC CCNAGANCTT
                                                                      120
TCTTGAAGAC NTTGAATTAA GATTACCAAN CGATGGGGGA CACAGGAAGG TCCACCCCCA
                                                                      180
NGCTCTGATA TNTGCCATCA CAGTTGCTAC AATCAGCTCT TTCCAATTTG GCTACCAACA
                                                                      240
CTGGGGTCAT CAATGCTCCT GAGAAGATCA TAAAGGAATT TATCAATAAA ACTTTGACGG
                                                                      300
ACAAGGGAAA TGCCCCACCC TCTGAGGTGC TGCTCACGTC TCTCTGGTCC TTGTCTGTGG
                                                                      360
CCATATNITC CGTCGGGGN ATGATCGGCT CCTTTTCCGT CGGACTCTTC GTCAACCGCT
TTGGCAGGCG CAATTCAATG CTGATTGTCA ACCTGTTGGC TGTCACTGGT GGCTGCTTTA
                                                                      480
TGGGACTGTG TAAAGTAGCT AAGTCGGTTG AAATGCTGAT CCTGGGTCGC TTGGTTATTG
                                                                      540
ACCTCTTCTG CGGGTCGACG ACCTCTTTGG CCCTCGAGAC A
                                                                      581
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- (2) INFORMATION FOR SEQ ID NO:78:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 523 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GTCAACCTGG	GAGGCTCTCC	CCCACCTTCT	TTCAATCTCT	TCTCAAACTC	TGCATCCTCA	60
GAGGGGCCTT	GCCTGATTGG	CCTTCTTAAA	ATGGATCTGC	CCCACCCCAC	TTTGTACTTG	120
CTGTGCCCTC	TGCTTTCAGG	CGTGTTCTCA	AACAGGATCT	CAACAAGGCC	TCCCCTGACC	180
ACACTTTAAA	ACTGCATGCC	CTATATATAC	CCCATCTCTC	TTATTTTTAT	TTGTCTCCCT	240
AATGCTTATC	CCCAGTATAC	TCTGTTTATT	GTCTGTCTCT	CCTCACTACA	AAATAAACTC	300
CCCAAGGCCT	AGAGTTTTTT	CTGTCTTGTC	CCTGCTATAT	ACCAGTGCTT	AGAACAGCGC	360
CCTGCACAGA	ATAGAGGCCC	AATTCAATAT	GGATTCGCTA	CCACTACATC	CTATTTGTTT	420
CCTTCCCATC	ACTTTTCGAA	CACTCATCTA	TTCAGCTCTG	CTGACCTGTT	TCACATCTGG	480
<b>ATCCTGTATA</b>	GCAACGTCGA	CGGCCTCTTT	GGCCCTCGAG	ACA		523

- (2) INFORMATION FOR SEQ ID NO:79:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 434 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

```
GTNGACTGAT ACTCGAGTAC CTGGATCAGC GGCTGAAAGC TGCAGAGAAC AAGTTTGCCA
                                                                      60
AGTGCCTCAT GACCTGTCTC AAATGCTGCT TCTGGTGCCT GGAGAAGTTC ATCAAATTCC
                                                                      120
TTAATAGGAA TGCCTACATC ATGATTGCCA TCTACGGCAC CAATTTCTGC ACCTCGGCCA
                                                                      180
GGAATGCCTT CTTCCTGCTC ATGAGAAACA TCATCAGAGT GGCTGTCCTG GATAAAGTTA
                                                                      240
CTGACTTCCT CTTCCTGTTG GGCAAACTTC TGATCGTTGG TAGTGTGGGG ATCCTGGCTT
                                                                      300
TCTTCTTCTT CACCCACCGT ATCAGGATCG TGCAGGATAC AGCACCACCC CTCAATTATT
                                                                      360
ACTGGGTTCC TATACTGACG GTGATCGTTG GCTCCTACTT GATTGCGTCG ACGGCCTCTT
                                                                      420
TGGCCCTCGA GACA
                                                                      434
```

- (2) INFORMATION FOR SEQ ID NO:80:
  - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 573 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80: GAGGCCCCTC AANTTCTGCC ATTTTATTTT ATTTTTTTGA NCTGGAGTNT TGCTCTGTAT CCCAGGCTGG AGTGCAGTGG CGCAATCTCG GCTCACTGCA AGNTCCTCCT CCCGGGTTCA 120 CGCACATTCT CCTGCTTCAG CCTCCCTAGT AGCTGGGACT ACAGGAGCCC GCCACCACGN 180 CTTGTTAATT TTTTTGTAT TTTTAGTAGA GACAGGNTTT CACTNTNTTA GTCAGGATGG 240 TCTCATTNTT CTGANGTCAT GATCCGCCCA CCTCGGCCTC CCAAAGTGCT GGGAKTACAG 300 GMGCGARCCA CCGCGCCCGG CCTATTTTT GGKGGTTTNA WWTCTGGGTG ACTTGTCAGC 360 AGGAAGTTTT TGTTKTTTTT TTTCCANTGA AAAGATCTGG CCANAATAGT GGGNNTGTCA 420 AAGTATCTCT TTGCAGNTTT AATTTGCATT TTCCCANTGA CTAAGATGAT GTTGTGCAAT 480 TTTTTCAGAN ACTGTNTGCT ATCTGTATAT CATCTCTTTT TTTTTTTTTC TTTTGGAAGT 540 GGATCCGGTN CGNCCTCTTT GCCCCTCGAG ACA 573 (2) INFORMATION FOR SEQ ID NO:81: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 468 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81: GAANCCCCAT CCACTTCNCG GGAGGGGGGA GAGCGCGGNG ACGGGTCTCG CTCCCTCGGC CCCGGGATTC GGCGGGTGCA GNTGCCGGAT CCTTCAGCGT CTGNATCTCG GCGTCGCCCC 120 GCGTACCGTC GCCCGGCTCT CCCGCGGGGTT CGGGGCACTT GGGTCCCACA 180 GTCTGGTCCT GCTTCACCTT CCCCTGACCT GAGTAGTCRC CATGGCACAG GTTCTCAGAG 240 GCACTGTGAC TGACTTCCCT GGATTTGATG AGCGGGCTGA TGCAGAAACT CTTCGGAAGG 300 CTATGAAAGG CTTGGGCACA GATGAGGAGA GCATCCTGAC TCTGTTGACA TCCCGAAGTA 360 ATGCTCAGCG CCAGGAAATC TCTGCAGCTT TTAAGACTCT GTTTGKCAGG GATCTTCTGG 420 ATGACCTGCG GAAGTGGATC CGGTTCGGCC TCTTTGGCCC TCGAGACA 468 (2) INFORMATION FOR SEQ ID NO:82: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 462 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82: GAACCGGATC CACTTCCGGG AAAACCTCGG ATTAGCAAGC AATAAAAACA TGACCTCACT CTTCCTCAAA GGAGCCCCTG GTCTTCCCTG TGTGACTCAG TTCTTTCCAT CTGTTTGTCC 120 CGCTGCAAGC CTCTTTCTGC GCTGACTGTG ACATCGGAAC GTGGCCTTCC TGTCACCCCC 180 TCCGTGCCAC GCACTGAAGG CCACCCCCC CCACCTGGGA AACTAAGAAC TGGATATTTT 240

300

GCCTCATTCA CTTGTACTGT AACAATGTAT ATAATTTGGT TGGTATTTCA CTATTTAATT

TTTAAGAAGC CTATTTTACT AGTGTTTTAT ATGAACAAAG TACTGCAGAA GTTAAACCTG

CCAGGAAGTG GATCCGGTTC GGCCTCTTTG GCCCTCGAGA CA

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 498 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TGTTGTATTT TTTCTGAGAT GTTTTGCTTT AAGAGATACT TTTTGCTCAG TTTTTATATG

420

462

(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:	
GGCCCGATNC ACTTCCGTGG NAAGAGCCTG CAATCCCNCC TACTCAGGAG GCTGAGGCAG GAGAATCGCC CGAACCCGAA AGGTGGAGGT TGCAGTGAGC TGAGAATGTG CCACCGCACT CCAGCCTGGG TGACAGGGLG AGACTCTCTC AAAGTAAATA AATTAAAAAA ATTTAANAAG ATCATCAAAG AACAAACGAA ATTTTGTTAT TTCAGTAAGT CAATTTAAAC AATAGAAGCC AATTCTACCA CCAGAGGARC RMMATAAAAT CTCATTATTA ATTGAGGGTG GCTTCTCTMC CAGGTGRRAA ATTCTATAGR CAGGTATTTT GKTTACTACT GACAGGTAAT AAGATTGTTT CTWAGGTAAA GGTAAACCCA GCAACACAAC ATTCTTCACT TTTGTTTAAT GAACCTCNAN ATTCATCATA TTACTTNTAT TTGCTAGCAT GCTTTTTGTG GAAGTGGATC CGGTTCGGCC TCTTTGGCCC TCGAGACA  (2) INFORMATION FOR SEQ ID NO:84:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 409 base pairs (B) TYPE: nucleic acid	60 120 180 240 300 360 420 480 498
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:	
CGASCCGGAT CCACTTCCCC CTTACGTATC ATTTGTCACA CAGGCCTCAG CCTGAAAAAA AATTCCAGTT TTTGTGTATT GCAGTTCCCG TATGCTATTG TCAACCAACA GTTTCCGTGA TCCTTGTAGT CTAATGAGTT TGGATGCATC TATGTTCCTA CTGGATCCAC TGTCCCGTCT CGGCAGCTCT TCCTCACTGC TGCTACTCTT TTCTGGACAC TCCTTTTTTT CCATTTGTCA AATGTGGTAT TTATGTCTTT ACTGTATCTT TTTTACCCAT GTGAGTTTCA GGAGCCCCAG GGTGCAGGAA GGAGGAGCGG AGGCTTGTTG CTTGGACACT GCCAGGCTGC TCTGTGTTCT GTTCCTCTTG GRAAGTGGAT CCGGTTCGGC CTCTTTGGCC CTCGAGACA	60 120 180 240 300 360 409
(2) INFORMATION FOR SEQ ID NO:85:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 611 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:	
GAACCGGATC CACTTCCGAA GAGAAGGTCA GAGCGCACTG CAGGCAGCGC GGCTCTGGGA AGAACTTCAC GGAGCCCCTT CTTAGAGCAG GGAGGGGGCT TTCTCAGTGA AATGTTTGGT	60 120
122	

TTTCTGCTGC	CTCCTCTGCC	CCAGGCCCCC	CTCCAGGGTA	CTGCCTATCC	CAGATAGGTC	180
AGTGCACCAG	GGACCCGGCC	GCCAGCACCG	CCGACCCCTC	CCAGAGTGAC	GCCCTTGTTC	240
ACTGACAAAG	AGACCTGTCC	CAGGAGTGTC	CTCCACCGAG	CCGGTCAGCT	GTGGGTGGTT	300
TTCCTGTTAC	GACGCTCAGT	AGCCTGTAGC	AATAACAAAC	TCGTGGCTAT	GAATGCAGAT	360
GCAGTGTTCT	CATAGAATAA	CTGTTCCTGC	ACTTTTACAG	ACAAATCTAC	GACAAAAAA	420
AAGATCAACT	TTTTTTTTCC	GAACAACAAA	AAAAATGAAT	GATTACAATA	GGAAAGGGAA	480
ATAAATTAAA	GCTACATATC	ATTAACAAAT	TAATGTTCTT	CAAAAAATAC	CTACAAATTT	540
CTCTGTACAT	TCTTTACGCA	CAGCGTAACG	ATGGAAGTGG	ATCCGGTTCG	GCCTCTTTGG	600
CCCTCGAGAC	A					611

- (2) INFORMATION FOR SEQ ID NO:86:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 373 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GAACCGGATN	CACTTCCCCT	CCACGTAGTT	GGNAGGGGAA	CCAGCCAACC	CGGCCATAGA	60
TCTCCCCTCG	CCACCAGCCT	TGGTGTCCCT	TCTTGTTAAG	GATCTTGATG	ATGTCACCCT	120
CCTTGAGCGA	CAGCTCTGAT	CGGTCTCGGG	CGCAGAAGTC	ATAGCGGGCT	TTGGGTGTGC	180
CAAAATACTT	TGTGCTTCCC	ACTGNTGGNC	TGCTGATGGT	TCTCTTTTCA	NGCTCCTTGA	240
AGGGGAACTG	CAANGTGGTG	TCCAGAGACT	TGAAGCAATC	CNTTAGAGAG	TTCTGNTGGT	300
AAAACTCCAC	CAGNTCCGTA	AGCCCCCNGA	AAGNCTTTTT	CTCTGTGATC	CGGTACAGAA	360
CCTTCTTCTG	TCA					373

- (2) INFORMATION FOR SEQ ID NO:87:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 489 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GTTGACCGCC CACGATGAT	C TTGCCGCCAC	GCTTGCTGGT	CTTCTCCACT	GACAAGGCAG	60
TGCTCAGGCC CTGCTCATG	C TTCCCCAGAC	CCTGGCCCTC	CCGGAAGCCG	NACTTCTGCA	120
TGATCTTGTG CGCCACCGT	G CCCCCCATGT	TAGCGAGGAA	GGAGTTGCTA	GGTCCGGTTG	180
GAGATCTCGG TCTGTCTTG	T TCCTCGTACA	CTGGGGGAGG	AATGGCTGCT	TTGGAAGACT	240
GTGATCGAGG TCTTGAGTC	C TCTTCATAAG	GAAAATCTCG	GGGTAACTCT	TTGTCTTTCT	300
CTACCAGAGA AGTGGGTGG	G GCAATGGCAG	CTCCGCCCAT	ACTTCTCTTC	CTCCTCTCTC	360
GCTCATAATC TTCATCTTC	A TCAGAATCTG	GATCTGGTCT	CCTTGCAAAC	CCACTTGCTT	420
CATGTCTGTC TTTACGCCT	T TTTTCCCTTT	CTTCTATTTC	CGTCGACGGC	CTCTTTGGCC	480
CTCGAGACA					489

- (2) INFORMATION FOR SEQ ID NO:88:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 520 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

```
GACGACTTTG TGGGTATTAA TTTTTGTTTA AGTTTAAAAT AAAAGTAAAG ATTCATTTTG
                                                                       60
GATATCAGTT GAAACCCCTT AGTAACTCAG TTTCTGTTAT TCTTGTTCTC ATTTCCTTTA
                                                                      120
AATACACTTG TTCTTGGCTT TTGCCATTTT GATTCTGTGA AGTAGGCAGG AGCAGGGATT
                                                                      180
AATTTATACA GTATTCCTGT TCTGAACAAA ACCAGAAAAG TCACTGTATA AACTTGACTT
                                                                      240
AAAATAGTAT CTTTCTCTTY TCATGTATTT TCATTTGGGG GAAAAAAAAT CTCTTTAATT
                                                                      300
GTAACCTGAA TTCAAGCTGT ACCCCTCCAT GGTCCTACAC TCTAGAGCTA ATCTGGTTGG
                                                                      360
GCAGAAAGGC AGAAGGATGG TATATTGTCC CATTGTGCCT ATAATGTATT TTAAATTGGT
                                                                      420
CATTCCACCT TACCTAATGG AAATTCTTGC AGCTTTCCTA GTGCTCATCA GCGGTTTTAG
                                                                      480
GAATTCACTA ACGTCGACGG CCTCTTTGGC CCTCGAGACA
                                                                      520
```

- (2) INFORMATION FOR SEQ ID NO:89:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 463 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GTTGACGGCG	TGGTGGCGGG	TGCCTGTAAT	TCCAGCTACT	CAGGAGGCTG	AGGAAGGAGA	60
ATCATTTGAA	CCTGGGAAGT	GGGGGTTGCA	GTGAGCCAAA	ATCGTGCCAT	TGCACTCCAG	120
CCTGGGCAAC	AAGAGTGAAA	CTCCATCTCA	GAAAAAAAAA	ААААААААА	AAAAAAAAG	180
GAAGGAACCG	GTGGGGCAAG	CAGAGTTAAG	ATGCTTTGCT	AAGTTAAAAA	GTCTACTAAC	240
TACCAAATCT	TGCTGTGGYT	TATCCAGAGC	TCTCAAAATG	CTGCCAATCT	ATTTTTAAGA	300
AGACCTAAAT	CCTCATTTTG	GCTTTTAGGA	CACTAGGATT	TGCCTTCAAC	CCATGTCTCC	360
AGTCATATAT	TTTCTTACTA	TTCTTCAAAC	ATACCTTTTT	CTCTTTTCTT	CACTCTTCAT	420
TATGCTGTTT	AAATCGTCGA	CGGCCTCTTT	GGCCCTCGAG	ACA		463

- (2) INFORMATION FOR SEQ ID NO:90:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 534 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

```
GTACAAGAAG TGGTCCATTC CTTTGTCTGA AGGAGCGACA GGAGCATCTA CGGTTGAGAA 60
GACAGAAAGAT TTGGCTTCGT CGATGTCTTG CTGTGTGAAT TTTCCAGACT TAGCCCAGTC 120
GACAGCCTTC CCAAAAGACT GGAGCGTCTC TATTGTATTT GGGTCCCTGT AAGAGTAAAC 180
GGTGAAAATC CCATTGTGGC TGAGTTTTGC GCCTCCACCA TAAGCACCGC CTTTTTCTCG 240
AATTTCTGTA TGCAAGAATT TGGCAGTCAT CAAACGTGCA AGGATTTTAA GACTGGCATG 300
ATCTGGGTCC GTGTAGGGGA CAGTTCGGAT GCATTCACCC ACGTTATTCA CCGGGAAGGG 360
CATCAGGAAG TGAGTCTTCA TCTGCCAGGG CTTGAAGGTG GGTTCCATGA CCAGCTTCCT 420
AATGACCTGG GAGCCATGG GAACGTGGGC ACGCCTCTT TGGCCCTCGA GACA
```

(2) INFORMATION FOR SEQ ID NO:91:

> (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 450 base pairs

```
(B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:
GTCGACCAGG ACTAGATTCT GTCTCTCCAA AGTGGCCCAA GCCCTGTTCT CTGTACTAGG
                                                                       60
GAAGCCAGCT GTGTCTTTTC GAGGACAGTT GGTCCAGCCA GCAGGCTCAG TTCAGATACC
                                                                      120
AGACAACCAT TCCAGCACGA GGGCTCAGCG CCCTGGCCCC GGCGGTCGCT CCAGTGCCTG
                                                                      180
TGTGCCCACC AGCACATCCA TGAGGTAGTC CAATTCGGCC TCGTCCAGCT CCGGAGCTTC
                                                                      240
CTCCTTGGCC GGCCCATCCT CAGGGCCTGG TTTGAGGCCC TCAGAGGCTG GTGCCCAAAG
                                                                      300
TTCATTGTCA TACATAGAGG TGTCAATATC CTCAAACAGG CCCTCAAGCC CATCGTCCAG
                                                                      360
TAGACAGCCA GTGGCTGGGC CCAGCAGGTC CAAGGCACCC AGGCTGGGCG CTGCTCCCCC
                                                                      420
GATGCTACGG CCTCTTTGGC CCTCGAGACA
                                                                      450
(2) INFORMATION FOR SEO ID NO:92:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 449 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:
GTCGACGGCG GYCATGGCAA AGCAGTACGA CTCGGTGGAG TGCCCCTTTT TTGTGATGAA
                                                                       60
GTYTCCCAAA ATACGAAGAA GCTCGCCAAG ATCGGCCAAG GCACCTTCGG GGAGGTGTTC
                                                                      120
AAGGCCAGGC ACCGCAAGAC CGGCCAGAAG GTGGCTCTGA AGAAGGTGCT GATGGAAAAC
                                                                      180
GAGAAGGAGG GGTTCCCCAT TACASCCTTG CGGGAGATCA GGATCCTTCA GCTTCTAAAA
CACGAGAATG TGGTCAACTT GATTGAGATT TGTCGGAACC AAAGCTTCCC CCTTATAACC
                                                                      300
GCTGCAAGGG TAGTATWITA CCTGGTGTTC GACTTCTGCG AGCATGACCT TGCTGGGCTG
                                                                      360
TTGAGCAATG TTTTGGTCAA GTTCACGCTG TCTGAGATNC AAGAGGGTGA TGCAGATGCT
                                                                      420
GCTTAACGGC CTCTTTGGCC CTCGAGACA
                                                                      449
(2) INFORMATION FOR SEQ ID NO:93:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 493 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:
GTCGACAAAA CATGGAGTTG TTCCTTTGGC CACATATATG CGAATCTATA AGAAAGGTGA
                                                                        60
TATTGTAGAC ATCAAGGGAA TGGGTACTGT TCAAAAAGGA ATGCCCCACA AGTGTTACCA
                                                                       120
TGGCAAAACT GGAAGAGTCT ACAATGTTAC CCAGCATGCT GTTGGCATTG TTGTAAACAA
                                                                       180
ACAAGTTAAG GGCAAGATTC TTGCCAAGAG AATTAATGTG CGTATTGAGC ACATTAAGCA
CTCTAAGAGC CGAGATAGCT TCCTGAAACG TGTGAAGGAA AATGATCAGA AAAAGAAAGA
                                                                       300
AGCCAAAGAG AAAGGTACCT GGGTTCAACT AAAGCGCCAG CCTGCTCCAC CCAGAGAAGC
                                                                       360
ACACTTTGTG AGAACCAATG GGAAGGAGCC TGAGCTGCTG GAACCTATTC CCTATGAATT
                                                                       420
                                    125
```

CATGGCACAA TAGGTGTTAA AAAAAAAAA TAAAGGACCT CTGGGGTCAA CGGCCTCTTT GGCCCTCGAG ACA	480 493
(2) INFORMATION FOR SEQ ID NO:94:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 437 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:	
GTCGACGAGG GGGTCATGGY AGGCAGGGGC AGGTGCGTCA GAGATGGAGC GCAGGTCCTG CATGGAGAAG CTCCGCAGCC TGCCGGCCAG CGCCCCTGA CTCTTGGTGG CAGCCTGCAC AGCAGCGAG GCGCAATGT TGAGGCCCCG CTTCCCGAAG CTGAGCACGG TCTCGTAGCT GCGCTCCTTG GCCTGCACGA TGTACGGGTC GATCTCCTTC TCATGGCGGG ACAGGGACGG GTGGACAAAC TTGCGGTAAA GCAGGCTGGC GCCCTTGGTG TAGGGTGAGA GCAGCCACAG CACGAAGGCC ATCTTGATCT CATAGTAGAA AGGGAACCAG GAGATAAAAA TGTCTGTAAC GATCTCTGCT GCCATGAAGA GTGCARCMAA CTATCCAGTA CATCATCCAG TGGACGGCCT CTTTGGCCCT CGAGACA	60 120 180 240 300 360 420 437
(2) INFORMATION FOR SEQ ID NO:95:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 493 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:	
GTCNACCGCC CTTCTTGTCT CCTCCTCAGT NGTACACCTG TGTGGTCTCC ACCACCTCAG ACTTNCTCCG CCCCTTTCAG TNGGAAGAAG GNGCAGGCCC GTCTCGGGGT CCTCCACGCA CCGNTCCAGA AGTTGCCTGT ACGTGAGGTT CTCATGCGTG TTGGGGTNAA AGAAGCCCTT GGTGTCGTCG CTGGGGTCCG CCGGGACGCG GKTCATCTCC TCACTGAAGT AGCCCCGCTG GTAGRSCACG TCCACAGACA CGCGGTGGTT GTGYACGGGG TCGATGATRC CGCCCGTGGC GATCTGGGCC TCCAGNAGGN GGATNCCGTG CTGCNGGAGA ACCAGNCCCT TCTNNATGTC CTGGAAGAGA GAGATGGTCC CCCCCGAGTA GGGGTCTCTG TANCCGGTGA CGNCCTTCTC GACAGACAGC ATCTGCTCGT GAAGCTCGGG GCCCACCACG CCCGCCTTCA CGGCCTCTTT GGCCCTCGAG ACA	60 120 180 240 300 360 420 480 493
(2) INFORMATION FOR SEQ ID NO:96:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 571 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:	
GTTGACCCAC GTTAGTACGG TTGGATAGGA TATGCTCTCA TGGTAACGCG TCCAAGTTGG	60

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AATGGTCTTC CAGTCTCCAT GGNATCCACA TGCTACTGGC GTTAGTTCCA GATCTTGAGG
                                                                      120
AAGNTATCCC AGGACCCTGT CGCCACAGGC ATGNCATCGT CANTCACGCC CAGGCAGCTG
                                                                      180
ACGCGGTTGT CATGNCCAGN CAAGACAACT GCCCGGTCGG GTTTGNGTGC ATCCCAGACG
                                                                      240
TTGCAGTTGA AGTCGTCGTA CCCAGCAAGG AGGAGGSGSC CGCTCTTGGW GAAGGAGACA
                                                                      300
GAGKTGATCC CCCAGATGAT GTTGTCATGG GAGTAAGTCA TGAGCTCCYG GTCAGCACGA
                                                                      360
AGGTCAAACA GCCTGCNGGT GGCGTCGTCT GAGCCAGTGC CAAATGCATT GCCATTTGGA
                                                                      420
AAGAANCAAA TGNCATTGAT GTCAGACTCG TGCCCAGTGA AGGTCTNCCG GCACATGCCT
                                                                      480
TCTCGCACAT CCCAGAGTTT GTCTGAAGCA TCACAAGCAC CAGAGACGAA CAGTCTGGTG
                                                                      540
TCAGTCGACG GCCTCTTTGG CCCTCGAGAC A
```

- (2) INFORMATION FOR SEQ ID NO:97:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 526 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear

  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

```
GTCGACGTAC CACCAGCAAC CATCAATCCC GTCTCCTCT GCCTCCTCT CTGCAATCCA 60
CCCCGCCACG ACTATCGCCA TGGCAGCCCT GATCGCAGAG AACTTCCGCT TCCTGTCACT 120
TTTCTTCAAG AGCAAGGATG TGATGATTTT CAACGGCCTG GTGGCACTGG GCACGGTGGG 180
CAGCCAGGAG CTGTTCTCTG TGGTGGCCTT CCACTGCCC TGCTCCCCGC CCCGGAACTA 240
CCTCAACAAC CACACCTGGA ACCTCGTGCC CGCCCTGGTG CTCTTCATCA TTGGCATCAT 300
CCTCAACAAC CACACCTGGA ACCTCGTGCC CGAGTGCCAG CACCGGAAGGA CCAAGAACTG 360
CTCCGCCGCC CCCACCTTCC TCCTTCTAAG CTCCATCCTG GGACGTGCGG CTGTGGCCCC 420
TGTCACCTGG TCTGTCATCT CCCTGCTGCG TGGTGAGGCT TATGTCTTGG CTCTCAGTGA 480
GTTCGTGGAC CCTTCCTCAC TCACGGCCTC TTTGGCCCTC GAGACA 526
```

- (2) INFORMATION FOR SEQ ID NO:98:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 520 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

- (2) INFORMATION FOR SEO ID NO:99:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 501 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GAATTCGGCC AAAGAGGCCG	TTGACGGGGC	TGGAGGAGGA	AGAAGAGGTG	GATCCCCGGA	60
TCCAGGGAGA ACTGGAGAAG	TTAAATCAGT	CCACGGATGA	TATCAACAGA	CGGGAGACTG	120
AACTTGAGGA TGCTCGTCAG	AAGTTCCGCT	CTGTTCTGGT	TGAAGCAACG	GTGAAACTGG	180
ATGAACTGGT GAAGAAAATT	GGCAAAGCTG	TGGAAGACTC	CAAGCCCTAC	TGGGATGCAC	240
GGAGGGTGGC GAGGCAGGCT	CAGCTGGAAG	CTCAGAAAGC	CACGCAGGAC	CTCCAGAGGG	300
CCACAGAGGT GCTCCGCGCC	GCCAAGGAGA	CCATCTCCCT	GGCCGAGCAG	CGGCTGCTGG	360
AGGATGACAA GCGGCAGTTC	GACTCCGCCT	GGCAGGAGAT	GCTGAATCTC	GCCACTCAGA	420
GGGTCATGGA GGCGGAGCAG	ACCAAGACCA	GGAGCGAGCT	GGTGCATAAG	GAGGTCGACG	480
GCCTCTTTGG CCCTCGAGAC	A				501

- (2) INFORMATION FOR SEQ ID NO:100:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 525 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GTCGACCGTG	TCCAGAGCCC	ACCTCCCTCA	CACCCACACA	GCGCTTCCTA	<b>AAGGCAGGGA</b>	60
CAGGAGCTGG	CCTCCCTCGC	CTGCTGGCAT	GGGGCTGGAC	ACAGGAGGAA	GTGGCGTGGG	120
GGCTGCCTGA	GGGGAGTGAG	GCGGCAGGAT	AGCTTCCCCA	GCAGGTCTCT	GGCTCAGGTC	180
CAGGTATCTC	CTCCTCCCCA	TACCTCTGCC	TCTCGCCTCC	GCTCAGAAAA	GCAGGTGCCC	240
TTAAGAGCCA	TCTCCACCCC	CATGTAAACT	GCACACAGGA	AGGGAGAGGC	CACTCCGACT	300
GCTCTGAGGT	CCAGGTAGGA	TGGTTTCCCC	CAGTGTCTGG	GTGGGGAGCA	AGGAACTCCA	360
GGGGCGACCT	TGTGCCACCG	CATCACCTTC	CTGCTCAGGG	AAGGGCCCG	TGCTGCCGCT	420
TGGAGGGTGC	CATGCCCAGA	GCCTCTGCCC	CTAGCCTCAG	CCTCGCCTAC	TCACTGGGGG	480
CTCCAGCACC	CCCGGCCGTC	AACGGCCTCT	TTGGCCCTCG	AGACA		525

- (2) INFORMATION FOR SEQ ID NO:101:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 425 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GTCGACGCGA	GTGGAGACCT	GTGGTAGAGA	AGCTCCTTTT	GATGTCCTAC	AGGCTTTCCA	60
CTGTGGTGTC	TCCAGTCATT	CAGAGCTCAT	CCCCTGAAGG	CCTCATCCCA	ATGGACACTG	120
ATTCAGAGTC	AGCAASCCGC	TTACAGATGA	TTCTGAATGA	GATTCANCCT	CGAGATACTA	180
ATGATTATTT	TAACCAAGCC	AAAATATTGA	AAGAACATGA	TAGCTTTGAT	ATGAAGGACT	240
TGAATGCTAG	TGTGGTGAAT	ATTGATACTT	CTACAGAAAT	CAAAGGTAAA	GAAGTAAAAA	300
	AACTGCGCAG					360
CTTTACTTTT	AGGCATGTTG	TGCCAGCTTC	TGCCCATGTC	AACGGCCTCT	TTGGCCCTCG	420
AGACA						425

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(2) INFORMATION FOR SEQ ID NO:102:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 462 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:
GGGACGTAAT CAACCCAAGC TTATGACCCG CACTTACTGG GAANTCNTCG TTCATGGGGA
                                                                      60
AGAANTGCAA TCCCCGATCC GCCATCACGA ATGGGGGGCA CCGGGTTANC CGCGCCTCCC
                                                                      120
GGCGTAGGGT AGNCACACNC TGANNCAGTC AGTGTATCGC GCGTGCATCN CCGGACATCT
                                                                      180
AAGGGCATCA CAGACCTGTT NTTGNTCAAT CTCGGGTGGN TGNNCGCCAC TTGTCNCTCT
                                                                      240
AAGAANATGG GGGACGCCGC CCNCTCGGGG GTNGCGTAAC TAGNTAGNAT NCCAGAGTCT
CGTTCGTTAT CGGAAGTAAC CAGACANATC GCTCCCCCAN CTAAGANNGG CCATNCACCA
                                                                      360
CCACCCACGG AATCGAGANA GAGCTATCAA TCTGTTGTTA GGACATGCCC GGCTTGCTTG
                                                                      420
GTCATCATCT TGGTGTACNC GACCTCTTTG NCCCTCGAGA CA
                                                                      462
(2) INFORMATION FOR SEQ ID NO:103:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 446 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:
GTCGACAGAA ATCATTATTC TTTATTTGCA GNCATTCCAC CCCACCTATG TTTTCTTCTC
CTTCCTTCTT CTCTGTCAGG AGAGTTCTTG TCATGCTGAG CTTCTTCATT GTATGGCATT
                                                                      120
TATATTTTAG CACTGTTTTA TTATTGCCTT CTGTATCAGC ATGTTCAACA TTTTCTTCAA.
                                                                      180
ATATAACACA GGTCCCTAGA GTGTCTTCAT ACTCCCCAGC AAAGACACAG CTGTCCACTT
                                                                      240
GCAGAATGGG CCTCTCAGTG TCAATGCCCA AAACCTTGCA TTTATTTTCA CATTTTGAGA
                                                                      300
GGAAGTCTGA ATCAATAATT CCTGATAATT CCACCAGAAC CAACTGCTCC TCCTCTTCCT
                                                                      360
CGTCTTCTCC GTCCTCTGGA CTCCGCTCGT CCGCCGCCGC CGCCATGGTC CCGCGGCGGT
                                                                      420
TGACGGCCTC TTTGGCCCTC GAGACA
                                                                      446
(2) INFORMATION FOR SEQ ID NO:104:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 466 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:
GANTTCCAGT GAAGTTGCCT TTTTGCCNNC CCTAGNCATC CAACCTNTCN AAAACCAAGT
ANACNAGGCT GATTCTGGAA GTTCTTGAGG AAAAAGCAAG CTTTACAACC AAAATACCCA
                                                                      120
GATGCTGTGN CCACATGGCT AAACCCTTGA CCCATCTCAG AAGCAGAATC TCCTANCCCC
                                                                      180
ACAGAGTGCT GTGTCCTCTG AAGAAACCAA TGACTTTAAA CAAGAGACCC TNCCAAGTAA
                                                                     240
GTCCANCGAA AGCCATGACC ACATGGATGA TATGGATGAT GAAGATGATG ATGACCATGT
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GGACAGCCAG	GACTCCATTG	ACTCGANCGA	CTCTGATGAT	GTAGATGACA	CTGATGATTC	360
TCACCAGTCT	GATGAGTCTC	ACCATTCTGA	TGAATCTGAT	GAACCGGTCA	CTGATTTTCC	420
CACGGACCTG	CCANCAACGT	CGACGNCCTC	TTTGNCCCTC	GAGACA		466

- (2) INFORMATION FOR SEQ ID NO:105:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 568 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GTCGACAGCG ACCGCTCCTC	CCTTCCTTCC	TTGAATCAGA	GCACGGTAGA	AAGCTGCTGC	60
TCTATGCCGA AGTGTTCGGA	AATTCTTGGC	AGCTGCATAG	ACCGCGGGGC	TGTCCCCTAA	120
CCTTTGCTCT TGTCGCCTCC	TCCACCAGGA	GGGCCCCCCT	CCCTGTACCC	CAGCTTCCCA	180
CAGAGCTGCA GGCACAGCTT	GGCTGCCTCC	CGCTTCCAGA	CCCCTATCTC	CATCAGGTGG	240
GCCTGAGGCG GGGCTGACTC	TTTCTTTAGG	CCCCTCACAG	GGACTAGAGC	AGAATGGCAC	300
TCAGTAAGCA GGGGTGACAA	CTAGAGGAAT	GGCAGGGTGT	GTTCAGCTGG	GAGAACAGTT	360
ACCAGAGACG CTGTGATTCT	TCAGGTGTGA	GGGCAACTGT	TACAAGACTT	AAGTAGCAAC	420
AACAACCATG GTAGACGCTG	CCTTCGATTG	TGCCCTTGGG	AGTCCCAGGC	CTGGCACCAG	480
GCCCTACTCA TCCTTCATTT	CTTTTTCTTT	TCTTTTGTTT	TTTGTTTTTT	GGGTTTTTTG	540
GTCAACGGCC TCTTTGGCCC	TCGAGACA				568

- (2) INFORMATION FOR SEQ ID NO:106:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 475 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GATTCANTTT	GGATATCAAG	TTGNCNCCCC	CNTAGTAACT	CAGTTTCTGT	TATTCTTGTT	60
CTCANCTTCC	CNATAAAAAC	ACTTGTTCGT	GGCTNTTGCC	ANNTTGATTC	TGTGAAGTAG	120
GCAGGAGCAG	GGATTAATTN	ATANAGTATT	CCTGTTCTGA	NCGCAACCAG	AAAAGTCACT	180
GTATAAACTT	GACTTAAAAT	AGTATCTNTC	TCTTTTCATG	TATANTCAGG	TGGGGGGGNA	240
AAAATCTCTT	TAATTGTAAC	CTGAANTCAA	GCTGTACCCC	NCCATGGTCC	TACACTCTAG	300
AGCTAATCTG	GNTGGGCAGA	AAGGCAGAAG	GATGGTATAT	TGTCCCATTG	TGCCTATAAT	360
GTATNTTAAA	NTGGTCATTC	CACCTTACCT	AATGGAAATT	CTTGCAGCTT	TCCTAGTGCT	420
CATCAGCGGT	TTTAGGAAGT	CACTAACGTC	GACGGCCTCT	TTGGCCCTCG	AGACA	475

- (2) INFORMATION FOR SEQ ID NO:107:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 470 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CCTGAGTTGT	GTCTAAGGNN	CNCAAGACAA	GTACCCAAGT	TTCCTCTAGN	TNTTCTCTTT	60
AAGCTTCTCN	AGTCATACAT	TTNCAAGCGT	CCTTTTGTCA	ACCATNCCAG	TCNANATACA	120
TTATTTGTCC	TCCAATGGNT	GACTTGCCAG	CATCTACGTG	NCCAATGAAT	ACTACATTTA	180
CATGCTCTTT	CTTAGGAGCA	CCTGGCGGTG	CAACCACAGA	CTTAGGTNTT	GGGATTTCCT	240
CTTCCTCCTC	CATCATTTCA	TGGGCACTTT	TCTCTGGCGG	CCTTCCATCT	CCCAAGGAAC	300
CACCCCCTGG	CTCTGCTTCA	CTTATTTCTT	CTTTGTGCTC	CCATGATTCT	TCTGGAGACA	360
TTTCTGTCTC	TCCACTTTCT	ACAATAGGTT	CTGAAAGTTC	CATGCTAACA	GCTGAATTTG	420
				CCTCGAGACA		470

## (2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 396 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GAATTCGGCC	AAAGAGGCCT	ACTCACAGTC	ATCAATTATA	GACCCCACAA	CATGCGCCCT	60
GAAGACAGAA	TGTTCCATAT	CAGAGCTGTG	ATCTTGAGAG	CCCTCTCCTT	GGCTTTCCTG	120
CTGAGTCTCC	GAGGAGCTGG	GGCCATCAAG	GCGGACCATG	TGTCAACTTA	TGCCGCGTTT	180
GTACAGACCC	ATAGACCAAC	AGGGGAGTTT	ATGTTTGAAT	TTGATGAAGA	TGAGCAGTTC	240
TATGTGGATC	TGGATAAAAA	GGAGACCGTC	TGGCATCTGG	AGGAGTTTGG	CCGAGCCTTT	300
TCCTTTGAGG	CTCAGGGCGG	GCTGGCTAAC	ATTGCTATAT	TGAACAACAA	CTTGAATACC	360
TTGATCCAGC	GTTCCAACCA	CACTCAGGCC	GTCGAG			396

### (2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 524 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GAATTCGGCC	AAAGAGGCCT	ACCCGATTGC	TAAATGGATT	ATGAAAGCAA	ATTGCTACTG	60
GGAGGTGATG	GTCAAAAGCA	AACTTAGATG	GTTTTCACAC	CATCTGTCAT	CATGACTCAA	120
AGGGAAATGC	TAGCCACACC	ATTTTCCAGT	GAAGCCACTG	CTTTACACAG	.\AGATACACA	180
TAGCTTCCTA	TTGTTATTTT	CTTTTCTAAT	TATGTACATT	TAGAAAAAA	ATACAACACT	240
GTGTTAAACA	GCAGGACAGC	TAGCAATGGA	ACATACAACA	CTATGCTGAA	AAACCACAAC	300
AGCTTGGTTA	AGCGGAGGAG	AGAAACAGAG	ATGGCCTTCA	TGGAGTGAAG	CTGTCAATGC	360
CTGCCATCTC	CTTAGTCTGT	GACGGATCTG	CACTCTGAGG	GCAGGCCTTC	TGAGCGCCGC	420
CACTTTGCCA	GGCGCTGCTT	AAACCATTTC	TGGGTCTCCT	CCTCGGAAAG	GCCTGCCTCG	480
GCCGCGATGA	GGCACAGCGT	GGTGGAATCC	GGGTGCTTGT	CGAG		524

#### (2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 377 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

				GGCATATGTA		60
AAACATTTAA	TTTGGGAAAC	TTTGATTCTT	GAAAGAGAAA	ACAAAAGCAT	GTGAATAAAC	120
				TCTTTGTAAA		180
				TGTTCCCCTT		240
				GCCCCTGAGC		300
GATTTCTTCT	GGGCTGGACT	TCCCCGTTCT	CCACCAGCAG	CTCCAGTATC	CCTGTTGAAT	360
TCTAGACCTG	CGTCGAG					377

- (2) INFORMATION FOR SEQ ID NO:111:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 392 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: CDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GAATTCGGCC	AAAGAGGCCT	AGCGGACAAG	TTTGAGAGAC	CTGGCCTTGG	CCAAAGCCCT	60
CGATTCGCTG	TGTCAGAAAA	ACTGAGGTGA	GAAGAGACCA	CCACCCTCTC	CACCACCCTC	120
TCAGTAGGAA	AGCGGGATCA	ACAGAGATCA	GAAGGACAGC	ACACTCACAC	CTGCACATGA	180
ACACACCATC	TATGTCAGGA	AATCCAGGGG	AAGGGGAAGA	GGGGTGGAGT	GGCTCCGCAG	240
GGCTGACCTG	ACAGGGGACA	GGAACACTCC	CCTAGACCCA	GGGAAGTCGC	CCCAAATCCA	300
AAGCTCTTGA	AAGGAGGTAT	GGCCTCGAAA	CTCCAGAAGC	CTCTTCTGCC	AACGCACCGA	360
GGACCTGCAC	CTCCCATTCA	GCACGCGTCG	AG			392

- (2) INFORMATION FOR SEQ ID NO:112:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 341 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CAATTCGGCC	AAAGAGGCCT	ACAGCATTTC	TACTCCTTCC	AAGAAGAGCA	GCAAAGCTGA	60
AGTAGCAGCA	GCAGCACCAG	CAGCAACAGC	AAAAAACAAA	CATGAGTGTG	AAGGGCATGG	120
CTATAGCCTT	GGCTGTGATA	TTGTGTGCTA	CAGTTGTTCA	AGGCTTCCCC	ATGTTCAAAA	180
GAGGACGCTG	TCTTTGCATA	GGCCCTGGGG	TAAAAGCAGT	GAAAGTGGCA	GATATTGAGA	240
AAGCCTCCAT	AATGTACCCA	AGTAACAACT	GTGACAAAAT	AGAAGTGATT	ATTACCCTGA	300
AAGAAAATAA	AGGACAACGA	TGCCTAAATC	CCAAAGTCGA	G		341

- (2) INFORMATION FOR SEQ ID NO:113:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 203 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

GAATTCGGCC	AAAGAGGCCT	AGCAGTAGCA	TGTGCAGCAA	CCAATCAAGA	TGGAGAACTA	60
TACCTGCACT						120
AATCAAGATG						180
CAATCCTCTC	TGCTCCCGTC	GAG				203

- (2) INFORMATION FOR SEQ ID NO:114:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 585 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GAATTCGGCC	AAAGAGGCCT	ATGAAGATCA	GCTATTAGAA	GAGAAAGATC	AGTTAAGTCC	60
	ATCAGCTTGA					120
TCGGAAACGA	TGAAATATAC	AAGTTATATC	TTGGCTTTTC	AGCTCTGCAT	CGTTTTGGGT	180
TCTCTTGGCT	GTTACTGCCA	GGACCCATAT	GTAAAAGAAG	CAGAAAACCT	TAAGAAATAT	240
TTTAATGCAG	GTCATTCAGA	TGTAGCGGAT	AATGGAACTC	TTTTCTTAGG	CATTTTGAAG	300
AATTGGAAAG	AGGAGAGTGA	CAGAAAAATA	ATGCAGAGCC	AAATTGTCTC	CTTTTACTTC	360
AAACTTTTTA	AAAACTTTAA	AGATGACCAG	AGCATCCAAA	AGAGTGTGGA	GACCATCAAG	420
GAAGACATGA	ATGTCAAGTT	TTTCAATAGC	<b>AACAAAAAGA</b>	<b>AACGAGATGA</b>	CTTCGAAAAG	480
CTGACTAATT	ATTCGGTAAC	TGACTTGAAT	GTCCAACGCA	<b>AAGCAATACA</b>	TGAACTCATC	540
CAAGTGATGG	CTGAACTGTC	GCCAGCAGCT	AAAACAGGGG	TCGAG		585

- (2) INFORMATION FOR SEQ ID NO:115:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 361 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GAATTCGGCC	AAAGAGGCCT	ACTGGCGGCC	GCGGAGACGC	AGAGTCTTGA	GCAGCGCGGC	60
AGGCACCATG	TTCCTGACTG	CGCTCCTCTG	GCGCGGCCGC	ATTCCCGGCC	GTCAGTGGAT	120
CGGGAAGCAC	CGGCGGCCGC	GGTTCGTGTC	GTTGCCCGCC	AAGCAGAACA	TGATCCGCCN	180
CCTGGAGATC	GAGGCGGAGA	ACCATTACTG	GCTGAGCATG	CCCTACATGA	CCCGGGAGCA	240
GGAGCGCGGC	CACGCCGCGG	TGCGCAGGAG	GGAGGCCTTC	GAGGCCATAA	AGGCGGCCGC	300
CACTTCCAAG	TTCCCCCCGC	ATAGATTCAT	TGCGGACCAG	CTCGACCATC	TCAATGTCGA	360
G						361

- (2) INFORMATION FOR SEQ ID NO:116:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 430 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

60	GTTGTTTGTG	ACTTGGAGAA	GTTATCAACC	AAACAAAATG	AAAGAGGCCT	GAATTCGGCC
120	TGCAAAAATG	AGCATCCTGC	CTAGAAGTAC	TTTAAGAGAA	CAGCAACTAT	ACAAACGATG
180	CTTTGTTCTG	ATGGCACAAA	GAAGTTGGAG	GCAAGAGCAA	CTTCTCATAT	ATTGTAATGG
240	CCTGTCAGTT	TGAGGATTGG	GAAGAACTTC	GGAATTAGCT	GAGCTCTCCT	GTATTTGCTG
300	TCTTCCTAAT	CTCATGAGAT	TGCAGAAAAG	TGAAATAGCC	TAGAAGGTTA	TCAGAGGTCA
360	TCTACTTCGT	AAGTCTCATC	GATATTGATG	AAACCTTCGA	GTTCTGCAAA	TTGGTATGTT
420	TATTGCTCAG	TGGCCAAGCT	GAAGTATTTC	ATATGGTAAT	TGAGTAAACA	ACCTCCATAA
430						GCATGTCGAG

- (2) INFORMATION FOR SEQ ID NO:117:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 373 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GAATTCGGCC	AAAGAGGCCT	AGAAGAAGAT	GATCCTAAAC	AAAGCTCTGA	TGCTGGGGGC	60
CCTCGCCCTG	ACCACCGTGA	TGAGCCCTTG	TGGAGGTGAA	GACATTGTGG	CTGACCACGT	120
TGCCTCTTAC	GGTGTAAACT	TGTACCAGTC	TTACGGTCCC	TCTGGCCAGT	TCACCCATGA	180
ATTTGATGGA	GACGAGGAGT	TCTATGTGGA	CCTGGAGAGG	AAGGAGACTG	TCTGGAAGTT	240
GCCTCTGTTC	CACAGACTTA	GATTTGACCC	GCAATTTGCA	CTGACAAACA	TCGCTGTGCT	300
AAAACATAAC	TTGAACATCC	TGATTAAACG	CTCCAACTCT	ACCGUTGCTA	CCAATGAGGT	360
TCCTGAGGTC	GAG					373

- (2) INFORMATION FOR SEQ ID NO:118:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 307 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GAATTCGGCC	AAAGAGGCCT	ACTTAACCAG	AATGACAGTC	TTTCCCCTAT	CTTCCTTCTT	60
TATTCTTATC	TTCTATCTTT	CCCTCCCAAA	CTCTTTCCCC	GACATAACAG	AAAACATGAA	120
GGAATTAAAG	GAGGCCAGGC	CGCGCAAAGA	TAACAGGCGT	CCAGATCTGG	AAATCTATAA	180
GCCTGGCCTT	TCTCGGCTAA	GGAACAAGCC	CAAAATCAAG	GAACCCCCTG	GGAGTGAGGA	240
ATTCAAAGAT	GAAATTGTTA	ATGACCGAGA	TTGCTCTGCT	GTTGAAAATG	GTACACAGCC	300
CGTCGAG						307

- (2) INFORMATION FOR SEQ ID NO:119:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 253 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

GGAGCTGCAC ATGGTACTTT	TGGAGAGCCT	GGTGGAAATC	ATTTTGGTTG	CTGTTCAGCA	60
TGTGGATTAT AGTCTTCGAT	GTGAGCAGGA	TCCAGAGAAG	AAAGCTTTTA	TCAGACAGAA	120
TGCATCCTTT TTATATGAAA	CAGTCCTCCC	TGTGGTGGAG	AAAAGGTTTG	AAGAAGGTGT	180
GGGGAAACCT GCCAAGCAAC	TCCAAGATCT	GAGGAATGCA	TCTAGACTTA	TTCGTGTGAA	240
TCCTGAAGTC GAG					253

- (2) INFORMATION FOR SEQ ID NO:120:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 428 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: CDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GAATTCGGCC AAAGAGGCCT					60
CTGCTTAGAC CCAGTACTCA					120
TTCCACTGGG AAAAGAAAAG	ATTGCAGATG	CAAGAAGAAA	GGAATTGGCA	AAGGATACTA	180
GAAGTGATCA CTTAACAGTT	GTGAATGCGT	TTGAGGGCTG	GGAAGAGGCT	AGGCGACGTG	240
GTTTCAGATA CGAAAAGGAC					300
TGCTGCATAA CATGAAAGGA					360
GTAGAAATCC TAAAGATCCA	GAATCTAATA	TAAATTCAGA	TAATGAGAAG	ATAATTAAAG	420
CTGTCGAG					428

- (2) INFORMATION FOR SEQ ID NO:121:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 526 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GAATTCGGCC	AAAGAGGCCT	ACAAGACGTC	ATTTCACAAA	GTGCGCCATT	CTGAGGATAT	60
GCAGTTTGCC	TTCTCTTATT	TTTATTATCT	CATGAGTGCA	GTGCAGCCAC	TGAATATATC	120
TCAAGTCTTT	GATGAAGTTG	ATACAGATCA	ATCTGGTGTC	TTGTCTGACA	GAGAAATCCG	180
AACACTGGCT	ACCAGAATTC	ACGAACTGCC	GTTAAGTTTG	CAGGATTTGA	CAGGTCTGGA	240
ACACATGCTA	ATAAATTGCT	CAAAAATGCT	TCCTGCTGAT	ATCACGCAGC	TAAATAATAT	300
TCCACCAACT	CAGGAATCCT	ACTATGATCC	CAACCTGCCA	CCGGTCACTA	AAAGTCTAGT	360
AACAAACTGT	AAACCAGTAA	CTGACAAAAT	CCACAAAGCA	TATAAGGACA	AAAACAAATA	420
TAGGTTTGAA	ATCATGGGAG	AAGAAGAAAT	CGCTTTTAAA	ATGATTCGTA	CCAACGTTTC	480
TCATGTGGTT	GGCCAGTTGG	<b>ATGACATAAG</b>	AAAAAACCCT	GTCGAG		526

- (2) INFORMATION FOR SEQ ID NO:122:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 340 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GGGTGGCAAT	ATGGACTTCC	TCTTTTCTGC	CANCCCANAC	CCATACATCG	GGATTCCTAT	60
AATACCTTCG	TTGGTCTCCC	TAACATGTAG	GTGGNGGNGG	GGAGATATAC	AATAGAACAG	120
ATACCAGACA	AGACATAATG	GGCTAAACAA	GACTACACCA	ATTACACTGC	CTCATTGATG	180
GTGGNACATA	ACGAGCTAAT	ACTGTAGCCC	TAGACTTGAT	AGCCATCATC	ATATCGAAGT	240
TTCACTACCC	TTTTTCCATT	TGCCATCTAT	TGAAGTAATA	ATAGGCGCAT	GCAACTTCTT	300
TTCTTTTTTT	TTCTTTTCTC	TCTCCCCCGT	TGTTGTCGAG			340

- (2) INFORMATION FOR SEQ ID NO:123:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 300 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GAATT	CGCC	AAAGAGGCCT	ACGTCCTTTT	AAATCTTAAT	GAAATATCAT	GGAATATTGT	60
ATGGT	TTCA	TATCGTTCTA	TATAATGCAA	ATGGTGAACT	GCTCTGTTCT	TTGCTTTCCT	120
GAAAGO	ATCC	ATCCGATCAG	TAGCTTTCCC	AATAGAAAAA	CCTGCAGCTC	CTTTTCCGTT	180
CCCCAC	AGCC	ACCAAGACAC	GGATCGATTT	CTTTCTTCCC	TCTTTCGCAG	TCATAGTGAA	240
AACGTT	TCTT	ACCTCAAGTA	TCCTGGTATC	AAAATCCTCA	TATGTTTCTC	CACAGTCGAG	300

- (2) INFORMATION FOR SEQ ID NO:124:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 373 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GAATTCGGCC	AAAGAGGCCT	ACCAGCTTTG	AGGTTGACCT	GTTTCTCTTT	GTCTGCCTTC	60
CCAAAACACC	AGCCCCCAGG	AAGACATTAA	GCAGCCTTAA	GCTTAAATTC	CTACTCCCTC	120
TTCCAAATTT	GGCTCACTTG	CCTTAGATCC	AAGGCAGGGA	AAGGAAAAGA	AGGGGGGTCT	180
CTGGCTTTAT	TACTCCCCTA	AGTCTTTACT	CTGACTTCCC	CAAACCCAGA	AAGATTTTCT	240
CCACAGTGTT	CATTTGAAAG	AGGAGTATTT	TGTCCCATTT	TCCCCTTCCT	CATTATCAAA	300
CAGCCCCAGT	CTTCCTTGTC	TCTGCTAAGA	AAGTAGAGGC	ATGATGATCT	GCCTCTCAAC	360
TGCCCTAGTC	GAG					373

- (2) INFORMATION FOR SEQ ID NO:125:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 644 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

# (2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 469 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GAATTCCCCC AAACAGGGG					
GAATTCGGCC AAAGAGGCCT	ACGITATACT	ATTAGATCCT	TTCATTATCA	ATCCCTTTTA	60
AAGGCAAGGA AACAGGTTCA	GCAAGATCAG	CTGACTTCTC	TGTGTAAGTG	GGACCTGAGA	120
TTTCAAACTT CACACCACA				CONCCIONON	120
TTTGAAAGTT GAGAGCAGCA	TGTTTTGCCC	ACTGAAACTC	ATCCTGCTGC	CAGTGTTACT	180
GGATTATTCC TTGGGCCTGA	<b>ልጥሮልር ጥጥር አ</b> አ	TOTTTOOCCO	CCTC > CCT > >	G1 CMCC	
	ATOACTIONA	101110000	CCIGAGCIAA	CAGTCCATGT	240
GGGTGATTCA GCTCTGATGG	GATGTGTTTT	CCAGAGCACA	CAACACAAAT	<b>CTATATECA</b> A	300
CATACACTICA ACROMOROS			or broncing of 1	GININITCAM	300
GATAGACTGG ACTCTGTCAC	CAGGAGAGCA	CGCCAAGGAC	GAATATGTGC	TATACTATTA	360
CTCCAATCTC AGTGTGCCTA	TTCCCCCCC	001011000			
CTCCAATCTC AGTGTGCCTA	TIGGGCGCTT	CCAGAACCGC	GTACACTTGA	TGGGGGACAA	420
CTTATGCAAT GATGGCTCTC	TCCTCCTCCA	AGATGTGCAA	CATCTCCAC		
	100100100	MONTOTOCAM	GWIGICGWG		469

- (2) INFORMATION FOR SEQ ID NO:127:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 435 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GAATTCGGCC	AAAGAGGCCT	AGAGGGGACT	CGCCGCCATC	TCAGGTCTCT	TGGCTTTGCC	60
AGGGCCCACC	GGAGAAAACT	GACGACCCGT	TTCTCTAATC	CTTATCCCAC	ACCAACCTTG	
TGCCTCCGGG	AGATCCACTC	TCCCACCTCC	3330003000	CARCOTATE	CTCCAAAAAA	120
COCOTCO	CTCCCTCCC	COOCACCIGG	MAACGCACGG	GAAGCCAAGC	CTCCAAAAAA	180
CACTCTACCC	CICGCICCGC	GIIGGGATTA	TCCGGAAGGA	ACTCCCAACG	GAGGTAGTAC	240
CACICIACCC	TCCGCACCTC	CTCCTGCATC	AGCCGGCCTG	AAGTCGCACC	CTCCTCCTCC	300
GGAGAAGTAG	AGAAATAAAT	TTCTCCCACC	CTAAACCAGT	CTTTGAGTGA	TTGCAGTATG	360
ACTCCATTTC	CCTGGTGCAT	TCATATAATA	GTTCACCTGG	TGAAAACAAT	GAAGATTATT	420
TACAATGCTA	CCCGG					435
		4				435

- (2) INFORMATION FOR SEQ ID NO:128:
  - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 base pairs

(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:	
GAATTCGGCC AAAGAGGCCT AACCAAGCAG AAGCTGTACC ACAAGAAGAT CTTCCGGACT	60
GCCATGCTGT TCCAGTTTGT GAACGTGCTG CTCCAGGTCC TGGTCCACAA GTCCCATGAT	120
CTTCTGCAGG AGGAGATTGG CATCGCCATC TACAACATGG CCTCAGTCGA G	171
(2) INFORMATION FOR SEQ ID NO:129:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTY: 372 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:	
GAATTCGGCC AAAGAGGCCT AGTCATGACT CCCCTGATTT GGCTCCTAAT GTCACTTATT	60
CCCTGCCCAG AACCAAAAGT GGTAAAGCCC CAGAAAGAGC CTCTAGCAAG ACTTCTCCAC	120
ATTGGAAGGA GTCAGGAGCC TCCCATTTGT CATTCCCAAA GAACAGCAAA TATGAGTATG	180
ACCCTGACAT CTCTCCTCCA CGAAAAAAGC AAGCAAAATC CCATTTTGGA GACAAGAAGC	240
AGCTTGATTC CAAAGGTGAC TGCCAGAAAG CAACTGATTC AGACCTTTCT TCTCCACGGC	300
ATAAACAAAG TCCAGGGCAC CAGGATTCTG ATTCAGATCT GTCACCTCCA CGGAATAGAC	360
CTAGACACCG GG	372
(2) INFORMATION FOR SEQ ID NO:130:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 378 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:	
GAATTCGGCC NAAGAGGCCT AGGGTGGGAC AAGAGAGTGA GACTAGAATA TAAATATCCG	60
TAAACAGCAT CTGAGCATTA GTCTTTAACA GGGAGGAGGA ACCACTGGTG TATATTAATT	120
TAGGACACAG GATCATTATA GGGGTNGGGC CAGCTGGTGT TAATGGCATG CAGGCATATG	180
TGATGCCAAC CATGAGGGCT GGAAGAACCA GAAGCCAAAG AAGAATATGA CCGCATCTAT	240
TCTAAAGCTA CTGTGGTGGT TTCTCATGCT TCAGAGTCTC GTAAGTCTCC TGGTTCCTGG	300
TGCTCAGGCC CGTGTAAACA CCATCTGATT TCTCATAGCT GGTTATAGCT GCCTTTCGCA	36
CTTGGATCTT CAGTCGAG	37
(2) INFORMATION FOR SEQ ID NO:131:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 414 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	

WO 98/45435	PCT/US98/06954
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:	-
GAATTCGGCC AAAGAGGCCT AGGTGCCGCG GTCCTGTCTT GCTGTGCCTG ( TCGGAACCAA TTCATTCCTG CACGGCCTGG GGCAGGAGCC CTTCGAGGGA (	CGGCAGGGGC 60 GCTCGGTCAC 120
TGTGTTGCAG GTCCTCGCCT AGAGACCTGC GAGATGGAGA AAGAGAGCAC	GAGGCGGCAC 180
AAAGGAAAGC CCCAGGAGCA GAGTCTTGCC CATCTCTCCC TCTGAGCATC	ICGGACATTG 240
GGACTGGATG TCTTTCGTCA CTGGAAAACC TCAGACTGCC GACGCTGCGG	GAAGAGTCAT 300
CCCCTCGAGA GCTCGAGGAC TCGAGCGGAG ACCAGGGCCG GTGCGGTCCC	ACACACCAGG 360
GATCCGAGGA TCCTTCGATG CTCTCGCAGG CCCAGTCCGC TACCGAGGGT (	CGAG 414
(2) INFORMATION FOR SEQ ID NO:132:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 295 base pairs	•
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(D) TOPOLOGI: Tinear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:	
AAGCGTGCTC GTGCCCGTAT TNCCNAGGGG NTCAGTCTGT NNCGCCCANA	GNCCAAGNCC 60
AAGCCCAAGN CCNAGNCCAA GGATCCANNC CAAGGCCCAG GCTGCAGCCC	CAGCTTCAGT 120
TCCAGCTCAG GCTCCCACAC GTACCCAGGC CCCCACAAAG GCTTCAGAGN I	AGATATCTCT 180
CCCAACATGA GGACAGAAGG ACTGGTGCGA CCCCCCACCC CCGCCCCTGG	
GCATGGGGCT GGGTCCTCCT GTGCTATTTG TACAAATAAA CCTGAGGCAG	rcgag 29!
(2) INFORMATION FOR SEQ ID NO:133:	
(i) SEQUENCE CHARACTERISTICS:	•
(A) LENGTH: 352 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(b) lorologi: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:	
ATGGACTICC TCTTTTCTGC CANCCCACAC CCATACATCG GGAGCCTATA	ATACCCTTCG 6
TTGNTCTCCC TAACATGTAG GTGGCGGAGG GGAGATATAC AATAGAACAG	
AGACATAATG GGCNNAACAA GACNACACCA ATTACNCTNC CTCATTGATG	GTGGNACATA 18
ACGAGCTAAT ACTGTANCCC TAGACNTGAT AGCCATCATC ATATCGAAGT	
TTTTTCCATT TGCCATCTAT TGAAGTAATA ATAGGCGCAT GCAACTTCTT	
TTCTTTTCTC TCTCCCCCGN TGTTGTCTCA CCATATCCGC AATGACGTCG	AG 35:

- (2) INFORMATION FOR SEQ ID NO:134:
  - (i) SEQUENCE CHARACTERISTICS:

    - (A) LENGTH: 350 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

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GAATTCGGCC AAAGAGGCCT ACGTTATCCG CGATGCGTTT CCTGGCAGCT ACATTCCTGC 60
TCCTGGCGCT CAGCACCGCT GCCCAGGCCG AACCGGTGCA GTTCAAGGAC TGCGGTTCTG 120
TGGATGGAGT TATAAAGGAA GTGAATGTGA GCCCATGCCC CACCCAACCC TGCCAGCTGA 180
GCAAAGGACA GTCTTACAGC GTCAATGTCA CCTTCACCAG CAATATTCAG TCTAAAAGCA 240
GCAAGGCCGT GGTGCATGGC ATCCTGATGG GCGTCCCAGT TCCCTTTCCC ATTCCTGAGC 300
CTGATGGTTG TAAGAGTGGA ATTAACTGCC CTATCCAAAA AGACGTCGAG 350
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- (2) INFORMATION FOR SEQ ID NO:135:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 254 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

GAATTCGGCC	AAAGAGGCCT	ATTGAATTCT	AGACCTGCGT	CGACCTCCCT	TCCAGCCCCC	60
AGAAAGCTCG	GTCACTTGAG	TGTTTTCTAG	AATCCTGGGG	TGCTCCCGGG	CCGCTCTCAG	120
AGAAGTGGCA	GGTŢTCACGT	TCAGCCGTGT	GGCGGATCGT	GTGGCTTCCA	AAGCCTTTTA	180
CAGCCCCCGC	CCCCCATCCC	GTGGTCTGTC	TGCAGGAACT	CTCCCGTCTG	TGAGAAGCCT	240
CTTTCCGAGT	CGAG					254

- (2) INFORMATION FOR SEQ ID NO:136:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 424 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GAATTCGGCC	AAAGAGGCCT	ACTAGAGGG	TCAGTGGCCC	CGCACGGTGG	GGTGGCCGCT	60
CAGGGCCTAG	GGAGCAGGTG	GGAGGGGCTT	GGAGGGCAGA	ACAGAGGGCC	TGGGGGCTGC	120
TCTGCTGGCC	ACCACTGCTT	TCTGGTTGAA	CCAGATAAGT	AGCTGGTGGT	GACGGCTGTG	180
GGCCCTGAGT	CGGGGGAGAA	GAGGCAGAGG	GAGCAGTGGG	CTGGGCTAGT	GGGGACATGA	240
GTGGGTGGTG	ATCATGCCTG	TGTCGGGGGA	GCTGAGGCAG	AGAGTGGGGC	AGCGAGCATC	300
CCCTGAGGGC	AGGAGGAGAG	GGGTGGGGAC	AGGGAAGGGT	CGGGGGTGGT	CCCAGCCCTG	360
AAGACAGGAG	TGGCGAGGGC	AGGTGTGGTC	TAGGTGCTTG	TCGAGGTGGA	CAACATGGGT	420
CGAG						424

- (2) INFORMATION FOR SEQ ID NO:137:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 705 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

	AAAGAGGCCT					60
	CGCCGGATCC					120
	AAGACGATGA					180
	TGAATATTGA					240
	TACTGCAGCA					300
	TTCAACAGAA					360
	ATGATATGGA					420
ACTGAAAGAA	AGGGTACCCA	GTGTGTTGAA	CAAATTCAAG	AGTTGGTTCT	ACCCTTCTGT	480
GAGAAGAACT	GTGAAAAGAG	CATGGTTGAA	CAGCTGGACA	AGTTTTTAAA	TGACACCACC	540
AAGCCTGTGG	GCCTTCTCCT	AAGTGAAAGA	TTCATTAATG	TCCCTCCACA	GATCGCTCTG	600
CCCATGTACC	AGCAGCTTCA	GAAAGAACTG	TCGGGGGCAC	ACAGAACCAA	TAAGCCATGT	660
GGGAAGTGCT	ACTTTTACCT	TCTGATTAGT	AAGACATTTG	TCGAG		705

- (2) INFORMATION FOR SEQ ID NO:138:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 350 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

GAATTCGGCC	AAAGAGGCCT	ACCCAGCTCA	GAATCTTGCT	GCTCGGCCCC	CAGGAGAGCA	6.0
ACAACACAAC	GGGAACGATG	TGGAAGGTGT	CAGCTCTGCT	CTTCGTTTTG	GGAAGCGCGT	60 120 180 240 300
CGCTCTGGGT	CCTGGCAGAA	GGAGCCAGCA	CAGGCCAGCC	AGAAGATGAC	ACTGAGACTA	180
CAGGTTTGGA	AGGCGGCGTT	GCCATGCCAG	GTGCCGAAGA	TGATGTGGTG	ACTCCAGGAA	240
CCAGCGAAGA	CCGCTATAAG	TCTGGCTTGA	CAACTCTGGT	GGCAACAAGT	GTCAACAGTG	300
TAACAGGCAT	TCGCATCGAG	GATCTGCCAA	CTTCAGAAAG	CCCAGTCGAG		350

- (2) INFORMATION FOR SEQ ID NO:139:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 450 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GAATTCGGCC	AAAGAGGCCT	AGTGGACAGG	AAGTAGAATT	TATTGGTGAG	TATTAAGAGG	60
GGGGCAGCAC	ATTGGAAGCC	CTCATGAGTG	CAGGGCCCGT	CACTTGTCCA	GAGGGCCACG	120
ACTGGGGATG	TACTTGACCC	CACAGCCATC	TGGGATGAGC	CGCTTTTCAG	CCACCATGTC	180
TTCAAATTCA	TCAGCATTGA	ACTTGGTGAA	GCCCCACTTC	TTTGAGATGT	GGATCTTCTG	240
GCGGCCAGGA	AACTTGAACT	TGGCCCTGCG	CAGGGCCTCA	ATCACATGCT	CCTTGTTCTG	300
CAGCTTGGTG	CGGATGGACA	TGATAACTTG	GCCAATGTGA	ACCCTGGCCA	CAGTGCCCTG	360
GGGCTTTCCA	AAGGCACCTC	GCATGCCTGT	TTGGAGCCTG	TCAGCCCCAG	CACAGGACAA	420
CATCTTGTTG	ATGCGGATGA	CGTGGTCGAG			•	450

- (2) INFORMATION FOR SEQ ID NO:140:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 585 base pairs

- (B) TYPE: nucleic acid (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GAATTCGGCC	AAAGAGGCCT	ATGAAGATCA	GCTATTAGAA	GAGAAAGATC	AGTTAAGTCC	60
TTTGGACCTG	ATCAGCTTGA	TACAAGAACT	ACTGATTTCA	ACTTCTTTGG	CTTAATTCTC	120
TCGGAAACGA	TGAAATATAC	AAGTTATATC	TTGGCTTTTC	AGCTCTGCAT	CGTTTTGGGT	180
TCTCTTGGCT	GTTACTGCCA	GGACCCATAT	GTAAAAGAAG	CAGAAAACCT	TAAGAAATAT	240
TTTAATGCAG	GTCATTCAGA	TGTAGCGGAT	AATGGAACTC	TTTTCTTAGG	CATTTTGAAG	300
AATTGGAAAG	AGGAGAGTGA	CAGAAAAATA	ATGCAGAGCC	AAATTGTCTC	CTTTTACTTC	360
AAACTTTTTA	AAAACTTTAA	AGATGACCAG	AGCATCCAAA	AGAGTGTGGA	GACCATCAAG	420
GAAGACATGA	ATGTCAAGTT	TTTCAATAGC	AACAAAAAGA	AACGAGATGA	CTTCGAAAAG	480
CTGACTAATT	ATTCGGTAAC	TGACTTGAAT	GTCCAACGCA	AAGCAATACA	TGAACTCATC	540
CAAGTGNTGG	CTGAACTGTC	GCCAGCAGCT	AAAACAGGGG	TCGAG		585

- (2) INFORMATION FOR SEQ ID NO:141:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 471 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GAATTCGGCC	AAAGAGGCCT	ATTGGAGTTT	GAGTATAGTA	AATTATGATC	CTTAAATATT	60
TGAGAGTCAG	GATGAAGCAG	ATCTGCTGTA	GACTTTTCAG	ATGAAATTGT	TCATTCTCGT	120
AACCTCCATA	TTTTCAGGAT	TTTTGAAGCT	GTTGACCTTT	TCATGTTGAT	TATTTTAAAT	180
TGTGTGAAAT	AGTATAAAAA	TCATTGGTGT	TCATTATTTG	CTITGCCTGA	GCTCAGATCA	240
AAATGTTTGA	AGAAAGGAAC	TTTATTTTTG	CAAGTTACGT	ACAGTTTTTA	TGCTTGAGAT	300
ATTTCAACAT	GTTATGTATA	TTGGAACTTC	TACAGCTTGA	TGCCTCCTGC	TTTTATAGCA	360
GTTTATGGGG	AGTCACTTGA	AAGAGCGTGT	GTACATGTAT	TTTTTTTCTN	GGCAAACATT	420
GAATGCAAAC	GTGTATTTTT	TTAATATAAA	TATATAACTT	CCTGCGTCGA	G	471

- (2) INFORMATION FOR SEQ ID NO:142:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 477 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

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GAATTCGGCC AAAGAGGCCT ATGTTTGGCA ACTGGGGTGA AGGGATTGCC CTCCCCCTGC 60
TGGGATCCCC CCAGCCCCTC CGGTCTGGCA GGAAGGGGGC AGCCTGCAAC CCCCAAGGGC 120
AGGTGTGGGG CTGCCAGATG CTCCAGGCAG GGGGCCAGAA GGGGTCACA AAGGCTTGCC 180
CTCCAGGGAG ATGACGGCAC TGCCCCCAG CTTCTCTGCC AGGGTGCAGC GGTCCTTGAC 240
CTCCTCGTAG CAGTTTGCTT GCAATTCATG CTTGATCCCT GTCAGCTTCT TCTTGATGGC 300
GTCCTTGGAG CTGGCATAAA TCATTTTGCT CTTAAGGGGG GCAGACTCGG GGGCCCAGAA 360
GATAAACACC AGATCCTCT TCTTGCTCTC CYTGGTCTCA TAGGTTGCAT CATAGAGGGC 420
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ATAGCGGCAG TCCTTATCTG GCAGCATCTT GACAAAGGTG GCGTAGGGAT CGTCGAG	477
(2) INFORMATION FOR SEQ ID NO:143:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 411 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:	
GAATTCGGCC CAAAGAGGCC YMAAAGATCA GCTATTAGAA GAGAAAGATC AGTTAAGTCC TTTGGACTTG ATCAGCTTGA TACAAGAACT ACTGATTTCA ACTTCTTTGG CTTAATTCTC TCGGAAACGA TGAAATATAC AAGTTATATC TTGGCTTTTC AGCTCTGCAT CGTTTTGGGT TCTCTTGGCT GTTACTGCCA GGACCCATAT GTAAAAGAAG CAGAAAACCT TAAGAAAATT TTTAATGCAG GTCATTCAGA TGTAGCGGAT AATGGAACTC TTTCTTAGG CATTTTGAAG AATTGGAAAG AGGAGAGTGA CAGAAAAATA ATGCAGAGCC AAATTGTCTC CTTTTACTTC AAAACTTTTA AAAACTTTAA AGATGACCAG AGCATCCAAA AGAGTGTCGA G	60 120 180 240 300 360 411
(2) INFORMATION FOR SEQ ID NO:144:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 427 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:	
GAATCGGCCC AAAGAGGCCT ACTGAAGATC AGCTATTAGA AGAGAAAGAT CAGTTAAGTC CTTTGGACCT GATCAGCTTG ATACAAGAAC TACTGATTC AACTTCTTTG GCTTAATTCT CTCGGAAACG ATGAAATATA CAAGTTATAT CTTGGCTTTT CAGCTCTGCA TCGTTTTGGG TTCTCTTGGC TGTTACTGCC AGGACCCATA TGTAAAAGAA GCAGAAAACC TTAAGAAATA TTTTAATGCA GGTCATTCAG ATGTAGCGGA TAATGGAACT CTTTTCTTAG GCATTTTGAA GAATTGGAAA GAGGAGAGTG ACAGAAAAAT AATGCAGAGC CAAATTGTCT CCTTTTACTT CAAACTTTTT AAAAACTTTA AAGATGACCA GAGCATCCAA AAGAGTGTGG AGACCATCAA GGTCGAG	60 120 180 240 300 360 420 427
(2) INFORMATION FOR SEQ ID NO:145:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 598 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:	
GAATTCGGCC AAAGAGGCCT AGAGAAGATA AAACTGGACA CTGGGGAGAC ACAACTTCAT GCTGCGTGGG ATCTCCCAGC TACCTGCAGT GGCCACCATG TCTTGGGTCC TGCTGCTGT ACTTTGGCTC ATTGTTCAAA CTCAAGCAAT AGCCATAAAG CAAACACCTG AATTAACGCT CCATGAAATA GTTTGTCCTA AAAAACTTCA CATTTTACAC AAAAGAGAGA TCAAGAACAA	60 120 180 240

CCAGACAGAA AAGCATGGCA AAGAGGAAAG GTATGAACCT GAAGTTCAAT ATCAGATGAT	300
CTTAAATGGA GAAGAAATCA TTCTCTCCCT ACAAAAAACC AAGCACCTCC TGGGGCCAGA	360
CTACACTGAA ACATTGTACT CACCCAGAGG AGAGGAAATT ACCACGAAAC CTGAGAACAT	420
GGAACACTGT TACTATAAAG GAAACATCCT AAATGAAAAG AATTCTGTTG CCAGCATCAG	480
TACTTGTGNC GGGTTGAGAG GATACTTCAC ACATCATCAC CAAAGATACC AGATAAAACC	540
TCTGAAAAGC ACAGACGAGA AAGAACATGC CGTCTTTACA TCTAACCAGG AGGTCGAG	598
(2) INFORMATION FOR SEQ ID NO:146:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 238 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:	
GAATTCGGCC AAAGAGGCCT AGAGCTAAGG CGAAGACCAA GACACGTGAC ATTCATGCTT	60
TGGTGTGGGG TCCAAAGCAC TCTTATTTAA CATAGATTCC AAACTTTTTA CACCCATGGG	120
GTCATATATA CTCTTTATTT TACCCTTCAT TATTTTAAAA ATCACAACAT CACCCATTGC	180
CCCCGTGTCC AAAGGAATCG CTTGTAATAA ATCAGCAGGT CTAGAATTCA ATCGGGAG	238
(2) INFORMATION FOR SEQ ID NO:147:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 304 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:	
GAATTCGGCC AAAGAGGCCT AGAGCTAAGG CGAAGACCAA GACACGTGAC ATTCATGCTT	60
TGGTGTGGGG TCCAAAGCAC TCTTATTTAA CATAGATTCC AAACTTTTTA CACCCATGGG	120
GTCATATATA CTCTTTATTT TACCCTTCAT TATTTTAAAA ATCACAACAT CACCCATTGC	180
CCCCGTGTCC AAAGGATTCG CTTGTAATAA ATCAGCAGGT CTAGAATTCA ATCGGGAGGT	240
TCTCCCTATA GTGAGTCGTA TTAATTTCAG AGGAGTATTT AGAAGAGAAG	300
CGAG	304
(2) INFORMATION FOR SEQ ID NO:148:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 397 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:	
	•
GAATTCGGCC AAAGAGGCCT ACGACAGTTG GTGTAAAGGA AAACTTCTGA GCTCCGTCAG	60
TTCACCTGGT ACATTGGAAT TAAAGTGCTT GGATGTTTTT CCCCCACTTT AAAAAAACTT	120
TTGAGGTTTT TTTTTTTTT TGTCTTTTAA AAACATCGTA ACATTAACAC ATGGCCGTTC	180

TCACAGTAAC GGTTCTGACC AGTCCTCCAG GTCGCACGTG GATGCGACAG GGGTGGGGAG GGAGGAGGAA GTGACTGTCC CACCTCTGCA GGACCATGGG AGTGGGCAAG GTGTTCTCCG GGGCGCACCC CTGAACCCAG GGGTGCTGCA GGACNTG 3
(2) INFORMATION FOR SEQ ID NO:149:
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 592 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:
GAATTCGGCC AAAGAGGCCT ATAAGAATTT AAGATGCATT TTTGCATTTG CTATATTTCT TTAAATTCTA GATAGTTATT TTCAAGTGTT GGTAAACATA AATCTTAGGC TTAGGAACCA 1: TTGGATTAGT AACAGCATTA TGCTAATCAA AACTTTAAAA AAATGAGTTC AAAATTGTTA 1: TAATGTAATT TTATAGATTT TCTTTTATCC TCAACCTGCA GAAGCCGGAA AGTGAGGCAC 2: ATAGCCCCAC ATAGGCAGAA ATTAAAGCCT AGGCAATAAC TTAGTGAAAA TGGAATTTTC 3:
AGAACATTCC ACTTCTTGTT TAGTACAATT TTATGGCCAT GGTGCTAGCT AATGGAAATG GCTAGTATAC TATTTATAGG CCAGCAATAT TTTGGTGAAT TTAAGCGAAA CTATGCTCAG TATCATTGAA ATGGGGGTGG GGTGGGCTTG AGACATGAAA TCAATCATAC AAAGTCAAAA ACTATTTTAA CCCAGGAATA AGTTAAATTC CTGTCACCCA GTCGAGGTTC TCCCTATAGT GAGTCGTATT AATTTCAGAG GAGTATTTAG AAGAGAAGCT GAAGCTGTCG AG 5
(2) INFORMATION FOR SEQ ID NO:150:
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 348 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:
GAATTCGGCC AAAGAGGCCT AGATGATGAT ATGTTTAACC ACCAAGTTCC TTATTTGTGG CTGATTTACT GCCTTTGTCA TCCTCTTCAA TCAAGTATTA AAGAAACAGT GGAGGCATAT 1 GAGGCAGCAT TAGGGGTGGC TATGACATGT GATATAGTAC AGAAGATATG GATGGATTAT 1 CTTGTCTTTG CAAATAATAG AGCTGCTGGA TCCAGAAACA AAGTTCAAGA ATTCAAATTT 2 TTTACTGATT TAGTGAATAG ATGTTTGGTT ACAGNCCCTG CCCGATACCC CATTCCTTTT 3 AGCAGNGCTG ATTACTGGTC CAACTATGAA TTTCATAATA GGGTCGAG 3
(2) INFORMATION FOR SEQ ID NO:151:
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 455 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

145

ACCTTCCTCT	GTCTGCCATG	GACCAACAAG	CAATATATGC	TGAGTTAAAC	TTACCCACAG	120
ACTCAGGCCC	AGAAAGTTCT	TCACCTTCAT	CTCTTCCTCG	GGATGTCTGT	CAGGGTTCAC	180
CTTGGCATCA	ATTTGCCCTG	AAACTTAGCT	GTGCTGGGAT	TATTCTCCTT	GTCTTGGTTG	240
TTACTGGGTT	GAGTGTTTCA	GTGACATCCT	TAATACAGAA	ATCATCAATA	GAAAAATGCA	300
GTGTGGACAT	TCAACAGAGC	AGGAATAAAA	CAACAGAGAG	ACCGGGTCTC	TTAAACTGCC	360
CAATATATTG	GCAGCAACTC	CGAGTCGAGG	TTCTCCCTAT	AGTGAGTCGT	ATTAATTTCA	420
GAGGAGTATT	TAGAAGAGAA	GCTGAAGCTG	TCGAG			455

- (2) INFORMATION FOR SEQ ID NO:152:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 348 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GAATTCGGCC	AAAGAGGCCT	AAAAATCTCT	TATTAAAGGT	AGAACCTCTG	CTAGCCAGAC	60
AACTATATTA	TTTTGCTCAA	CAAAACAGTG	GACATTTCCT	GAGGGGCTAC	GATTTACCAG	120
AACACATCAG	CAATCCAGAA	GATTACCACA	GATCTATCCG	CCATTCCTCT	ATTCAAGAAT	180
GAAAAATGTC	AAGATGAGTG	GTTTTCTTTT	TCCTTTTTTT	TTTTTTTTT	TTTTGATACG	240
GGGATACGGG	GTCTTGCTCT	GTCTCCCAGG	CTGGAGTGCA	GTGACACAAT	CTCAGCTCAC	300
TGTGACCTCC	GCCTCCTGGG	TTCAAGAGAC	TCTCCTGCCT	CAGTCGAG		348

- (2) INFORMATION FOR SEQ ID NO:153:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 360 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

GAATTCGGCC	AAAGAGGCCT	ACCTTAAAGC	CGTATACTTA	TGAATTTAAA	GTGGAAAATT	60
TTTTTGGTGG	CCCTGGCCCC	CTTGCCAGAT	TCCAGCTGGC	CGTCAGTGCT	CGCGTGTCTC	120
TCTGAAGAGG	CTCTGCGGTT	CTGGTCCCTG	TGCCTGAGCT	CCAGGTGCCG	CCAGACATTA	180
TACAACGTGA	AGGCTGAGAT	CTTTCCCCCT	TCGGGAATGG	AGTATTGCAG	AACAGGCTCC	240
CTCTGCTCCC	TGGAGGTTTT	GATCACGAGG	CTCTCAGACC	TCTTGGAGGT	GGATAAAGAT	300
GAAGCACTGA	CTGAATCTGA	TGAGCATTTT	TCGACAAAGC	TTATGTATGA	AGTTGTCGAG	360

- (2) INFORMATION FOR SEQ ID NO:154:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 582 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

```
CCCCTTCAAG TCCTGGGGTC CCAGCCTGTG CCCCCAGCTT CCTGCCCACC CAGCCCCGAG
                                                              120
CATTCTCACA CAGAGAAAGA ACAAGCAAGG GCTCCAGGGG GACAGGATGG GGCAGGGCAT
                                                              180
240
GGGTTTTTT TTTCTTCTT TTTTCTCCCC TTTACTCTTT GGGTGGTGTT GCTTTTCCTT
                                                              300
TCCTTTTCCC TTTGAGATTT TTTTGTTGTT GTTTCCTTTT TGTATTTTAC TGATATCACC
AGGATAGTTT ACTCTCCTTC TAGCTTTCTG CTTACCGCAC ACTGGATAAC ACACACATAC
                                                              420
ACACCCACAA AAATGCTCAT GAACCCAATC CGGAGAAGGT TCCAGCAGGT CCCCCACCCT
                                                              480
CCCCTCCTCC TCCTACTTCT CCTCTTGACA GCGAGGACAG GAGGGGGACA AGGGGACACC
                                                              540
TGGGCAGACC CGCCGGCTCT CCCCCCACCC CACCCCGTCG AG
                                                              582
```

- (2) INFORMATION FOR SEQ ID NO:155:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 263 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GAATTCGGCC	AAAGAGGCCT	AGAAATAAAA	CATTCTACAC	CGTCTCCTAC	CAAATATTCA	60
CTATCACCAA	GTAAAAGTTA	CAAGGTAAAC	AGGAAAGAAT	GGAATCATTT	CATTGTGAAA	120
TTGTTTCTGT	TCTAAGTGTT	TTAAATGCTG	TTTTGTTATT	TTTATTTTTT	TTTTCAGTAT	180
TCTCCCGAAA	CACCACCTCG	ATGGACAGAA	GATCGGAATT	CTTTACTGAA	TATGATTTGC	240
CAACAAGTAG	AGGCCATGTC	GAG				263

- (2) INFORMATION FOR SEQ ID NO:156:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 555 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

G/	ATTCGGCC	AAAGAGGCCT	AATTTCTCAG	CTCCAAGCAT	TAGGTAAACC	CACCAAGCAA	60
T	CTAGCCTG	TGATGGCGTT	TGACGTCAGC	TGCTTCTTTT	GGGTGGTGCT	GTTTTCTGCC	120
GC	CTGTAAAG	TCATCACCTC	CTGGGATCAG	ATGTGCATTG	AGAAAGAAGC	CAACAAAACA	180
T	ATAACTGTG	AAAATTTAGG	TCTCAGTGAA	ATCCCTGACA	CTCTACCAAA	CACAACAGAA	240
T.	TTTTGGAAT	TCAGCTTTAA	TTTTTTGCCT	ACAATTCACA	ATAGAACCTT	CAGCAGACTC	300
A.	<b>IGAATCTTA</b>	CCTTTTTGGA	TTTAACTAGG	TGCCAGATTA	ACTGGATACA	TGAAGACACT	360
T	TCAAAGCC	ATCATCAATT	AAGCACACTT	GTGTTANCTG	GAAATCCCCT	GATATTCATG	420
G	CAGAAACAT	CGCTTAATGG	GCCCAAGTCA	CTGAAGCATC	TTTTCTTAAT	CCANNCGGGA	480
A.	TATCCAATC	TCGAGTTTAT	TCCAGTGCAC	AATCTGGAAA	ACTTGGAAAG	CTTGTATCTT	540
G	BAAGCAACG	TCGAG					555

- (2) INFORMATION FOR SEQ ID NO:157:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 414 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

GAATTCGCCC	AAAGAGGCCT	AGATGATGAT	ATGTTTAACC	ACCAAGTTCC	TTATTTGTGG	6
CTGATTTACT	GCCTTTGTCA	TCCTCTTCAA	TCAAGTATTA	AAGAAACAGT	GGAGGCATAT	12
					GATGGATTAT	186
CTTGTCTTTG	CAAATAATAG	AGCTGCTGGA	TCCAGAAACA	AAGTTCAAGA	ATTCAAATTT	24
					CATTCCTTTT	
						300
				GGGTCGAGGT		360
GTGAGTCGTA	TTAATTTCAG	AGGAGTATTT	AGAAGAGAAG	CTGAAGCTGT	CGAG	414

- (2) INFORMATION FOR SEQ ID NO:158:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 590 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

GAATTCGGCC	NAAGAGGCCT	AAGCAGATGC	TGATCTCATT	ATGCTTGGCC	TTGCCACACA	60
TGAACCGAAC	TTTACCATTA	TTAGAGAAGA	ATTCAAACCA	AACAAGCCCA	AACCATGTGG	120
TCTTTGTAAT	CAGTTTGGAC	ATGAGGTCAA	AGATTGTGAA	GGTTTGCCAA	GAGAAAAGAA	180
GGGAAAGCAT	GATGAACTTG	CCGATAGTCT	TCCTTGTGCA	GAAGGAGAGT	TTATCTTCCT	240
TCGGCTTAAT	GTTCTTCGTG	AGTATTTGGA	AAGAGAACTC	ACAATGGCCA	GCCTACCATT	300
CACATTTGAT	GTTGAGAGGA	<b>GCATTGATGA</b>	CTGGGTTTTC	ATGTGCTTCT	TTGTGGGAAA	360
TGACTTCCTC	CCTCATTTGC	CATCGTTAGA	GATTAGGGAA	AATGCAATTG	ACCGTTTGGT	420
TAACATATAC	AAAAATGTGG	TACACAAAAC	TGGGGGTTAC	CTTACAGAAA	GTGGTTATGT	480
CAATCTGCAA	AGAGTACAGA	TGATCATGTT	AGCAGTTGGT	GAAGTTGAGG	ATAGCATTTT	540
TAAAAAGAGA	AAGGATGATG	AGGACAGTTT	TAGAAGACGA	CAGGGTCGAG		590

- (2) INFORMATION FOR SEQ ID NO:159:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 322 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

GAATTCGGCC	AAAGAGGCCT	AGACGGGCCT	CGGTCAGCAG	CACGGGGTGC	TCCTCGGGAG	60
CCACACGCAG	CTCATTGTAG	AAGGTGTGGT	GCCAGATTTT	CTCCATGTCG	TCCCAGTTGG	120
TGACGATGCC	GTGCTCGATG	GGGTACTTCA	GGGTGAGGAT	GCCTCTCTTG	CTCTGGGCCT	180
CGTCGCCCAC	ATAGGAATCC	TTCTGACCCA	TGCCCACCAT	CACGCCCTGG	TGCCTGGGGC	240
GCCCCACGAT	GGAGGGGAAG	ACGGCCCGGG	GGGCATCGTC	CCCCGCGAAG	CCGGCCTTGC	300
ACATGCCGGA	GCCGTTGTCG	AG				322

- (2) INFORMATION FOR SEQ ID NO:160:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 349 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

GGGTTGACAA	ATATGGACTT	CCTCTTTTCT	GCCNNCCCAA	ACCCATACAT	CGGGATTCCT	60
ATAATACCTT	CGTTGGTCTC	CCTAACATGT	AGGTGGCGGA	GGGGAGATAT	ACAATAGANC	120
AAGATACCAG	ACAAGACATA	ATGGGCTAAA	CAAGACTACA	CCAATTACAC	TGCCTCATTG	180
ATGGTGGTAC	ATAACGAACT	AATACTGTAG	CCCTAGACTT	GATAGCCATC	ATCATATCGA	240
AGTTTCACTA	CCCTTTTTCC	ATTTGCCATC	TATTGAAGTA	ATAATAGGCG	CATGCAACTT	300
CTTTTCTTTT	TTTTTCTTTT	CTCTCTCCCC	CGTTGTTGTC	TCACCATAG		349

- (2) INFORMATION FOR SEQ ID NO:161:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 688 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

GAATTCGGCC AAAGAGGCCT	ACTATAAGAG	AGATCCAGCT	TGCCTCCTCT	TGAGCAGTCA	60
GCAACAGGGT CCCGTCCTTG	ACACCTCAGC	CTCTACAGGA	CTGAGAAGAA	GTAAAACCGT	120
TTGCTGGGGC TGGCCTGACT	CACCAGCTGC	CATGCAGCAG	CCCTTCAATT	ACCCATATCC	180
CCAGATCTAC TGGGTGGACA	GCAGTGCCAG	CTCTCCCTGG	GCCCCTCCAG	GCACAGTTCT	240
TCCCTGTCCA ACCTCTGTGC	CCAGAAGGCC	TGGTCAAAGG	AGGCCACCAC	CACCACCGCC	300
ACCGCCACCA CTACCACCTC	CGCCGCCGCC	GCCACCACTG	CCTCCACTAC	CGCTGCCACC	360
CCTGAAGAAG AGAGGGAACC	ACAGCACAGG	CCTGTGTCTC	CTTGTGATGT	TTTTCATGGT	420
TCTGGTTGCC TTGGTAGGAT	TGGGCCTGGG	GATGTTTCAG	CTCTTCCACC	TACAGAAGGA	480
GCTGGCAGAA CTCCGAGAGT	CTACCAGCCA	GATGCACACA	GCATCATCTT	TGGAGAAGCA	540
AATAGGCCAC CCCAGTCCAC	CCCCTGAAAA	AAAGGAGCTG	AGGAAAGTGG	CCCATTTAAC	600
AGGCAAGTCC AACGTCGAGG	TTCTCCCTAT	AGTGAGTCGT	ATTAATTTCA	GAGGAGTATT	660
TAGAAGAGAA GCTGAAGCTG	TCGAGACA				688

- (2) INFORMATION FOR SEQ ID NO:162:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 180 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

GAATTCGGCC	AAAGAGGCCT	AATGATTTTG	ATAGGAAGAA	TGTCAGCCCA	GGTTCCCATG	60
AACATGACCA	TCACAGGTTG	TATGATGACG	TTTTACAGGA	CTACGCCGGC	TGTGCTGTTC	120
TGGCAGTGGA	TTAACCAGTC	CTTCAATGCC	GTCGTCAATT	ACACCAACAA	AAGTGTCGAG	180

- (2) INFORMATION FOR SEQ ID NO:163:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 600 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

GAATTCGGNC	AAAGAGGCCT	ACCACCTTCT	CTGCCAGAAG	ATACCATTTC	AACTTTAACA	6 C
CAGCATGATC	GAAACATACA	ACCAAACTTC	TCCCCGATCT	GCGGCCACTG	GACTGCCCAT	120
CAGCATGAAA	ATTTTTATGT	ATTTACTTAC	TGTTTTTCTT	ATCACCCAGA	TGATTGGGTC	180
AGCACTTTTT	GGTGTGTATC	TTCATAGAAG	GTTGGNCAAG	ATAGAAGATG	AAAGGRAWYY	240
TYMATKRARR	WTTTKKKWTY	MWKRAAACSR	WWMCARRRRW	KSMAMMMMRG	RRRRRRRWCC	300
YYWWYCYTWC	YTKRWSYTKK	KRRGRRRWTW	AAARCCMRKT	TKGWRGGSYT	TKKKRWRGRW	360
TTWTWWKKTW	AAMMAMRRRG	RRRMSRCGRR	RARRAAAMMR	CYTTTGNAAT	NCNCCNAGGT	420
GATCAGAATC	CTCACATTGC	GGCACATGTC	ATAAGTGAGG	CCANCAGTAA	AACAACATCT	480
GTGTTACAGT	GGGCTGANAA	AGGATACTAC	ACCATGAGCA	ACAACTTGGT	AACCCTGGAA	540
AATGGGAAAC	AGCTGNCCGT	TAAAAGACAA	<b>GGACTCTATT</b>	ATATCTATGC	CCAAGTCGAG	600

- (2) INFORMATION FOR SEQ ID NO:164:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 352 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

NCCTGTTTCA TTAATTAAAT	TTCCCGAAAG	AACCTGAGTC	ATTTTCCNAC	ATGAGAATAC	60
TAGAAGAATG ACCAAGACTT	GCGAGACGCG	ATTTNCCGGG	TGGTGCGAAC	AATAGANCGA	120
CCATGACCTT GAAGGTGAGA	CGCGCATAAC	CGCTAGAGTA	CTTTGAAGAG	GAAACANCAA	180
TAGGTTGCTA CCAGTATAAA	TAGACAGGTA	CATACAACAC	TGGAAATGGT	TGTCTGTTTG	240
AGTACGCTTT CAATTCATTT	GGGTGTGCAC	TTTATTATGT	TACAATATGG	AAGGGAACTT	300
TACACTTCTC CTATGCACAT	ATATTAATTA	AAGTCCAATG	CTAGTAGAGA	AG	352

- (2) INFORMATION FOR SEQ ID NO:165:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 387 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

GAATTCGGCC AAAGAGGCCT	AAAGAAGACA	AAGATGATAG	GCGGCACAGA	GATGACAAAA	60
GAGATTCCAA GAAAGAGAAA	AAACACAGTA	GAAGCAGAAG	CAGAGAAAGG	AAACACAGAA	120
GTAGGAGTCG AAGTAGAAAT	GCAGGGAAAC	GAAGTAGAAG	TAGAAGCAAA	GAGAAATCAA	180
GTAAACATAA AAATGAAAGT	AAAGAAAAAT	CAAATAAACG	AAGTCGAAGT	GGCAGTCAAG	240
GAAGAACTGA CAGTGTTGAA	AAATCAAAAA	AACGGGAACA	TAGTCCCAGC	AAAGAAAAT	300
CTAGAAAGCG TAGTAGAAGC	AAAGAACGTT	CCCACAAACG	AGATCACAGT	GATAGTAAGG	360
ACCAGTCAGA CAAACATGAC	CGTCGAG				387

- (2) INFORMATION FOR SEQ ID NO:166:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 518 base pairs
    - (B) TYPE: nucleic acid

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- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

GAATTCGGCC	AAAGAGGCCT	AAGGAAGTTG	GATGTTTTGA	TTTTACTGTT	TATAGATGTT	60
AGATTGTACA	GATTTGTCTG	TATTTCTCAC	CATATCTAAT	GATACTTTTT	TCATTAGATT	120
GGTCTTCAAG	AACAGTATTA	GTTATAATTA	TTTTGGTTAT	TCAGTATATA	GTTAGCTCTT	180
ACAGTTTAGC	TTTATTCACC	ATATTTATAC	TGTGGATTCA	CAGCGAGAGG	TAGAGGTTAT	240
TCCAGGAGAG	TTGATGACCT	TCATTTAAAG	TCCAACTAAA	ATCAGTAGTA	GAAACATAAG	300
AAAACATCTT	TGCAATATTT	ACTTTTGTTT	CTGTTTGCCG	TAAATAGTAA	CATTGTTTTT	360
TTTTATTTTG	TGTTTGTTAT	AAAACAGTTG	CATTCACAAT	ATTATTGGCC	TGAGATATTG	420
ATGATATTGT	GATGGTATGA	AAATGTGTAC	ATTCCCTGTG	CAACATCAGA	TTTGCAGGAA	480
AAATGAAGCA	CTTACTGAAA	TCGCTGGTAC	TCGTCGAG			518

- (2) INFORMATION FOR SEQ ID NO:167:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 393 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

GAATTCGGCC	AAAGAGGCCT	AGGACAAAAC	AAAACATTTT	CCTTTGGGTT	TTTTTTTTCT	60
TTCTTTTTTC	TCCCCTTTAC	TCTTTGGGTG	GTGTTGCTTT	TCCTTTCCTT	TTCCCTTTGA	120
GATTTTTTTG	TTGTTGTTTC	CTTTTTGTAT	TTTACTGATA	TCACCAGGAT	AGTTTACTCT	180
CCTTCTAGCT	TTCTGCTTAC	CGCACACTGG	ATAACACACA	CATACACACC	CACAAAAATG	240
CTCATGAACC	CAATCCGGAG	AAGGTTCCAG	CAGGTCCCCC	ACCCTCCCCT	CCTCCTCCTA	300
CTTCTCCTCT	TGACAGCGAG	GACAGGAGGG	GGACAAGGGG	ACACCTGGGC	AGACCCGCCG	360
GCTCTCCCCC	CACCCCACCC	CGGCACCCTC	GAG			393

- (2) INFORMATION FOR SEQ ID NO:168:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 421 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

GAATTCGGCC	AAAGAGGCCT	ACGAAGTTAC	AGAACTGAGA	TTCTCGGGTC	CCAGACACGC	60
ACCTATGTAC	CTCCCACTGG	TGTCCCTGCA	AAGCCTGGCG	CTTTTGACAT	CAATAATAAA	120
AGTGGCAGGG	CTGAGCAACA	CCTCAGGAGT	TACTCTGGAA	GGATGGAGGA	GTTATGTAAC	180
ACACGAGAGT	CAGGAGCCCT	GTGGAAGTGC	TTTTATTAGC	AGTAAGGCTG	ATCGTACAAA	240
AAATTCTCAG	AGCTTCATAG	GACAAGGTAG	TACAAGTATG	GATGATACAG	GACTGAGGAA	300
CGGGGGACGG	CTCAAAAGAA	ATCAACATCG	TCTGGGGCAT	CCAGGTCCCG	ATATTCCACA	360
ATGGCCCTTG	GGTCTCCACG	AACCATCCTG	TGAGGTGAGA	GGTACAGGAT	CAGACCTCGA	420
G						421

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 365 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:
TAGGAGATCT GGATGGCATC TACTTCGTAT GACTATTGCA GAGTGCCCAT GGAAGACGGG
                                                                       6.0
GATAAGCGCT GTAAGCTTCT GCTGGGGATA GGAATTCTGG TGCTCCTGAT CATCGTGATT
                                                                      120
CTGGGGGTGC CCTTGATTAT CTTCACCATC AAGGCCAACA GCGAGGCCTG CCGGGACGGC
                                                                      180
CTTCGGGGAG TGATGGAGTG TCGCAATGTC ACCCATCTCC TGCAACAAGA GCTGACCGAG
                                                                      240
GCCCAGAAGG GCTTTCAGGA TGTGGAGGCC CAGGCCGCCA CCTGCAACCA CACTGTGATG
                                                                       300
GCCCTAATGG CTTCCCCTGG ATGCAGAGAA GGCCCAAGGA CAAAAGAAAG TGGAAGNATC
                                                                      360
TCGAG
                                                                       365
(2) INFORMATION FOR SEQ ID NO:170:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 463 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:
GAATTCGGCC AAAGAGGCCT AACACAGGAA ACATTACAAT TGAACAATGC CTCAGCTATA
CATTTACATC AGATTATTGG GAGCCTATTT GTTCATCATT TCTCGTGTTC AAGGACAGAA
                                                                       120
TCTGGATAGT ATGCTTCATG GCACTGGGAT GAAATCAGAC TCCGACCAGA AAAAGTCAGA
                                                                       180
AAATGGAGTA ACCTTAGCAC CAGAGGATAC CTTGCCTTTT TTAAAGTGCT ATTGCTCAGG
                                                                       240
GCACTGTCCA GATGATGCTA TTAATAACAC ATGCATAACT AATGGACATT GCTTTGCCAT
                                                                       300
CATAGAAGAA GATGACCAGG GAGAAACCAC ATTAGCTTCA GGGTGTATGA AATATGAAGG
                                                                       360
ATCTGATTTT CAGTGCAAAG ATTCTCCAAA AGCCCAGCTA CGCCGGACAA TAGAATGTTG
                                                                       420
TCGGACCAAT TTATGTAACC AGTATTTGCA ACCCACGCTC GAG
                                                                       463
(2) INFORMATION FOR SEQ ID NO:171:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 353 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:
GAATTCGGCC AAAGAGGCCT ACTTAGCTTC AAATCCCTAC TCCTTCACTT ACTAATTTTG
TGATTTGGAA ATATCCGCGC AAGATGTTGA CGTTGCAGAC TTGGCTAGTG CAAGCCTTGT
TTATTTTCCT CACCACTGAA TCTACAGGTG AACTTCTAGA TCCATGTGGT TATATCAGTC
                                                                       180
CTGAATCTCC AGTTGTACAA CTTCATTCTA ATTTCACTGC AGTTTGTGTG CTAAAGGAAA
                                                                       240
AATGTATGGA TTATTTTCAT GTAAATGCTA ATTACATTGT CTGGAAAACA AACCATTTTA
                                                                       300
CTATTCCTAA GGAGCAATAT ACTATCATAA ACAGAACAGC ATCCACGCTC GAG
 (2) INFORMATION FOR SEQ ID NO:172:
```

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(i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 419 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:
GAATTCGGCC AAAGAGGCCT ACACTCGTCT CTTTTTTTCC CCATCTCATT GCTCCAAGAA
TTTTTTTCTT CTTACTCGCC AAAGTCAGGG TTCCCTCTGC CCGTCCCGTA TTAATATTTC
                                                                  120
CACTTTTGGA ACTACTGGCC TTTTCTTTT AAAGGAATTC AAGCAGGATA CGTTTTCTG
                                                                  180
TTGGGCATTG ACTAGATTGT TTGCAAAAGT TTCGCATCAA AAACAACAAC AACAAAAAAC
                                                                  240
CAAACAACTC TCCTTGATCT ATACTTTGAG AATTGTTGAT TTCTTTTTTT TATTCTGACT
                                                                  300
TTTAAAAACA ACTTTTTTT CCACTTTTTT AAAAAATGCA CTACTGTGTG CTGAGCGCTT
TTCTGATCCT GCATCTGGTC ACGGTCGCGC TCAGCCTGTC TACCTGCAAC ACACTCGAG
                                                                  419
(2) INFORMATION FOR SEQ ID NO:173:
     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 361 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:
GAATTCGGCC AAAGAGGCCT ACCCAGAAAC ATCCAATTCT CAAACTGAAG CTCGCACTCT
                                                                  60
CGCCTCCAGC ATGAAAGTCT CTGCCGCCCT TCTGTGCCTG CTGCTCATAG CAGCCACCTT
CATTCCCCAA GGGCTCGCTC AGCCAGATGC AATCAATGCC CCAGTCACCT GCTGCTATAA
                                                                  180
CTTCACCAAT AGGAAGATCT CAGTGCAGAG GCTCGCGAGC TATAGAAGAA TCACCAGCAG
                                                                  240
CAAGTGTCCC AAAGAAGCTG TGATCTTCAA GACCATTGTG GCCAAGGAGA TCTGTGCTGA
                                                                  300
CCCCAAGCAG AAGTGGGTTC AGGATTCCAT GGACCACCTG GACAAGCAAC CCAAACTCGA
                                                                  361
(2) INFORMATION FOR SEQ ID NO:174:
     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 368 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:
ACTCTTTGGG TGGTGTTGCT TTTCCTTTCC TTTTCCCTTT GAGATTTTTT TGTTGTTGTT
                                                                  120
TCCTTTTTGT ATTTTACTGA TATCACCAGG ATAGTTTACT CTCCTTCTAG CTTTCTGCTT
                                                                  180
ACCGCACACT GGATAACACA CACATACACA CCCACAAAAA TGCTCATGAA CCCAATCCGG
                                                                  240
AGAAGGTTCC AGCAGGTCCC CCACCCTCCC CTCCTCCTCC TACTTCTCCT CTTGACAGCG
                                                                  300
360
CCCGGCAC
                                                                  368
(2) INFORMATION FOR SEQ ID NO:175:
```

(i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 382 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

```
(ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:
GAATTCGGCC AAAGAGGCCT AGACTAACCC AGAAACATCC AATTCTCAAA CTGAAGCTCG
                                                                       60
CACTCTCGCC TCCAGCATGA AAGTCTCTGC CGCCCTTCTG TGCCTGCTGC TCATAGCAGC
CACCTTCATT CCCCAAGGGC TCGCTCAGCC AGATGCAATC AATGCCCCAG TCACCTGCTG
                                                                      180
CTATAACTTC ACCAATAGGA AGATCTCAGT GCAGAGGCTC GCGAGCTATA GAAGAATCAC
                                                                      240
CAGCAGCAAG TGTCCCAAAG AAGCTGTGAT CTTCAAGACC ATTGTGGCCA AGGAGATCTG
                                                                       300
TGCTGACCCC AAGCAGAAGT GGGTTCAGGA TTCCATGGAC CACCTGGACA AGCAAACCCA
                                                                      360
AACTCCGAAG ACTTCAC I'CG AG
                                                                      382
(2) INFORMATION FOR SEQ ID NO:176:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 496 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:
GAATTCGGCC AAAGAGGCCT AGTATAATAC TAAGTTGAGA TGATATCATT TACGGGGGAA
                                                                       60
GGCGCTTTGT GAAGTAGGCC TTATTTCTCT TGTCCTTTCG TACAGGGAGG AATTTGAAGT
AGATAGAAAC CGACCTGGAT TACTCCGGTC TGAACTCAGA TCACGTAGGA CTTTAATCGT
                                                                      180
TGAACAAACG AACCTTTAAT AGCGGCTGCA CCATCGGGAT GTCCTGATCC AACATCGAGG
TCGTAAACCC TATTGTTGAT ATGGACTCTA GAATAGGATT GCGCTGTTAT CCCTAGGGTA
                                                                      300
ACTTGTTCCG TTGGTCAAGT TATTGGATCA ATTGAGTATA GTAGTTCGCT TTGACTGGTG
AAGTCTTAGC ATGTACTGCT CGGAGGTTGG GTTCTGCTCC GAGGTCGCCC CAACCGAAAT
                                                                       420
TTTTAATGCA GGTTTGGTAG TTTAGGACCT GTGGGTTTGT TAGGTACTGT TTGCATTAAT
                                                                       480
AAATTAAAGC CTCGAG
                                                                       496
(2) INFORMATION FOR SEQ ID NO:177:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 390 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:
TINGGCCAAA GGGGCTTAGG ACAAAACAAA ACATTTTCCT TIGGGTTTNA NITTCTNTCT
                                                                        60
TTNTTCTCCC ATTTANTNNT GGGGTGGTGT TGCTTTTCCT TTCCTTTTCC CTTGGAGATT
                                                                       120
TINTINGTIGT NGTITICCTIT TIGITATINIA NIGATATCAC CAGGATAGIT TACTCTCNIT
                                                                       180
NTAGCTNTGT GCTTACCGCA CANTGGATAA CACACATA CACACCCACA AAAATGNTCA
TGAACCCAAT CCGGAGAAGG TTCCAGCAGG TCCCCCACCC TCCCCTCCTC CTCNTACTTC
                                                                       300
TCCTCTNGAC AGCGAGGACA GGAGGGGGAC AAGGGGACAC CTGGGCAGAC CCGCCGGCTN
                                                                       360
TTCCCCCCAC CCCACCCCGG CACCCTCGAG
                                                                       390
                                    154
```

- (2) INFORMATION FOR SEQ ID NO:178:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 356 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

GAATTCGGCC	AAAGAGCAAT	TCTCAAACTG	AAGCTCGCAC	TCTCGCCTCC	AGCATGAAAG	60
TCTCTGCCGC	CCTTCTGTGC	CTGCTGCTCA	TAGCAGCCAC	CTTCATTCCC	CAAGGGCTCG	120
CTCAGCCAGA	TGCAATCAAT	GCCCCAGTCA	CCTGCTGCTA	TAACTTCACC	AATAGGAAGA	180
TCTCAGTGCA	GAGGCTCGCG	AGCTATAGAA	GAATCACCAG	CAGCAAGTGT	CCCAAAGAAG	240
CTGTGATCTT	CAAGACCATT	GTGGCCAAGG	AGATCTGTGC	TGACCCCAAG	CAGAAGTGGG	300
TTCAGGATTC	CATGGACCAC	CTGGACAAGC	AAACCCAAAC	TCCGAAGACT	CTCGAG	356

- (2) INFORMATION FOR SEQ ID NO:179:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 480 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

GAATTCGGCC	AAAGAGGCCT	ACCGAGACTG	ACACACTGAA	CTCCACTTCC	TCCTCTTAAA	60
TTTATTTCTA	CTTAATAGCC	ACTCGTCTCT	TTTTTTCCCC	ATCTCATTGC	TCCAAGAATT	120
TTTTTCTTCT	TACTCGCCAA	AGTCAGGGTT	CCCTCTGCCC	GTCCCGTATT	AATATTTCCA	180
CTTTTGGAAC	TACTGGCCTT	TTCTTTTTAA	AGGAATTCAA	GCAGGATACG	TTTTTCTGTT	240
GGGCATTGAC	TAGATTGTTT	GCAAAAGTTT	CGCATCAAAA	ACAACAACAA	CAAAAAACCA	300
AACAACTCTC	CTTGATCTAT	ACTTTGAGAA	TTGTTGATTT	CTTTTTTTTA	TTCTGACTTT	360
TAAAAACAAC	TTTTTTTTCC	ACTTTTTTAA	AAAATGCACT	ACTGTGTGCT	GAGCGCTTTT	420
CTGATCCTGC	ATCTGGTCAC	GGTCGCGCTC	AGCCTGTCTA	CCTGCAGCAC	CACTCTCGAG	480

- (2) INFORMATION FOR SEQ ID NO:180:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 462 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

GAATTCGGCC	AAAGAGCCTA	ACACAGGAAA	CATTACAATT	GAACAATGCC	TCAGCTATAC	60
ATTTACATCA	GATTATTGGG	AGCCTATTTG	TTCATCATTT	CTCGTGTTCA	AGGACAGAAT	120
CTGGATAGTA	TGCTTCATGG	CACTGGGATG	AAATCAGACT	CCGACCAGAA	AAAGTCAGAA	180
AATGGAGTAA	CCTTAGCACC	AGAGGATACC	TTGCCTTTTT	TAAAGTGCTA	TTGCTCAGGG	240
CACTGTCCAG	ATGATGCTAT	TAATAACACA	TGCATAACTA	ATGGACATTG	CTTTGCCATC	300
ATAGAAGAAG	ATGACCAGGG	AGAAACCACA	TTAGCTTCAG	GGTGTATGAA	ATATGAAGGA	360
TCTGATTTTC	AGTGCAAAGA	TTCTCCAAAA	GCCCAGCTAC	GCCGGACAAT	AGAATGTTGT	420

462

CGGACCAATT TATGTAACCA GTATTTGCAA CCCACGCTCG AG

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 463 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:181: GAATTCGGCC AAAGAGGCCT AACACAGGAA ACATTACAAT TGAACAATGC CTCAGCTATA CATTTACATC AGATTATTGG GAGCCTATTT GTTCATCATT TCTCGTGTTC AAGGACAGAA 120 TCTGGATAGT ATGCTTCATG GCACTGGGAT GAAATCAGAC TCCGACCAGA AAAAGTCAGA 180 AAATGGAGTA ACCTTAGCAC CAGAGGATAC CTTGCCTTTT TTAAAGTGCT ATTGCTCAGG 240 GCACTGTCCA GATGATGCTA TTAATAACAC ATGCATAACT AATGGACATT GCTTTGCCAT 300 CATAGAAGAA GATGACCAGG GAGAAACCAC ATTAGCTTCA GGGTGTATGA AATATGAAGG 360 ATCTGATTTT CAGTGCAAAG ATTCTCCAAA AGCCCAGCTA CGCCGGACAA TAGAATGTTG 420 TCGGACCAAT TTATGTAACC AGTATTTGCA ACCCACGCTC GAG 463 (2) INFORMATION FOR SEQ ID NO:182: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 369 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:182: TACGAGAAGT CCTGTAAGAC GTAAATATTT TTAAAATTCA CTGAATTTTT GTCTTTCTCG 60 GTACCATAGA ACACCACAGC CAAGAGATCT CGATCACTGC TTATGATCTT ACTGATGTAC 120 ACACTTTGGA TACACTGGAT GCTCATGTCA AAAGGTGTCA ACTCATCTTC ATCTCCATCC 180 TCTTCCTCAC CATCACCTTC TTCTTCCTCC TCCTCTTCCT CCCCACCTTC TTCCTCTTCT 240 TCGTCTACCT CATTGTCAGC CTCCTGCTCC CCATTTTCCT CATTAGCATT CCCGTTAGCA 300 GGGGCGTCTC TTCCATTTTC TGCCTCTTCC ACAACTTCCT TCTTCTCCTT TAAGTCCTTG 360 GTGGTGAGT (2) INFORMATION FOR SEQ ID NO:183: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 309 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:183: GAATTCGGCC NAAGANGCCT ATGATCNTCT TCTTTGAAGA AACATGAAGT TACACTATGT 60 TGCTGTGCTT ACTCTANCCA TCCTGATGTT CCTGACATGG CTTCCACAAT CACTGAGCTG 120 TNACAAAGCA CTCTGTGCTA NTGATGTGAG CAAATGCCTC ATTCAGGAGC TCTGCCNGTG 180 CCGGCCGGGA GAAGCAATTG CTCCTGCTGT NAGGAGTGCA TGCTGTGTCT TGGGGCCCTT 240 156

TGGGACGANT GCTGTGACTG TGTTGGTATG TGTAATCCTC GAAATTATAG TGACACACCG

300 309

(2) INFORMATION FOR SEQ ID NO:184:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 334 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:	
GAATTCGGCC AAAGAGGCCT AATTCTGGTT TAAGATTCTA TCCATTTCTC ACTCTCAGAT CTGTTTGTTC CACCCTCTCC CCCTAAATAT TTGGATTTTA TATAGACCAG TAGGCTAAGG TAGGGAAGAC CACTGACAAG TATAAATTTA AGAGTTTACA AAACCAAGGA GGCCATCCAG CCCCTAGTTC TAAGCCATGT TCAGCACAGT GCCAACTTTG CCTTCCCTGG CTGTCCTTGC TTGCTTTCTG GTTGCTGTAA TTCTGAGGGG CAACCAGGCT TGCTGTAGAG AGGAGAGCCA GATGATGTGG AAGCCTAAGG CCCACACCCCT CGAG  (2) INFORMATION FOR SEQ ID NO:185:	60 120 180 240 300 334
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 522 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:	
TAACCAGCCT TGAAAAGCCC TTCCTCTGC TTGCTAGGAA GCTCATTGGA GACCCTAACT TGGAATTTGT TGCCATGCCT GCTCTCGCC CACCAGAAGT TGTCATGGAC CCAGCTTTGG CAGCACAGTA TGAGCACGAC TTAGAGGTTG CTCAGACAAC TGCTCTCCCG GATGAGGATG ATGACCTGTG AGAATGAAGC TGGAGCCCAG CGTCAGAAGT CTAGTTTTAT AGGCAGCTGT CCTGTGATGT CAGCGGTGCA GCGTTGTGC CACCTCATTA TTATCTAGCT AAGCGGAACA TGTGCTTCAT CTGTGGGATG CTGAAGGAGA TGAGTGGCCT TCGGAGTGAA TGTGCCAGTT TAAAAAAATAA CTTCATTGTT TGGACCTGCA TATTTAGCTG TTTTTGGAACG CAGTTGATTC CTTGAGTTTC ATATATAAGA CTGCTGCAGT TAGAATCAGA AT	120 180 240 300 360 420 480 522
(2) INFORMATION FOR SEQ ID NO:186:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 393 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:	
GAATTCGGCC AAAGAGGCCT AGGACAAAAC AAAACATTTT CCTTTGGGTT TTTTTTTCT TTCTTTTTTC TCCCCTTTAC TCTTTGGGTG GTGTTGCTTT TCCTTTCCTT	69 129 189

CCTTCTAGCT TTCTGCTTAC CGCACACTGG ATAACACACA CATACACACC CACAAAAATG CTCATGAACC CAATCCGGAG AAGGTTCCAG CAGGTCCCCC ACCCTCCCCT CCTCCTCCTA CTTCTCCTCT TGACAGCGAG GACAGGAGGG GGACAAGGGG ACACCTGGGC AGACCCGCCG GCTCTCCCCC CACCCCACCC CGGCACCCTC GAG	240 300 360 393
(2) INFORMATION FOR SEQ ID NO:187:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 349 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:	
GAATTCGGCC AAAGAGGCCT ATTCTAGGAC AAGAGCCAGG AAGAAACCAC CGGAAGGAAC CATCTCACTG TGTGTAAACA TGACTTCCAA GCTGGCGTG GCTCTCTTGG CAGCCTTCCT GATTTCTGCA GCTCTGTGT AAGGTGCAGT TTTGCCAAGG AGTGCTAAAG AACTTAGATG TCAGTGCATA AAGACATACT CCAAACCTTT CCACCCCAAA TTTATCAAAG AACTGAGAGT GATTGAGAGT GGACCACCA AGGAAAACTG GGTGCAGAGG GAGCTCGAG AGGACCTCTGT CTGGACCCCA AGGAAAACTG GGTGCAGAGG GAGCTCGAG	60 120 180 240 300 349
(2) INFORMATION FOR SEQ ID NO:188:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 366 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:	
GAATTCGGCC AAAGAGGCCT ACAAGAAAGC AAGCTCATCA TACTGGCTAG TGGTGGACCC CAAGCTTTAG TAAATATAAT GAGGACCTAT ACTTACGAAA AACTACTGTG GACCACAAGC AGAGTGCTGA AGGTGCTATC TGTCTGCTCT AGTAATAAAGC CGGCTATTGT AGAAGCTGGT GGAATGCAAG CTTTAGGACT TCACCTGACA GATCCAAGTC AACGTCTTGT TCAGAACTGT CTTTGGACTC TCAGGAATCT TCAGATGCT GCAACTAAAC AGGAAGGGAT GGAAGGTCTC CTTGGGACTC TTGTTCAGCT TCTGGGTTCA GATGATATAA ATGTGGTCAC CTGTGCAGAT CTCGAG	60 120 180 240 300 360 366
(2) INFORMATION FOR SEQ ID NO:189:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 421 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:	
TACAGCCACA TCTGGATACA CACACACAC CTTACATTCA TACCCAGAGA CTGGTGCACA GACACACAC CATCCCCGT CCTGCCAATC AGTCCCAGGA ACACACAGGT CTCTATCAAC ACCCAGAAAT TCTGACACCA CAAGCACAGG CCAACCTACA GCTAGAGGAT TAATGTCCAG	60 120 180

ACCCACAGGC TGGTGTGCGC ATGTCCTTCC ACGTGAATGT CACATGGGAG GACAGACTGC ATGGATTTT TTAATGACAC TATTTTATT ATTTTTTGAG ACAGAGTCTC ACTCTGTCGC CCAGGATGGA GTGCAGTGGC GTGATCTCGG CTCACTACAA CCTCCGCCTC CTGGGTTCAA GCGATTCTCG TGCCTCAGCA TCCCAAGTAC CTGGGATTAC AGGCGCATGC CACCACGTCC A	240 300 360 420 421
(2) INFORMATION FOR SEQ ID NO:190:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 383 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:	
GAATTCGGCC AAAGAGGCCT AGGGAGATCT GGATGGCATC TACTTCGTAT GACTATTGCA GAGTGCCCAT GGAAGACGGG GATAAGCGCT GTAAGCTTCT GCTGGGGATA GGAATTCTGG TGCTCCTGAT CATCGTGATT CTGGGGGGTC CCTTGATTAT CTTCACCATC AAGGCCAACA GCGAGGCCTG CCGGGACGGC CTTCGGGCAG TGATGGAGTG TCGCAATGTC ACCCATCTCC TGCAACAAGA GCTGACCGAG GCCCAGAAGG GCTTTCAGGA TGTGGAGGCC CAGGCCGCCA CCTGCAACCA CACTGTGATG GCCCTAATGG CTTCCCTGGA TGCAGAGAAG GCCCAAGGAC AAAAGAAAAA GGAGGAGCTC GAG  (2) INFORMATION FOR SEQ ID NO:191:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 428 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	60 120 180 240 300 360 383
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:	
GAATTCGGCC AAAGAGGCCT ACCCCAGTCC AGATCCAGGA CTGAGATCCC AGAACCATGA ACCTGGCCAT CAGCATCGCT CTCCTGCTAA CAGTCTTGCA GGTCTCCCGA GGGCAGAAGG TGACCAGCCT AACGGCCTGC CTAGTGGACC AGAGCCTTCG TCTGGACTGC CGCCATGAGA ATACCAGCAG TTCACCCATC CAGTACGAGT TCAGCCTGAC CCGTGAGACA AAGAAGCACG GCAAATACAA CATGAAGGTC CTCTACTTAT CCGCCTTCAC TAGCAAGGAC GAGGGCACCT ACACGTGTGC ACTCCACCAC TCTGGCCATT CCCCACCCAT CTCCTCCCAG AACGTCACCA GTCTCGAG	60 120 180 240 300 360 420
(2) INFORMATION FOR SEQ ID NO:192:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 305 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

(ii) MOLECULE TYPE: cDNA

·	
GAATTCGGCC AAAGAGGCCT AAAGAGCTCT CACTTCAGTC TTACTTACCC CACTGCTATT CCCTGTGGAG AAAGCCGGCT AATTGTTTTG ATAAGGCTAT CTGCCATTGT AGAATACCTT TCTCTAGTAG CTGAATGACA ATCAACTATA CGTTCCATAC TAAACCATGCC AGAGATAGGA CTTTTAGGCC TTGCTTTACA AAACTGGTTT TTAACAGCTG ACATGAATAT TTCCCGTTTC TATTTTCTTT TTTTTTTTT TTTTTTTTT TGAGACGGAG TCTCGCTCTA TCCCCCACGC TCGAG	60 120 180 240 300 305
(2) INFORMATION FOR SEQ ID NO:193:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 0 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:	
(2) INFORMATION FOR SEQ ID NO:194:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 516 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:	
GAATTCGGCC AAAGAGGCCT AANAGAAGAT GCCCCTGCTG ATCACTCTAA CCTGCTCCTC TTCTGGCTCT CAGGCTACTC CATTGCCACT CAAATCACCG GTCCAACAAC AGTGAATGGC TTGGAGCGGG GCTCCTTGAC CGTGCAGTGT GTTTACAGAT CAGGCTGGGA GACCTACTTG AAGTGGTGGT GTCGAGGAGC TATTTGGCGT GACTGCAAGA TCCTTGTTAA AACCAGTGGG TCAGAGCAGG AGGTGAAGAG GGACCGGGTG TCCATCAAGG ACAATCAGAA AAACCGCACG TTCACTGTGA CCATGGAGGA TCTCATGAAA ACTGATGCTG ACACTTACTG GTGTGGAATT GAGAAAACTG GAAATGACCT TGGGGTCACA GTTCAAGTGA CCATTGACCC AGCACCAGTC ACCCAAGAAG AAACTAGCAG CTCCCCCAACT CTGACCGGCC ACCACTTGGA CAACAGGCAC AAGCTCCTGA AGCTCAGTGT CCTCCCACCC CTCGAG	60 120 180 240 300 360 420 480 516
(2) INFORMATION FOR SEQ ID NO:195:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 466 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:	
CANTERCOCC ANACHOROUS ACCOCCUSTON DOSCUSTON DESCRIPTION ON CONTRACT ON CONTRAC	
GAATTCGGCC AAAGAGGCCT AGCGCCCTGA AGACAGAATG TTCCATATCA GAGCTGTGAT CTTGAGAGCC CTCTCCTTGG CTTTCCTGCT GAGTCTCCGA GGAGCTGGGG CCATCAAGGC GGACCATGTG TCAACTTATG CCGCGTTTGT ACAGACGCAT AGACCAACAG GGGAGTTTAT GTTTGAATTT GATGAAGATG AGATGTTCTA TGTGGATCTG GACAAGAAGG AGACCGTCTG	60 120 180 240

300

GCATCTGGAG GAGTTTGGCC AAGCCTTTTC CTTTGAGGCT CAGGGCGGGC TGGCTAACAT

CAACGATCCC CCTGAGGTGA CCGTGTTTCC CAAGGAGCCT GTGGAGCTGG GCCAGCCCAA CACCCTCATC TGCCACATTG ACAAGTTCTT CCTACCAGTG CTCGAG	420 466
(2) INFORMATION FOR SEQ ID NO:196:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 191 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:	
TAGGCAGAAT GGGACTCCAA GCCTGCCTCC TAGGGCTCTT TGCCCTCATC CTCTCTGGCA AATGCAGTTA CAGCCCGGAG CCCGACCAGC GGAGGACGCT GCCCCCAGGC TGGGTGTCCC TGGGCCGTGC GGACCCTGAG GAAGAGCTGA GTCTCACCTT TGCCCTGAGA CAGCAGAATG TGGATCGACG T	60 120 180 191
(2) INFORMATION FOR SEQ ID NO:197:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 614 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:  GAATTCGGCC AAAGAGGCCT AATGGATCTC ATGTGCAAGA AAATGAAGCA CTGTGGTTCT	60
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:  GAATTCGGCC AAAGAGGCCT AATGGATCTC ATGTGCAAGA AAATGAAGCA CTGTGGTTCT TCCTCCTGCT GGTGGCGGCT CCCAGATGGG TCCTGTCCCA GCTGCAGCTG CAGGAGTCGG	120
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:  GAATTCGGCC AAAGAGGCCT AATGGATCTC ATGTGCAAGA AAATGAAGCA CTGTGGTTCT TCCTCCTGCT GGTGGCGGCT CCCAGATGGG TCCTGTCCCA GCTGCAGCTG CAGGAGTCGG GCCCAGGACT GGTGAAGCCT TCGGAGACCC TGTCCCTCAC CTGCACTGTC TCTGGTGGCT	120 180
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:  GAATTCGGCC AAAGAGGCCT AATGGATCTC ATGTGCAAGA AAATGAAGCA CTGTGGTTCT TCCTCCTGCT GGTGGCGGCT CCCAGATGGG TCCTGTCCCA GCTGCAGCTG CAGGAGTCGG GCCCAGGACT GGTGAAGCCT TCGGAGACCC TGTCCCTCAC CTGCACTGTC TCTGGTGGCT CCATCAGCAG TAGTAGTTAC TACTGGGGCT GGATCCGCCA GCCCCCAGGG AAGGGGCTGG	120 180 240
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:  GAATTCGGCC AAAGAGGCCT AATGGATCTC ATGTGCAAGA AAATGAAGCA CTGTGGTTCT TCCTCCTGCT GGTGGCGGCT CCCAGATGGG TCCTGTCCCA GCTGCAGCTG CAGGAGTCGG GCCCAGGACT GGTGAAGCCT TCGGAGACCC TGTCCCTCAC CTGCACTGTC TCTGGTGGCT CCATCAGCAG TAGTAGTTAC TACTGGGGCT GGATCCGCCA GCCCCCAGGG AAGGGGCTGG AGTGGATTGG GAGTATCTAT TATAGTGGGA GCACCTACTA CAACCCGTCC CTCAAGAGTC	120 180 240 300
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:  GAATTCGGCC AAAGAGGCCT AATGGATCTC ATGTGCAAGA AAATGAAGCA CTGTGGTTCT TCCTCCTGCT GGTGGCGGCT CCCAGATGGG TCCTGTCCCA GCTGCAGCTG CAGGAGTCGG GCCCAGGACT GGTGAAGCCT TCGGAGACCC TGTCCCTCAC CTGCACTGTC TCTGGTGGCT CCATCAGCAG TAGTAGTTAC TACTGGGGCT GGATCCGCCA GCCCCCAGGG AAGGGGCTGG AGTGGATTGG GAGTATCTAT TATAGTGGGA GCACCTACTA CAACCCGTCC CTCAAGAGTC GAGTCACCAT ATCCGTAGAC ACGTCCAAGA ACCAGTTCTC CCTGAAGCTG AGCTCTGTGA	120 180 240 300 360
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:  GAATTCGGCC AAAGAGGCCT AATGGATCTC ATGTGCAAGA AAATGAAGCA CTGTGGTTCT TCCTCCTGCT GGTGGCGGCT CCCAGATGGG TCCTGTCCCA GCTGCAGCTG CAGGAGTCGG GCCCAGGACT GGTGAAGCCT TCGGAGACCC TGTCCCTCAC CTGCACTGTC TCTGGTGGCT CCATCAGCAG TAGTAGTTAC TACTGGGGCT GGATCCGCCA GCCCCCAGGG AAGGGGCTGG AGTGGATTGG GAGTATCTAT TATAGTGGGA GCACCTACTA CAACCCGTCC CTCAAGAGTC GAGTCACCAT ATCCGTAGAC ACGTCCAAGA ACCAGTTCTC CCTGAAGCTG AGCTCTGTGA CCGCCGCAGA CACGGCTGTG TATTACTGTG CGAGACATTC TGGGCGCAGC AGCTGGTTCA	120 180 240 300
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:  GAATTCGGCC AAAGAGGCCT AATGGATCTC ATGTGCAAGA AAATGAAGCA CTGTGGTTCT TCCTCCTGCT GGTGGCGGCT CCCAGATGGG TCCTGTCCCA GCTGCAGCTG CAGGAGTCGG GCCCAGGACT GGTGAAGCCT TCGGAGACCC TGTCCCTCAC CTGCACTGTC TCTGGTGGCT CCATCAGCAG TAGTAGTTAC TACTGGGGCT GGATCCGCCA GCCCCCAGGG AAGGGGCTGG AGTGGATTGG GAGTATCTAT TATAGTGGGA GCACCTACTA CAACCCGTCC CTCAAGAGTC GAGTCACCAT ATCCGTAGAC ACGTCCAAGA ACCAGTTCTC CCTGAAGCTG AGCTCTGTGA	120 180 240 300 360 420
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:  GAATTCGGCC AAAGAGGCCT AATGGATCTC ATGTGCAAGA AAATGAAGCA CTGTGGTTCT TCCTTCCTGCT GGTGGCGCT CCCAGATGGG TCCTGTCCCA GCTGCAGCTG CAGGAGTCGG GCCCAGGACT GGTGAAGCCT TCGGAGACCC TGTCCCTCAC CTGCACTGTC TCTGGTGGCT CCATCAGCAG TAGTAGTTAC TACTGGGGCT GGATCCGCCA GCCCCCAGGG AAGGGGCTGG AGTGGATTGG GAGTATCTAT TATAGTGGGA GCACCTACTA CAACCCGTCC CTCAAGAGTC GAGTCACCAT ATCCGTAGAC ACGTCCAAGA ACCAGTTCTC CCTGAAGCTG AGCTCTGTGA CCGCCGCAGA CACGGCTGTG TATTACTGTG CGAGACATTC TGGGCGCAGC AGCTGGTTCA CGTCCTACTG GGGCCAGGGA ACCCTGGTCA CCGTCTCCTC AGGGAGTGCA TCCGCCCCAA	120 180 240 300 360 420 480
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:  GAATTCGGCC AAAGAGGCCT AATGGATCTC ATGTGCAAGA AAATGAAGCA CTGTGGTTCT TCCTCCTGCT GGTGGCGGCT CCCAGATGGG TCCTGTCCCA GCTGCAGCTG CAGGAGTCGG GCCCAGGACT GGTGAAGCCT TCGGAGACCC TGTCCCTCAC CTGCACTGTC TCTGGTGGCT CCATCAGCAG TAGTAGTTAC TACTGGGGCT GGATCCGCCA GCCCCCAGGG AAGGGGTTGG AGTGGATTGG GAGTACTAT TATAGTGGGA GCACCTACTA CAACCCGTCC CTCAAGAGTC GAGTCACCAT ATCCGTAGAC ACGTCCCAAGA ACCAGTTCTC CCTGAAGCTG AGCTCTTGA CCGCCGCAGA CACGGCTGTG TATTACTGTG CGAGACATTC TGGGCGCAGC AGCTGGTTCA CGTCCTTACTG GGGCCAGGGA ACCCTGGTCA CCGTCTCCTC AGGGAGTGCA TCCGCCCCAA CCCTTTTCCC CCTCGTCTCN TGTGAGAATT CCCCCGTCGGA TACGAGCAGC GTGGCCGTTG	120 180 240 300 360 420 480 540
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:  GAATTCGGCC AAAGAGGCCT AATGGATCTC ATGTGCAAGA AAATGAAGCA CTGTGGTTCT TCCTCCTGCT GGTGGCGGCT CCCAGATGGG TCCTGTCCCA GCTGCAGCTG CAGGAGTCGG GCCCAGGACT GGTGAAGCCT TCGGAGACCC TGTCCCTCAC CTGCACTGTC TCTGGTGGCT CCATCAGCAG TAGTAGTTAC TACTGGGGCT GGATCCGCCA GCCCCCAGGG AAGGGGTTGG AGTGGATTGG GAGTATCTAT TATAGTGGGA GCACCTACTA CAACCCGTCC CTCAAGAGTC GAGTCACCAT ATCCGTAGAC ACGTCCAAGA ACCAGTTCTC CCTGAAGCTG AGCTCTGTGA CCGCCGCAGA CACGGCTGTG TATTACTGTG CGAGACATTC TGGGCGCAGC AGCTGGTTCA CGTCCTACTG GGGCCAGGGA ACCCTGGTCA CCGTCTCCTC AGGGAGTGCA TCCGCCCCAA CCCTTTTCCC CCTCGTCTCN TGTGAGAATT CCCCGTCGGA TACGAGCAGC GTGGCCGTTG GCTGCCTCGC ACAGGACTTC CTTCCCGACT CCATCACTTT CTCCTGGAAA TACAAGAACA	120 180 240 300 360 420 480 540
(XI) SEQUENCE DESCRIPTION: SEQ ID NO:197:  GAATTCGGCC AAAGAGGCCT AATGGATCTC ATGTGCAAGA AAATGAAGCA CTGTGGTTCT TCCTCCTGCT GGTGGCGGCT CCCAGATGGG TCCTGTCCCA GCTGCAGCTG CAGGAGTCGG GCCCAGGACT GGTGAAGCCT TCGGAGACCC TGTCCCTCAC CTGCACTGTC TCTGGTGGCT CCATCAGCAG TAGTAGTTAC TACTGGGGGT GGATCCGCCA GCCCCCAGGG AAGGGGCTGG AGTGGATTGG GAGTATCTAT TATAGTGGGA GCACCTACTA CAACCCGTCC CTCAAGAGTC GAGTCACCAT ATCCGTAGAC ACGTCCAAGA ACCAGTTCTC CCTGAAGCTG AGCTCTGTGA CCGCCCGCAGA CACGGCTGTG TATTACTGTG CGAGACATTC TGGGCGCAGG AGCTGGTTCA CGTCCTTACTG GGGCCAGGGA ACCCTGGTCA CCGTCCTCTC AGGGAGTGCA TCCGCCCCAA CCCTTTTCCC CCTCGTCTCN TGTGAGAATT CCCCGTCCGA TACGAGCAGC GTGGCCGTTG GCTGCCTCGC ACAGGACTTC CTTCCCGACT CCATCACTTT CTCCTGGAAA TACAAGAACA ACTCTGAACT CGAG	120 180 240 300 360 420 480 540
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:  GAATTCGGCC AAAGAGGCCT AATGGATCTC ATGTGCAAGA AAATGAAGCA CTGTGGTTCT TCCTCCTGCT GGTGGCGGCT CCCAGATGGG TCCTGTCCCA GCTGCAGCTG CAGGAGTCGG GCCCAGGACT GGTGAAGCCT TCGGAGACCC TGTCCCTCAC CTGCACTGTC TCTGGTGGCT CCATCAGCAG TAGTAGTTAC TACTGGGGCT GGATCCGCCA GCCCCCAGGG AAGGGGCTGG AGTGGATTGG GAGTATCTAT TATAGTGGGA GCACCTACTA CAACCCGTCC CTCAAGAGTC GAGTCACCAT ATCCGTAGAC ACGTCCAAGA ACCAGTTCTC CCTGAAGCTG AGCTCTGTGA CCGCCGCAGA CACGGCTGTG TATTACTGTG CGAGACATTC TGGGCGCAGC AGCTGGTTCA CGTCCTACTG GGGCCAGGGA ACCCTGGTCA CCGTCTCCTC AGGGAGTGCA TCCGCCCCAA CCCTTTTCCC CCTCGTCTCN TGTGAGAATT CCCCGTCGGA TACGAGCAGC GTGGCCGTTG GCTGCCTCGC ACAGGACTTC CTTCCCGACT CCATCACTTT CTCCTGGAAA TACAAGAACA ACTCTGAACT CGAG  (2) INFORMATION FOR SEQ ID NO:198:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 0 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	120 180 240 300 360 420 480 540

(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 427 base pairs(B) TYPE: nucleic acid

(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(iii) MOLECULE TURN - DVA	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:	
, , , , , , , , , , , , , , , , , , , ,	
GAATTCGGCC AAAGAGGCCT ANACTGCAGC TCTTTTCATT TTGCCATCCT TTTCCAGCTC CATGATGGTT CTGCAGGTTT CTGCGGCCCC CCGGACAGTG GCTCTGACGG CGTTACTGAT	60 120
GGTGCTGCTC ACATCTGTGG TCCAGGGCAG GGCCACTCCA GAGAATTACC TTTTCCAGGG	180
ACGGCAGGAA TGCTACGCGT TTAATGGGAC ACAGCGCTTC CTGGAGAGAT ACATCTACAA	240
CCGGGAGGAG TTCGCGCGCT TCGACAGCGA CGTGGGGGGAG TTCCGGGCGG TGACGGAGCT	300
GGGGCGGCCT GCTGCGGAGT ACTGGAACAG CCAGAAGGAC ATCCTGGAGG AGAAGCGGGC AGTGCCGGAC AGGATG'.'GCA GACACAACTA CGAGCTGGGC GGGCCCATGA CCCTCACAGA	360 420
ACTCGAG	420
(2) INFORMATION FOR SEQ ID NO:200:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 322 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:	
TAGGGATGTC AACATGATCT TTTCATATAT GCTGGCTATA GAAATTGGTC TCGGTGAAGT	60
AATGGTCTGT CTGTCAAGCA TGACATCCTT GCCTGTGTTA AGTTTTTGTT GCTCTTCTGG	120
GATGTTGATC GTGACGTCTT GTCCGGGATT GAGAAGCTTC TGTTGCTCTT CTGGGATGTC ATTCATGATC TCTTCATATA TGCTGGCTAT AGAAATTGGG CTCTGTGAAG AAATAGTGTG	180 240
TCCCCAACCT TGGTACAGNC CCCCTGGGGA GGGTACCTTT GAAGAACCAG AAGTTAGANC	300
TTGTGAAGAA GAAGAAAGTA GG	322
(2) INFORMATION FOR SEQ ID NO:201:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 272 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:	
GAATTCGGCC AAAGAGGCCT ATGGAGTGTG AGAACAGCAA AAAATAATAA TTCAACCAGT	60
TGGTTATTAT GAACATCATT TTCATATTTT TAAAAATATG CTATATCATG GAATTCAATG	120
TAAAACCTCA AGAGATGCCA TCCTTGGAGA GGGCTGCACC AGCCTGTGCC CCAAGTTACC	180
CAGGATCACC CCCTACTTCT CCTGACGGCC CCCCGAGAAA GGCCTGCATT CTGGGCGACG TGGCCTTCAG GGGCTCAACC CTTGGCCTCG AG	240 272
IGGCCITCAG GGGCTCAACC CITGGCCTCG AG	212
(2) INFORMATION FOR SEQ ID NO:202:	
(i) SEQUENCE CHARACTERISTICS:	
162	
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(A) LENGTH: 401 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
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- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

GAATTCGGCC	AAAGAGGCCT	AGCCAATTTG	GTTTTCTAAG	TATTTTCACG	CCTTCTCCTC	60
					CATTTTAGTA	120
GTTTTTGGAT	TGGGCTCCCG	GCTGCTAATT	TTGTCCCCTT	TTCCACTATC	TTCCACATTG	180
TCACCGCAGT	CATGTTTCTA	AGGCAGAATC	TCACTGTGCC	CCACATCGTG	TTGCTGGGCC	240
CTTGCATGCC	GTACCCTGGC	CTTTGTGAAA	TGCCCTTCAT	CTGTGCTCTT	CCCTCCACCT	300
GGAATGTCCG	TCTCTCTTTT	TCTGCCAACC	CACNCGACCC	CTCCCTCCTN	CAAGCCCGTG	360
AGTGTCCCCN	CCCTCCATGT	CCTGTGGTGA	CAGAGCTCGA	G		401

- (2) INFORMATION FOR SEQ ID NO:203:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 395 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

CGGGCCGAAC AGCATGACGT CCGCTTTGGA GAACTACATC AACCGAACTG TTGCCGTTAT 18 TACATCAGAT GGGAGAATGA TTGTGGGAAC ACTGAAAGGT TTTGACCAGA CCATTAATTT 24 GATTTTGGAT GAAAGCCATG AACGAGTATT CAGCTCTTCA CAGGGGGTAG AACAAGTGGT 30 ACTAGGATTA TACATTGTAA GAGGTGACAA CGTTGCAGTC ATTGGAGAAA TCGATGAAGA 36	GAATTCGGCC	AAAGAGGCCT	ACGATATTTG	CTGCGACCCG	CAGGCGCTAT	CCGCTGCCGG	60
TACATCAGAT GGGAGAATGA TTGTGGGAAC ACTGAAAGGT TTTGACCAGA CCATTAATTT 24 GATTTTGGAT GAAAGCCATG AACGAGTATT CAGCTCTTCA CAGGGGGTAG AACAAGTGGT 30 ACTAGGATTA TACATTGTAA GAGGTGACAA CGTTGCAGTC ATTGGAGAAA TCGATGAAGA 36	GTTCTGGCGC	GCCCTTTCAG	TTCTGCTTGC	TGTCCGCACC	GNTGCGTTAC	CCGGAACCGC	120
GATTTTGGAT GAAAGCCATG AACGAGTATT CAGCTCTTCA CAGGGGGTAG AACAAGTGGT 30 ACTAGGATTA TACATTGTAA GAGGTGACAA CGTTGCAGTC ATTGGAGAAA TCGATGAAGA 36	CGGGCCGAAC	AGCATGACGT	CCGCTTTGGA	GAACTACATC	AACCGAACTG	TTGCCGTTAT	180
ACTAGGATTA TACATTGTAA GAGGTGACAA CGTTGCAGTC ATTGGAGAAA TCGATGAAGA 36	TACATCAGAT	GGGAGAATGA	TTGTGGGAAC	ACTGAAAGGT	TTTGACCAGA	CCATTAATTT	240
· · · · · · · · · · · · · · · · · · ·	GATTTTGGAT	GAAAGCCATG	AACGAGTATT	CAGCTCTTCA	CAGGGGGTAG	AACAAGTGGT	300
AACAGATTCT GCGCTTGATT AGGGGAACAC TCGAG 39	ACTAGGATTA	TACATTGTAA	GAGGTGACAA	CGTTGCAGTC	ATTGGAGAAA	TCGATGAAGA	360
	AACAGATTCT	GCGCTTGATT	AGGGGAACAC	TCGAG			395

- (2) INFORMATION FOR SEQ ID NO: 204:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 395 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

GAATTCGGCC	ANAGAGGCCT	AAGAGCCAGT	AAAAAATTG	TTAGAAAGCA	GATACCATCA	60
AATTGGTTCT	GGGAAGTGTG	AAATCAAAGT	TGCACAACCC	AAAGAGGTAT	ATAGGCAGCA	120
ACAGCAACAA	CAAAAAGGTG	GAAGAGGTGC	TGCAGCTGGT	GGACGAGGTG	GTACGAGGGG	180
TCGTGGCCGA	GGTCAGGGCC	AAAACTGGAA	CCAAGGATTT	AATAACTATT	ATGATCAAGG	240
ATATGGAAAT	TAÇAATAGTG	CCTATGGTGG	TGATCAAAAC	TATAGTGGCT	ATGGCGGATA	300
TGATTATACT	GGGTATAACT	ATGGGAACTA	TGGATATGGA	CAGGGATATG	CAGACTACAG	360
TGGCCAACAG	AGCACTTATG	GCAAGGCATC	TCGAG			395

(2) INFORMATION FOR SEQ ID NO:205:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 560 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

GAATTCGGCC AAAG	AGGCCT AGTTTGGTCG	TTCGTTGGGC	GGTGCTGGTT	TTTCGCTCGT	60
CGACTGCGGC TCTT	CCTCGG GCAGCGGAAG	CGGCGCGCG	GTCGGAGAAG	TGGCCTAAAA	120
CTTCGGCGTT GGGT	GAAAGA AAATGGCCCG	AACCAAGCAG	ACTGCTCGTA	AGTCCACCGG	180,
TGGGAAAGCC CCCC	GCCAAA CAGTTGNCCA	CGGAAANCCG	CCAGGAAAAG	CGCTCCNTCT	240
ACCGGCGGGG TGAA	GAAGCC TCATCGCTAC	AGGCCCGGGA	CCGTGGCGCT	TCGAGAGATT	300
CGTCGTTATC AGAA	GTCGAC CGAGCTGCTC	ATCCGGAAGC	TGCCCTTCCA	GAGGTTGGTG	360
AGGGAGATCG CGCA	GGATTT CAAAACCGAC	CTGAGGTTTC	AGAGCGCAGC	CATCGGTGCG	420
CTGCAGGAGG CTAG	CGAAGC GTACCTGGTG	GGTCTGTTCG	AAGATACCAA	CCTGTGTGCC	480
ATCCACGCTA AGAG	AGTCAC CATCATGCCC	AAAGACATCC	AGTTGGCTCG	CCGGATACGG	540
GGAGAGAGAG CTTT	CTCGAG				560

- (2) INFORMATION FOR SEQ ID NO: 206:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 411 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

GAATTCGGCC	AAAGAGGCCT	ACTAGTTTAC	TTTATCCCAT	CCATTTATAT	ATACATATAT	60
ATACACATAT	ATGTGTGTTG	TTTTTGTTTT	GTTTTGTTTT	GTTTTTTTGA	GATGGAGTCT	120
CGCTCTGTCG	CCCAGGCTGG	AGTGCAGTGG	TGTGATCTTG	GCTCACTGCA	ACCTCTGCCT	180
CCTGGGTTCA	AGCAATTCTC	CTGCCTCAGC	TTCCCCGAGT	AGCTGGGACT	ACAGGTGTGC	240
GCCACCACGC	CCGGCAAATT	TTTTTTTTT	TTTTTTTTT	TTGATATTTT	TAGCAGAGAT	300
GAGGTTTCCC	CÁCGTTGGCC	AGGCTGGTCT	CGAACTCTTG	ACCTCAGGTT	ATCTGCCTGC	360
CTTGGCCTCC	CAAAGTGTTG	GGATTACAGG	CGTGAGCCAC	CGAACCTCGA	G	411

- (2) INFORMATION FOR SEQ ID NO:207:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 0 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:
- (2) INFORMATION FOR SEQ ID NO:208:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 411 base pairs
    - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:	
GAATTCGGCC AAAGAGGCCT ACGTGGTGCG CGAGAGCGTA TCCCCAACTG GGACTTCCGA GGCAACTTGA ACTCAGAACA CTACAGCGGA GACGCCACCC GGTGCTTGAG GCGGGACCGA GGCGCACAGA GACCGAGGCG CATAGAGACC GAGGCACAGC CCAGCTGGGG CTAGGCCCGG TGGGAAAGGA GACCGTCGTT AATTTATTTC TTATTGCTCC TAATTAATAT TTATATGTAT TTATGTACGT CCTCCTAGGT GATGGAGATG TGTACGTAAT ATTTATTTTA ACTTATGCAA GGGTGTGAGA TGTTCCCNCT GCTGTAAATG CAGGTCTCTT GGTATTTATT GAGCTTTGTG GGACTGGTGG AAGCAGGACA CCTGGAACTG CGCCAAAGTA GGCGACTCGA G	60 120 180 240 300 360 411
(2) INFORMATION FOR SEQ ID NO: 209:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 152 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:	
GAATGCTGAT TGACCAGCTA AAAATCAAAT TACAAGATAG CCAAAATAAC TTACAGATTA ATGTATCTGA ACTTCAGACA TTGCAGTCTG AACATGNTAC ACTGCTAGAA AGGCACAACA AGATGCTGCA GGAAACTGTG TCTCAGCTCG AG  (2) INFORMATION FOR SEQ ID NO:210:	60 120 152
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 355 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:	
GAATTCGGCC AAAGAGGCCT ACACNTCTGC ACCTCAACCA CAGACTACAC TTGCTGAACT GGCTCCTGGG GCCATGAGGC TGTCACTGCC ACTGCTGCTG CTGCTGCTGG GAGCCTGGGC CATCCCAGGG GGCCTCGGGG ACAGGGCGCC ACTCACAGCC ACAGCCCCAC AACTGGATGA TGAGGAGATG TACTCAGCCC ACATGCCCGC TCACCTGCGC TGTGATGCCT GCAGAGCTGT GGCTTACCAG GTGAGTCCTT CACCACTGTC ACCCTGCCCT GCTCACACCC CTTCTCAAGC CAGACCCCTC CACCCACCTC ACATTCCACC ACCGGCCTTT GATCCCCGCC TCGAG	60 120 180 240 300 355
(2) INFORMATION FOR SEQ ID NO:211:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 403 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

GAATTCGGCC A	AAAGAGGCCT	AATTATAAGC	ACTCAATAAT	ACATTATCAA	CTATTATTAC	60
TCAATTAAAA (						120
TGAAAÇACAA	TTCTGTATGG	ATGTCAGAAA	CATGAAATAT	AAAATGTAAT	TAAAAAAA	180
ATTAAAAAACC (	CCTTAGCAAA	TGTTAAGGAG	CGTGTCAAAT	GATTCCTGTG	TTGAACCTTA	240
AGCATTTAGG 7	TGGCTGGAGC	CTTGAAAGTT	ACCATCCCCC	AATTTTCTGC	TGTGTCACTA	300
GGTTTTTTTC 1	TATTGAGCAA	TTCTTTCAGG	TCGCCTCCAC	TCTGCTCTGC	CTAAAGGACA	360
ACTTCATATA (	GTGCATTCGT	GTCTTAGACT	CCACGATCTC	GAG		403

- (2) INFORMATION FOR SEQ ID NO:212:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 308 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

GAATTCGGCC	AAAGAGGCCT	AAGCGCTAAG	CCTGGAGTGT	GGGCACTGCA	GTTTCAGAGG	60
CACCGATTAT	GAGAATGTGC	AGCTCCACAT	GGGCTCCATT	CATCCTGAGT	TCTGTGATGA	120
TATGGATGCC	GGGGGCCTGG	GCAAGCTCAT	CTTTTACCAG	AAGAGTGCAA	AGCTCTTCCA	180
TTGCCATAAG	TGCTTCTTCA	CCAGCAAGCT	GTACGCCAAT	GTGTACTATC	ACATCACGGC	240
CAGACACGCA	GCCTCGGACA	AGTGGAGTGA	GCAGCCGAAA	GAGCAGCCGA	GCAAAGACAC	300
CCGTCGAG						308

- (2) INFORMATION FOR SEQ ID NO:213:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 362 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

CAATTCCCCC	AAAGAGGCCT	A CTCTCCTA A	THE CHARLES COME	A A TTA CATTOCO	CACCCCCCC	60
GAATICGGCC	MANGAGGCCI	ACIGIGGIAA	TICIAGAGCI	MAIMCAIGCC	GACGGGGGG	60
GACCCCCTTC	GCGGGGGGA	TGCGTGCATT	TATCAGATCA	AAACCAACCC	GGTCAGCCCC	120
TCTCCGGCCC	CGGCCGGGGG	GCGGGCGCCG	GCGGCTTTGG	TGACTCTAGA	TAACCTCGGG	180
CCGATCGCAC	GCCCCCCGTG	GCGGCGACGA	CCCATTCGAA	CGTCTGCCCT	ATCAACTTTC	240
GATGGTAGTC	GCCGTGCCTA	CCATGGTGAC	CACGGGTGAC	GGGGAATCAG	GGTTCGATTC	300
CGGAGAGGGA	GCCTGAGAAA	CGGTTACCAC	ATCCAAGGAA	GGCAGCAGGC	GCGCACCTCG	360
AG						362

- (2) INFORMATION FOR SEQ ID NO:214:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 445 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

```
GAATTCGGCC AAAGAGGCCT ATTCTTTTT AAACTAATCA CCATATTGTA AATTCAGGG 60
TTTTTTTTTT GGTTAAGCT GACTCTINGC TCTAATTTTG GAAAAAAAGA AATGTGAAGG 120
GTCAACTCCA ACGTATGTGG TTATCTGTGA AAGTTGCACA GCGTGGCTTT TCCTAAACTG 180
GTGTTTTTCC CCCGCATTTG GTGGATTTTT TATTATTATT CAAAAACATA ACTGAGTTTT 240
TTAAAAGAGG AGAAAATTA TATCTGGGTT AAGTGTTTAT CATATATATG GGTACTTTGT 300
AATATCTAAA AACTTAGAAA CGGAAATGGA ATCCTGCTCA CAAAATCACT TTAAGATCTT 360
TTCGAAGCTG TTAATTTTC CTAGTGTTGT GGACACTGCA GACTTGTCCA GTGCTCCCAC 420
GGCCTGTACG GACACGACTC TCGAG
```

- (2) INFORMATION FOR SEQ ID NO:215:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 345 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

GAATTCGGCC	AAAGAGGCCT	ACTTCACTCT	CTCATTCTTA	GCTTGAATTT	GGAAATGACT	60
TTTGATGACC	TAAAGATCCA	GACTGTGAAG	GACCAGCCTG	ATGAGAAGTC	AAATGGAAAA	120
AAAGCTAAAG	GTCTTCAGTT	TCTTTACTCT	CCATGGTGGT	GCCTGGCTGC	TGCGACTCTA	180
GGGGTCCTTT	GCCTGGGATT	AGTAGTGACC	ATTATGGTGC	TGGGCATGCA	ATTATCCCAG	240
GTGTCTGACC	TCCTAACACA	AGAGCAAGCA	AACCTAACTC	ACCAGAAAAA	GAAACTGGAG	300
GGACAGATCT	CAGCCCGGCA	ACAAGCAGNA	GAAGCTGTTC	TCGAG		345

- (2) INFORMATION FOR SEQ ID NO:216:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 511 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

GAATTCGGCC	AAAGAGGCCT	ACTGGGGAGT	CTGCTATATT	GTTGTTAAGG	TCTCTTTGTT	60
AGTGGTGGTA	GAAATTGGAG	TATTCCCTCT	CATTTGTGGT	TGGTGGCTGG	ATATCTGTTC	120
CTTGGAAATG	TTTGATGCTA	CTCTGAAAGA	TCGAGAACTG	AGCTTTCAGT	CGGCTCCAGG	180
TACTACCATG	TTTCTGCATT	GGCTAGTGGG	AATGGTATAT	GTCTTCTACT	TTGCCTCCTT	240
CATTCTATTA	CTGAGAGAGG	TACTTCGACC	TGGTGTCCTG	TGGTTTCTAA	GGAATTTGAA	300
TGATCCAGAT	TTCAATCCAG	TACAGGAAAT	GATCCATTTG	CCAATATATA	GGCATCTCCG	360
AAGATTTATT	TTGTCAGTGA	TTGTCTTTGG	CTCCATTGTC	CTCCTGATGC	TTTGGCTTCC	420
TATACGTATA	ATTAAGAGTG	TGCTGCCTAA	TTTTCTTCCA	TACAATGTCA	TGCTCTACAG	480
TGATGCTCCA	GTGAGTGAAC	TGTCCCTCGA	G			511

- (2) INFORMATION FOR SEQ ID NO:217:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 336 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

(ii)	MOLECULE	TYPE:	CDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

(	GAATTCGGCC	AAAGAGGCCT	AGTTTATACC	CACAGAATTT	TTTCATAAAA	TTAACCAAAC	60
(	CCTTTTCACT	TTGCTTAAGA	CTTCAGTTTT	GTCCCATTAC	TCTTTAAGGT	TAAGACCATC	120
•	TATAAAATCC	TCTGAACTGG	ACAAAATTAC	ATTCTCTTTA	NCAAAATCCA	TATTCCTATG	180
(	CCTTCTTATA	ATCTTTTACC	AAAAACACCT	TCCCTATACA	CCTTGTACGT	AAAACTGTTT	240
(	CTCCAGTGGT	CTCAACTACA	TATTATACTG	TTAACTCTTA	CTCCTTTTAG	CATAGCTAGT	300
1	AGGCATGGCT	CTCCATATGT	TCCCAGGCAT	CTCGAG			336

#### (2) INFORMATION FOR SEQ ID NO:218:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 167 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

GAATTCGGCC	AAAGAGGCCT	AGTGGGTAGA	TACAGACCCT	AACTTTGAGC	TCTAAGATGA	60
AATTTGTTTA	TAAATCCCTA	GTTTCCATTC	AGTTTTTTCA	ATATTTATCA	AACACCTACT	120
GTGCCAGGCA	TTGTTTAGGC	ACAGGGGATA	CAGCAGAAAA	ACTCGAG		167

- (2) INFORMATION FOR SEQ ID NO:219:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 377 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

GAATTCGGCC	AAAGAGGCCT	ACACACGCCT	TTGGCACAAT	GAAGTGGGTA	ACCTTTATTT	60.
CCCTTCTTTT	TCTCTTTAGC	TCGGCTTATT	CCAGGGGTGT	GTTTCGTCGA	GATGCACACA	120
AGAGTGAGGT	TGCTCATCGG	TTTAAAGATT	TGGGAGAAGA	AAATTTCAAA	GCCTTGGTGT	180
TGATTGCCTT	TGCTCAGTAT	CTTCAGCAGT	GTCCATTTGA	<b>AGATCATGTA</b>	AAATTAGTGA	240
ATGAAGTAAC	TGAATTTGCA	AAAACATGTG	TTGCTGATGA	GTCAGCTGAA	AATTGTGACA	300
AATCACTTCA	TACCCTTTTT	GGAGACAAAT	TATGCACAGT	TGCAACTCTT	CGTGAAACCT	360
ATGGTGAAAC	CCTCGAG					377

- (2) INFORMATION FOR SEQ ID NO:220:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 310 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

CTTGGGGGTG GGTTCNNNT ANNAAAAATT ANAGNCGTTG GGGGTTGGGG GGCNGAGAAG GAANANAGAA CCCCNGGNAA AATTTGAAAA CNGGGTNATT TATCCNGTNT TTTNAANGAG AATCCCANNC CCGGAAAAAA AAAAAAANAG AGGAANANAN AGATTGTAAG TTAAAACAAA AATCTATCTG TATAAGTCTT TACTTGTACA AGTCTGTACA AGTCAGTNAG GTTTGGTCTC TGCAGAGCCA GAACTTCAGA GAAGGTGATT TAATTGTAGG CNTCTTTGGT AGGCCTCTTT GGCCGAATTC	60 120 180 240 300 310
(2) INFORMATION FOR SEQ ID NO:221:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 313 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:	
GAATTCGCCC AAGAGGCCTA AAGAGGCCTA GAAGCCAAAA AACTTTTCCC GAAAGGAGTC TTCACCAAAG AGCTCCCATC TGGCAAGAAA TACCTCCGCT ACACACCCCA GCCTTAAGTC TCTTGGAGAA GCTGGTGCTG TGAGCCAGAG GATGTCAGCT GCCAATTGTG TTTTCCTGCA GCAATTCCAT AAACACATCC TGGTGTCATC ACAGCCAAGG TTTTTAGGTT GCTATACCAA TGGCTTATTA AATGAAAATG GCACTAAAAG TTTCTTGAGA TTCTTTATAC TCTCTGCCTT CAGCAATCCC GAG	60 120 180 240 300 313
(2) INFORMATION FOR SEQ ID NO:222:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 357 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:	
GAATTCGGCC AAAGAGGCCT AGGAACCACT GGCTTGGTGG ATTTTGCTAG ATTTTTCTGA TTTTTAAACT CCTGAAAAAT ATCCCAGATA ACTGTCATGG AGCTGGTAAC TATCTTCCTG CTGGTGACCA TCAGCCTTTG TAGTTACTCT GCTACTGCCT TCCTCATCAA CAAAGTGCCC CTTCCTGTTG ACAAGTTGGC ACCTTTACCT CTGGACAACA TTCTTCCCTT TATGGATCCA TTAAAGCTTC TCTGAAAAC TCTGGGCATT TNTGTTGGGC ACCTTGTGGA GGGGCTAAGG AAGTGTGTAA ATGAGCTGG ACCAGAGGCT TCTGAAGCTG TGGAGCAACC GCTCGAG	60 120 180 240 300 357
(2) INFORMATION FOR SEQ ID NO:223:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 208 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:	
GAATTCGGCC AAAGAGGCCT ATTAAATGTG TCATTGGAAG CCATCCCTTT TTTTACATTT CATACAACAG AAACCAGAAA AGCAATACTG TTTCCATTTT AAGGATATGA TTAATATTAT	60 120

TAATATAATA ATGATGATGA TGATGATGAA AACTAAGGAT TTTTCAAGAG ATCTTTCTTT

CCAAAACATT TCTGGACAGT ACCTCGAG	208
(2) INFORMATION FOR SEQ ID NO:224:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 348 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:	
TNAAACCAAT AGTTTTTAA AAGACAAGCT TGGGTGGGTG CANGNTGGGG ACAGTGCTGG TCTTTCACNG CAGCCCAGGC ACCCNTTGAG AGTCCCAGNG NGNGTNATGC CCCGAGCCAG TNAAGATGAA GGGAGAGCGG GTGCGGGGGC CATCNTCGGN GTCCCAGCCC GGCCCATGGG ANTGAGTNGC GGCCTCTGCT TGTCGACNTG GGNGCTGGCT GTCCNATTTT ACTACTATTG ACCCTGAAGG CCATCGAGGA GGCACGATG GAGGAGATCC AAGAGGAGGT CCGGCAGAAG AAATCATCAC GGAAGCGCAA GCGAGACTAG GCNTCTNTGG CCGAATTC	60 120 180 240 300 348
(2) INFORMATION FOR SEQ ID NO:225:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 483 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:	
GAATTCGGCC AAAGAGGCCT ACTTTCTCTG CAGATCATGG GGCCCTTGAT TGTGCTTGTG GGATTGTGTT TCTTCGTGGT TGCCCATGTT AAGAAGAGAA ACACGCTGAA TGCTGGCCAG GATGCCTCTG AGAGAGAAGA GGGACAGATC CAGATTATGG AGCCTGTCCA GGTCACTGTA GGTGACTCGG TAATAATATT TCCACCCCCT CCACCACCTT ACTTTCCTGA ATCTTCAGCT TCTGCGGTCG CTGAGAGTCC TGGAACTAAC AGTCTGCTTC CGAATGAAAA CCCCCCTTCA TATTACAGTA TTTTCAACTA TGGCAGGACC CCAACTTCAG AGGGTGCAGC CTCTGAAAGA GATTGTGAAT CTATTATAC CATTTCTGGG ACGAATTCAT CTTCTGAGGC CTCACACACT CCACATCTTC CATCTGAATT GCCTCCTAGA TATGAAGAAA AAGAAAATGC TGCAGCACTC GAG	60 120 180 240 300 360 420 480 483
(2) INFORMATION FOR SEQ ID NO:226:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 500 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:	
GAATTCGGCC AAAGAGGCCT ACGATTACAA TCATGATTTC CAGAATGGAG AAGATGACGA TGATGATGAA GATATTGATT ATGTTTGCTC TTGGAATGAA CTACTGGTCT TGCTCAGGTT TCCCAGTGTA CGACTACGAT CCATCCTCCT TAAGGGATGC CCTCAGTGCC TCTGTGGTAA	60 120 180

AAGTGAATTC CCAGTCACTG AGTCCGTATC TGTTTCGGGC ATTCAGAAGC TCATTAAAAA GAGTTGAGGT CCTAGATGAG AACAACTTGG TCATGAATTT AGAGTTCAGC ATCCGGGAGA CAACATGCAG GAAGGATTCT GGAGAGAGCCC TGAAGGTATC TGCCTTCCAG AGGGACTACT ATGTGTCCAC AGCTGTTTGC AGAAGCACCG TGAAGGTATC TGCCCAGCAG GTGCAGGGCG TGCATGCTCG CTGCAGCTG TCCTCCCAC CGTCTGAGTC TTACAGCAGC GAAGAGATGA TTTTTGGGGA CACTCTCGAG	240 300 360 420 480 500
(2) INFORMATION FOR SEQ ID NO:227:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 497 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	•
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:	
GAATTCGGCC AAAGAGGCCT AGGAGAAAGA AGATATTGAC ACCATCTACG GGCACCATGG AACTGCTTCA AGTGACCATT CTTTTTCTTC TGCCCAGTAT TTGCAGCATT AACAGCACAG GTGTTTTAGA GGCAGCTAAT AATTCACTTG TTGTTACTAC AACAAAACCA TCTATAACAA CACCAAACAC AGAATCATTA CAGAAAAATG TTGTCACACC AACAACTGGA ACAACTCCTA AAGGAACAAT CACCAATGAA TTACTTAAAA TGTCTCTGAT GTCAACAGCT ACTTTTTTAA CAAGTAAAGA TGAAGGATTG AAAGCCACAA CCACTGATGT CAGGAAGAAT GACTCCATCA	60 120 180 240 300 360
TTTCAAACGT AACAGTAACA AGTGTTACAC TTCCAAATGC TGTTTCAACA TTACAAAGTT	420
CCAAACCCAA GACTGAAACT CAGAGTTCAA TTAAAACAAC AGAAATACCA GGTAGTGTTC TACAACCAGA NCTCGAG	480 497
(2) INFORMATION FOR SEQ ID NO:228:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 154 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:	
GAATTCGGCC AAAGAGGCCT ACTTTTTTAA TATAAATTTT GTTGATATGG AATTAGGTAA GTTTAAGTGT CTATGTGCAT ATGTTTTTTA TATAAGTTTT TTCTATTCAG TTTCACNGAT CCAACTGGCA GTGGGTAAAT ATGGCGAGCT CGAG	60 120 154
(2) INFORMATION FOR SEQ ID NO:229:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 387 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:	
GAATTCGGCC AAAGAGGCCT AGGAATGGTT TTNATTTGGT CCTTATTTTT AACCTGCCCC TGAGACTTAT ATGCTTGTTT ATACCATGTA CGTAGTGTGT GATTGTATGT GTTTGTATTT	60 120

GTCCACATGT CCCAAAACAT GGGCTGTTAC TCCCTTTTCT ATCTTGGTTT CCTTATTCCC	180
ACCOTTCTCT TTCCACCCAG GTATCTGGAC AGGAAGACTT CTACCATCAG CTTTACCAGA	240
GGAAGCTGCA GGCCCCACTG TGGCCCAGCT CCCTGGGCAT CACTGATTGC TATCAGTATG	300
TCACCTCCTG TCACCCCAAG AGATCAGAGA GACGCAAGTA TGGCCGAGAC TTCCTGCTAC	360
GTTTCCGCTT CTGCAGCATC GCTCGAG	387
(2) INFORMATION FOR SEQ ID NO:230:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 336 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(b) TOPOLOGY: Tinear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:	
CARMINOCCCC ARRONGCOM ACCOMMINE COMMINE AND ARRONGCO OF COMMINE	
GAATTCGGCC AAAGAGGCCT ACCTTCATTT GTTAGATTAT ATCAGTACCC CAACTTTGCT GGACCTCATG CAGCTTTAGC TAATAAAAGT TTCTTTAAGG CAGATAAAGT TACAATGCTG	60 120
TGGAATAAAA AAGGTATGTT AAGTATATTT TATCCCTCCC TTTGTTTATC AGTTGTTAAT	180
TTAGGCTATA TTCCTATGTG TATAACAGAA GAATCAATGC CCATTTGTGT TTTAAATCTA	240
ATTAAAGTTT TTACTGTTAT AGCTACTGCT GTGTTGGTAA TAGCTAGCAC AGATGTTGAC	300
AAGACAGGAG CTTCCTACTA TGGAGAACGA CTCGAG	336
(2) INFORMATION FOR SEQ ID NO:231:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 479 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:	
ANDRESSES AND ASSESSED ASSESSED COMMENTS OF THE ASSESSED AS A PROPERTY OF THE ASSESSED AS A PROP	
GAATTCGGCC AAAGAGGCCT AGGGACATTG GTTGAATTGG CATGACTAGA ATAGTTGGGA ATGTTTGGGA ATGGGGAGAG ATTGCTAATG GGATGTCTGC CAGGGGCAAT ACTGAAATCT	60 120
GCTGGTTGGT AAAGGTAGTG CCTGAGCCCA GTGCTAACCA TAGTAGTTGG AAAATTGTGT	180
ACGTTGGCTG TGGAATCCTT ATGCGAATAT TTGTCCAATC CATCTAAATT TCTCTCTGCA	240
GCATTTTTAA AAAGACATAT AGCTGAAATT TTGTCAGTCC TAAAAATATT TTGTATTTCT	300
CTGCCCAGAT TTGCATTTGG GTAGATCGTG CTGTAGAAGA TATATCTTGC TTTAAGATAG	360
CTGCCACTGA TTAGTTTATT TTAGTCTATT TTAATCAACT TATTGCCTTG TAATCTTTCC	420
TTTTTCATTC TCTAAATTTC TGAAATTCTA TCTTTCATGT TCCCCAGGAA ACACTCGAG	479
(2) INFORMATION FOR SEQ ID NO:232:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 338 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(C) STRANDEDNESS: GOUDIE (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	

172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

60

CATICCTITI TITGAAGATA TGTGTAAAGG CATTAAAGCT GGTGACACCT GTGAGAAGCT	120
GGTGGGATAT TCTNCCGTGT ATAGAGTCTG TTTTGGAATG GCTTGTTTCT TCTTTATCTT	180
CTGTCTACTG ACCTTGAAAA TCAACAACAG CAAAAGTTGT AGAGCTCATA TTCACAATGG	240
CTTTTGGTTT CTTTAAACTT CTGCTGTTGG GGGCCATGTG CTCAGGAGCT TTCTTCATTC	300
CAGATCAGGA CACCTTTCTG AACGCCGGGC AGCTCGAG	338
(2) INFORMATION FOR SEQ ID NO:233:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 363 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:	
GAATTCGGCT TCATGGCCTA CCCCGAACCA CTCAGGGTCC TGTGGACAGC TCACCTAGTG	
GCAATGGCTC CAGGCTCCCG GACGTCCCTG CTCCTGGCTT TTGCCCTGCT CTGCCTGCC	60
TGGCTTCAAG AGGCTGGTGC CGTCCAAACC GTTCCGTTAT CCAGGCTTTT TGACCACGCT	120
ATGCTCCAAG CCCATCGCGC GCACCAGCTG GCCATTGACA CCTACCAGGA GTTTGAAGAA	180
ACCIATATCC CAAAGGACCA GAAGTATICA TICCIGCATG ACTCCCAGAC CICCITCTGC	240
TECTORICE CHARGONICA GRAGITATICA TICCTGCATG ACTCCCAGAC CTCCTTCTGC	300
TTCTCAGACT CTATTCCGAC ACCCTCCAAC ATGGAGGAAA CGCAACAGAA ATCCAATCTC	360
GAG	363
(2) INFORMATION FOR SEQ ID NO:234:	
(i) CROUDICE CHARLED TORSE	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 374 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:	
GAATTCGACC TTCATGACCT AGCGTAAGAG GAGAGAGACA CATTCAGCAG CCAAAGGACT	60
CGGTGGAAAG AGCAGAACAC CATAGACAAT ATGTCGCTCT TGGGACCCAA GGTGCTGCTG	120
TTTCTTGCTG AATTCATCAT CACCTCTGAC TGGATACCCC TGGGGGTCAA TAGTCAATCG	180
AGGAGACGAT GTGACTCAAG CGACTCCAGA AACATTCACA GAAGATCCTA ATCTGGTGAA	240
TGATCCCGCT ACAGATGAAA CAGTTTTGGC TGTTTTGGCT GATATTGCAC CTTCCACAGA	300
TGACTTGGAG TGCTGGGATG AGAAATTTAC CTGCAGCAAG GCTCTACTCT GTGCATCGGC	360
CGGTTAAACT CGAG	374
(2) INFORMATION FOR SEQ ID NO:235:	
(i) CROVIDVOR GUADA COMPANIA	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 330 base pairs	
(B) TYPE: hucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:	

GAATTCGGCC TTCTGGCCTA GGGTGGGATA AGTGATTNGT ATTTGTTTNG GTTTAAAAAC

ATACTTTGAT AGAAATTAGT CCCTTTCTTT TCCTTCTCTT CTACAATGTC AATTGCCCAT TTCATTTGTG TGTTTCTAAC ATTTTCTTTT GTTAAGAAAT GTTGGGGCTA TAATTTTTTT GAAATCACTG AAGGAGGGGG AAAAATAATT TTAACAACCT GTGTTGAAAC CTTCCATAGC TTAATTGACT GGAATAATCC TGCCATCATT AATAAGATGT ACAAGGTGTA CCTTGGAGAT ATACCACTGA AGACAANAGA GGAGCTCGAG	120 180 240 300 330
(2) INFORMATION FOR SEQ ID NO:236:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 107 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:	
TTACACCCTG GAAACCAAGC ATAAGCACAC TNTTAGCAGA TGACTTAGAA ATTAAGTTGT TTGAATCNAG TGAACACACT GAAGACTCCA ACAACCCACA ACTCGAG	60 107
(2) INFORMATION FOR SEQ ID NO:237:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 338 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:	
GAATTCGGCC TTCATGGCCT ACCCGTCGTT AGTGAAGGGG AAATGGGTTG TATCCTAAGG GATTGGGAAA TGGGAACTGA ATTTCAGGAG ATTGTGGACT ACAAGGTATG TGTTTACGTT AGGTGATGAG CAGTGTCAGG ATAGTGAACT GTGGACAGTG TCAAATGCTT TTCTGTAGGG AAGATGAAGT TAGCATCATC TTATCACTTT TGCCAAAGCC TCTGTACTAT TTTTTGTTTTG	60 120 180 240 300 338
(2) INFORMATION FOR SEQ ID NO:238:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 455 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	
(ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:	

GTACCACCGT GTACTGTGAT GCCCATGAAC TCGAG

# PCT/US98/06954

GTACCACCGT GTACTGTGAT GCCCATGAAC TCGAG	455
(2) INFORMATION FOR SEQ ID NO:239:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 431 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:	
GAATTCGGCC AAAGAGGCCT AGGGGGGTGA TGGTGTGTGC TTTGGACTGT GTGCCTACAG GGTTTTTTTG TTTTGTTTTG TTTTACTGTA ATGGAAATGG GTTTAGGATA AGCATACTCA AAGCTCCACA GTGTATCCTT GAGCTTTCCA TGACTGCCAG TTACACACTG GAGAGGGTTA AATGAATCTT AAAGTGTTCA TGATTACTAT TAAATATCAT TATAAAACAA ATTCTTTCGG GGGGCACAA ATGCTAATAT GTACAAGAAA ATCTTAGACT TGAAAATATC TTTAAAATGA AAATAACTTT TTTTTTCAGC TGACTGTATT CACAACCTTG ATGGATGTTA CCAAAGGTCA ATTTGAAAGT CACCTTCGAG ATTGCCCAGA CCCTTGTATA GGCTGGTGAG CACACGTTGG CCAGCCTCGA G	60 120 180 240 300 360 420 431
(2) INFORMATION FOR SEQ ID NO:240:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 178 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:	
GAATTCGGCC TTCATGGCCT ACTACAATCC GTGGCTGCTC NTTCTTGCCT ACTTTACTCT CCCACTGAAG CAGGTTANCG TTGAAGGTGG TATGGAAAAG CCTGCATGCC TGTTCAATTC TTTTGTTTCT TCTCCTTCCC CCTCCCCCTA CCTCCTTCCC CTACCTCCTT CGCTCGAG	60 120 178
(2) INFORMATION FOR SEQ ID NO:241:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 232 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:	
GAATTCGGCC TTCATGGCCT ACATCAACAG CATCAAGTCC AGACTAAGCA AAAGTGGGCA CATACAAACT CTGCTTAGAG CATTTGAAGC TCGTGATCGA AACATACAAG AAAGCAACTT TGATAGAGTC AATTTCTGGT CTATGGTTAA TTTAGTGGTC ATGGTGGTGG TGTCAGCCAT TCAAGTTTAT ATGCTGAAGA GTCTGTTTGA AGATAAGAGG AAAAGTCTCG AG	60 120 180 232
(2) INFORMATION FOR SEQ ID NO:242:	

<ul><li>(A) LENGTH: 195 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:	
GAATTCGGCC TTCATGGCCT ACAAAACCTA ACTTGCGCAG AAAACAAGAT GAGATTGGCA TGGCTTTATT TGTTTTTTTT GTTTTGTTTT GGTTTTTTTT TTTTTT	60 120 180 195
(2) INFORMATION FOR SEQ ID NO:243:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 325 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:	
GAATTCGGCC TTCATGGCCT ACATATCCTC AAATGGTAGT CATCTGGGGA CTAAGCAACA GGTGTTTCAA GGAACTAATT CTCTGGGTTT GAAAAGTTCA CAGTCTGTGC AGTCTATTCG TCCTCCATAT AACCGAGCAG TGTCTCTGGA TAGCCCTGTT TCTGTTGGCT CAAGTCCTCC AGTAAAAAAT ATCAGTGCTT TCCCCATGTT ACCAAAGCAA CCCATGTTGG GTGGGAATCC AAGAATGATG GATAGTCAGG AAAATTATGG CTCAAGTATG GGAGACTGGG GCTTACCAAA CTCAAAGGCC GGCAGCGGAC TCGAG	60 120 180 240 300 325
(2) INFORMATION FOR SEQ ID NO:244:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 342 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:	
(XI) SEQUENCE DESCRIPTION: SEQ ID NO:244:	
GAATTCGGCC TTCATGGCCT AGGAGGCTAT TTTAGGATTT CAATGAGAAG CAAAATCATA TCCAAATCAA AGTAAAGGTC ATCGGTGGCC AATGAAGAGC GGAGAAAACG GAGGCGGGAG AACAGACGCG ACCTCAAGAC AGAAGAATGG AAGACGCAAC TTTCAAAGAAA AGAGGAACTG AAACGAAAAG AGAGGCACAG TCCAAATGAG GAAGAGAACA AGGAGCCTTC AGTCTCCTGG GGGCCAGGGA GCCTCGCCAC GCGGTCACAG GTACACGGGG ACATTTAGAG GCCATCTCCT TTAAAGCCAG ACATTCTTCT TACTGGAATC TAGGCCATGA AG	120 180 240 300 342
(2) INFORMATION FOR SEQ ID NO:245:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 373 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

GIGAACGCTG CTGTGACTTA CTCGAAGCCT CGATTCCCCA CAMPUTTCCCCA	GTGAA GTTGA	ACGCTG AGCTGG	CTGTGACTTA TTCCTCCCAC	CCAATTTGTC CTCGAAGCCT CCCTGCTGAG	CGTAACCTTG CGATTGGCCA ATCCCTAGAG	TGGAGAAGAC CATTTTGGTA	CTACGCCAAG	60 120 180
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- (2) INFORMATION FOR SEQ ID NO:246:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 514 base pairs
    - (B) TYPE: nucleic acid .
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

GAATTCCCCC	<b>ですべきかべべべべか</b>	*****				
	TICATOCCCI	AAACAGGACC	TGCTTCACAC	CACCAAGCAT	CAGGATGTGT	60
TGCTCAGTGA	GCAGACCCGA	CTCCAGAAGG	ΔΟΔΤΟΛΩΤΟΛ	ATCCCCANAN	AGGTTTGAAG	
ACTOTOTOTOTA	ACMA CACCA	200000000	MUNICACIOA	WIGGGCWWWI.	AGGTTTGAAG	120
ACTO! CHOMA	MUNAGAGGAG	ACAAAACAAC	AACAACTTCA	AGTGCTTCAG	AATGAGATTG	180
AAGAAAACAA	GCTCAAACTA	GTCCAACAAC	CARATCATION	MMG1 G1 G1 G	CCAGAAAGAG	100
30303330mo	**********	orcanamo	GAMATGATGT	TTCAGAGACT	CCAGAAAGAG	240
ACACAAAG TG	AAGAAAGCAA	ATTAGAAACC	AGTAAAGTGA	CACTGAAGGA	GCAACAGCAC	200
CAGCTGGAAA	AGGAATTAAC	ACACCACAAA	1001110mag		CONCACCAC	300
20000000		AGACCAGAAA	AGCAAACTGG	ACCAAGTGCT	CTNCAAAGGT	360
GCIGGCAGCT	GAAGAGCGTG	TTAGGACTCT	GCAGGAAGAG	GAGAGGTGGT	CTCACACOCT	
GGAGAAGACA	CTCTCCCAAA	CM3.3.3.000.03		ONGNOG1001	GIGAGAGCCT	420
oo.io.inchch	CTCTCCCAAA	CIMAACGGCA	GCTTTCAGAA	AGGGAGCAGC	AATTGGTGGA	480
GAAATCAGGT	GAGCTGTTGG	CCCTCACGCT	CCAC			
			COND			514

- (2) INFORMATION FOR SEQ ID NO:247:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 425 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

GAATTCGGCC TGTTCACCCT AAAAGTGTCT TAAAGAATGG GTGCTAATTA CAACAACAGC CCCGTTTCTC	TGCAGTTTTT AAACGACGTT TTGGGCAATG TCCTGTTTTC AACAACAACT	ATGCTCCTGG GGAATTTGCA TGCGGCAAAC TGTGTCCAGA TTGATGATGA	CCCAATTGGT AGAAGAAGTG AAAGGGACTG CAAAGACTAC CTACTGCTTC	CTCAGGTAAT CAAACCTGAA CTGTGTTCCA AAGAATTTCA GATGTCTTCG	TGGTATGTGA GAGATGCATG GCTGACAGAC, ACAGTAACAG ATGGCTCCTA	60 120 180 240 300 360 420
TCGAG		· · · · · · · · · · · · · · · · · · ·	CCICIGICIC	CIGCICIAGG	ATCCCCACGC	420 425

- (2) INFORMATION FOR SEQ ID NO:248:
  - (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 352 base pairs

(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:	
GAATTCGGCC TTCATGGCCT ACAAAAGGAA AGAAGAAAAA GGGCCAAAAG CCAAAATGAA ACTGATGGTA CTTGTTTTCA CCATTGGGCT AACTTTGCTG CTAGGAGTTC AAGCCATGCC TGCAAATCGC CTCTCTTGCT ACAGAAAGAT ACTAAAAGAT CACAACTGTC ACAACCTTCC GGAAGGAGTA GCTGACCTGA CACAGATTGA TGTCAATGTC CAGGATCATT TCTGGGATGG GAAGGGATGT GAGATGATCT GTTACTGCAA CTTCAGCGAA TTGCTCTGCT GCCCAAAAGA CGTTTTCTTT GGACCAAAGA TCTCTTTCGT GATTCCTTGC AACAATCTCG AG	60 120 180 240 300 352
(2) INFORMATION FOR SEQ ID NO:249:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 400 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:	
GAATTCGGCC TTCATGGCCT ACACAATGGT GTTCGCATTT TGGAAGGTCT TTCTGATCCT AAGCTGCCTT GCAGGTCAGG TTAGTGTGGT GCAAGTGACC ATCCCAGACG GTTTCGTGAA CGTGACTGTT GGATCTAATG TCACTCTCAT CTGCATCTAC ACCACCACTG TGGCCTCCCG AGAACAGCTT TCCATCCAGT GGTCTTTCTT CCATAGAAAG GAGATGGAGC CAATTTCTAT TTACTTTTCT CAAGGTGGAC AAGCTGTAGC CATCGGGCAA TTTAAAGATC GAATTACAGG GTCCAACGAT CCAGGTAATG CATCTATCAC TATCTCGCAT ATGCAGCCAG CAGACAGTGG AATTTACATC TGCGATGTTA ACAACCCCCC AAGACTCGAG	60 120 180 240 300 360 400
(2) INFORMATION FOR SEQ ID NO:250:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 278 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:	
GAATTCGGCC AAAGAGGCCT AAGAGATTCA GGACCTGCAG AGTCGCCAGA AGCATGAAAT TGAATCTTTG TATACTAAAC TGGGCAAGGT TCCCCCTGCT GTCATTATTC CCCCAGCTGC TCCTCTGTCG GGGAGAAGAA GGAGACCCAC TAAAAGCAAA GGCAGCAAGT CTAGTCGCAG CAGCTCATTG GGCAATAAAA GCCCACAGCT TTCAGGCAAC CTGTCTGGTC AGAGTGGAAC TTCAGTCTTA CACCCCCAAC AGACCCTCCA CAGTCGAG	60 120 180 240 278
(2) INFORMATION FOR SEQ ID NO:251:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 187 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	

(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:	
GAATTCGGCC TTCATGGCCT AGTTTATATA CTTTCTCTGA AGGATCCTAA TGATAGTTAA CCATTTCTCA TTTTTATTTT GCTGGATTGT TTTCTGTTTT TTGCTTCAGC ATTCTTGCTT TTGCTGTGCT TACTTTTGGA GTTTTGATTC CCTGTGTCAC TGTTTTCTTT CGCATCCACC	120
(2) INFORMATION FOR SEQ ID NO:252:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 392 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:	
GAATTCGGCC TTCATGGCCT ACTTCTCTGG AAAGGTCACT GATTGTTTGT TTTTTCGAGA CAGGGTCTCG CTCTTCACCC AGACTGCAAT GCAGTGGCAC AATCATAGCT TATTGCAACC TCAAACTCGT GGGCTCAAGC AATGCTCGCT CCTCCCAAGT AGCTAGGACC ACAGGCATGC ACCACGATGC CCACCTAGTT TTTTGTATTT TCTATAGAGA NGGGGGGTCTC ACTGTGTTTC TCAAGCTGGT CACATACTCT TGGCCTCAGG CAGTTCTCCC ACATCAGANT CTCAAAGCAC TGGGCTTACA GCTGNGAGCC NGNCCTTTTT AAAAAAAAAAA AAAAAATCAA AACAAAACAA AACAAGATTA TGTCTTTCCC ACGCATCTCG AG	120 180 240 300
(2) INFORMATION FOR SEQ ID NO:253:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 320 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:	
GAATTCGGCC TTCATGGCCT ACTTGGGAAT TAACATCTTC GATAAATCCC AGAAGTCTTT AAGTGACAGT AGAGAGCCTA CAGAGAAGCC TGGGAAAGCA GAAAAATCTA AGAGCCCAGA AAAAGTGTCA TCGTTCTCAA ACTCCTCCTC CAACAAGGAA TCAAAAGTAA ACAATGAGAA GTTTCGTACT AAGAGCCCCA AGCCTGCCGA AAGCCCCCAG TCAGCCACTA AGCAGTTGGA TCAGCCCACT GCTGCTTATG AGTATTATGA TGCTGGCAAT CACTGGTGCA AAGACTGCAA CACCATCTGT GGGACTCGAG	120 180 240
(2) INFORMATION FOR SEQ ID NO:254:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 367 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: cDNA

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

GAATTCGGCC	TTCATGGCCT	AATCAGAAGC	TTTTCAAAAT	TCCGTCTTCA	AGAAGAAACA	60
CCCGTGGAGG	AAGAAGACAT	TATACAAAAC	AAATTTAGAA	ACTGGGATCA	TGAGTGGAAA	120
AACAAAGGCA	AGAAGGGCTG	CCATGTTTTT	TAGACGTTGC	TCTGAAGACG	CCAGCGGTAG	180
CGCCAGTGGC	AATGCTTTGT	TATCAGAGGA	CGAAAATCCT	GATGCGAATG	GGGTAACTCG	240
ATCATGGAAG	ATTATTCTAA	GTACAATGCT	TACACTGACT	TTTCTTCTTG	TAGGACTCCT	300
AAATCATCAG	TGGCTTAAAG	AAACAGATGT	TCCTCAGAAA	TCCAGACAAT	TATATGCCAT	360
GCTCGAG				•		367

### (2) INFORMATION FOR SEQ ID NO:255:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 447 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

GAATTCGGCC TTCATGGCCT	AAAGTAGTTC	TGTTATAAAA	AGCCAGGAAT	CCTAAAACCA	60
AAATATTAGA ACGAAAACAG	AAACATGGCT	CACTATATTA	CATTTCTCTG	CATGGTTTTG	120
GTGCTGCTTC TTCAGAATTC	TGTGTTAGCT	GAAGATGGGG	AAGTAAGATC	AAGTTGTCGT	180
ACTGCTCCGA CAGATTTAGT	TTTCATCTTA	GATGGCTCTA	ATTGTGTTGG	CCCAGAAAAC	240
TTTGAAATAG TGAAAAAGTG	GCTTGTCAAT	ATCACAAAAA	ACTTTGACAT	AGGGCCGAAG	300
TTTATTCAAG TTGGAGTGGT	TCAATATAGT	GACTACCCTG	TGCTGGAGAT	TCCTCTCGGA	360
AGCTATGATT CAGGAGAACA	TTTGACGGCA	GCAGTGGAAT	CCATACTCTA	CTTAGGAGGA	420
AACACAAAGA CAGGGAAGAA	CCTCGAG				447

## (2) INFORMATION FOR SEQ ID NO:256:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 391 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

GAATTCGGCC	TTCATGGCCT	AAATGAAGCA	AAATTCCATA	CATCATTTTG	AAAATAGTGT	60
TTCTTTCCCT	GATAGGCCTG	TTCTGCATCA	TTCTTTTAGC	TTCCTTCTGC	CCTGTTTATC	120
ACTTGGTCCC	ACTTTTATAT	TTTTCCTCTT	CGGTCCAGAA	TTTCTTATTT	AGTTTCTTGT	180
ATTTTGCCTA	CTCCCTCCCT	TCTCCATGAT	TCAGCCTAGT	CTTTCCGTCC	TCTGTGGACT	240
TGGGTGTGCC	TTCCTCTGGG	CCACCTCGTC	TTTTGCTGCT	GTTAGCCCTC	CCGCCTGCGC	300
ACCTGCCACT	TCACCCTCGC	CTGTGGTCCA	CTTACGTTCC	ACTCAGCCCG	GTCAGTCCTG	360
CTTTGTTCTT	CTCCACCGCC	TAGGTCTCGA	G			391

### (2) INFORMATION FOR SEQ ID NO:257:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 70 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MC	DLECULE TYPE: cDNA	
(xi) SE	EQUENCE DESCRIPTION: SEQ ID NO:257:	
GAATTTAAGT T AGATCCTGAG	TCCAGTATGA GATCTTCAAA GCTGTCTTTT TTTTTTCTTC TTCCGTTCTC	60 70
(2) INFORMAT	TION FOR SEQ ID NO:258:	
(A (B (C	QUENCE CHARACTERISTICS: A) LENGTH: 362 base pairs B) TYPE: nucleic acid C) STRANDEDNESS: double D) TOPOLOGY: linear	
(ii) MC	OLECULE TYPE: cDNA	
(xi) SE	EQUENCE DESCRIPTION: SEQ ID NO:258:	
AGATTGCGTT T GAAGTAGAGA A TCCGTTTTGA A CAATGAAGAA A	AAAGAGGCCT AGTCAAATTC TTACCTCGCT CTTTCACTGC TAGTAAGATC ICTTTCAGTT ACTCTTCAAT CGCCAGTTTC TTGATCTGCT TCTAAAAGAA AGATAAATCC TGTCTTCAAT ACCTGGAAGG AAAAACAAAA TAACCTCAAC AAAAAACATT CCAAGAACTT TCATCAGAGA TTTTACTTAG ATGATTTACA AGTACATGCA CTTTGGGCTT CTGTATGCCT GCTGCTTAAT CTTGCCCCTG IGCTGATTCT GAGGAAGATG AAGAACACAC AATTATCACA GATACACTCG	60 120 180 240 300 360 362
(2) INFORMAT	TION FOR SEQ ID NO:259:	
(i) SEC (A (E	QUENCE CHARACTERISTICS: A) LENGTH: 453 base pairs B) TYPE: nucleic acid C) STRANDEDNESS: double D) TOPOLOGY: linear	
(ii) MC	OLECULE TYPE: cDNA	
(xi) SE	EQUENCE DESCRIPTION: SEQ ID NO:259:	
CAAAAGAAGA ATGATTCTAG TTTGATGATG CTAAAAGGAGG AAATGGGCAG ATAGCCCTGA	CCTGCCTCGA GTGCGGATCC AGCCGGAGGC GAAGAGAAGC ACTTTGGGGG GAAAAATGAA GACGGGACAT TTTGAAATAG TCACCATGCT GCTGGCAACC TGGACATTTT CCAGGTGAAG GCTGAAGTGT TAGACATGGC AGATAATGCA AATACCTGAA ATGTACGGAC AGGATGGAAA TTAAATACGT TCCCCAACTG AAAAGCAAG CCACCAGCAA TTAGATACTG TGTGGGAAAA TGCAAAAGCC CCCGAAAGAC TCAAATCTTT CTCCCTATGA ATTTTAAGGA TAACCATGGA TGGCATATAT TTCCGAAGCT CAAGAGCAAA CTCCCTTTTA CCATCTCTC TGAAGATGGC TGGCCAACTC GAG	60 120 180 240 300 360 420 453
(2) INFORMA	TION FOR SEQ ID NO:260:	
() (1	QUENCE CHARACTERISTICS:  A) LENGTH: 465 base pairs  B) TYPE: nucleic acid  C) STRANDEDNESS: double	

(ii) MOLECULE TYPE: cDNA

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

GAATTCGGCC	TTATGGCCTA	CTTTAAAAAA	AAACCAATAC	CAAAGAAGCC	TACAATGTTG	60
GCCTTAGCCA	AAATTCTGTT	GATTTCAACG	TTGTTTTATT	CACTTCTATC	GGGGAGCCAT	120
GGAAAAGAAA	ATCAAGACAT	AAACACAACA	CAGAACATNG	CAGAAGTTTT	TAAAACAATG	180
GAAAATAAAC	CTATTTCTTT	GGAAAGTGAA	GCAAACTTAA	ACTCAGATAA	AGAAAATATA	240
ACCACCTCAA	ATCTCAAGGC	GAGTCATTCC	CCTCCTTTGA	ATCTACCCAA	CAACAGCCAC	300
GGAATAACAG	ATTTCTCCAG	TAACTCATCA	GCAGAGCATT	CTTTGGGCAG	TCTAAAACCC	360
ACATCTACCA	TTTCCACAAG	CCCTCCCTTG	ATCCATAGCT	TTGTTTCTAA	AGTGCCTTGG	420
AATGCACCTA	TAGCAGATGA	AGATCTTTTG	CCCATCTCCC	TCGAG		465

- (2) INFORMATION FOR SEQ ID NO:261:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 491 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

GAATTCGGCC	TTCATGGCCT	AGCGGCGGG	CGAGCGCCTC	CACGCAGCAA	CTCCGGAGTC	60
CCCCGCTTGC	CCGAGCGCAG	TTTCTCCGCT	GCTGTTTCCA	CCGGCTTTGT	AACACTGGGA	120
ATTTACATCC	TCACCCGCAC	CCCTCACGCC	CGAGGATTTT	AAACTCACCT	TTACTCTCGA	180
ACTGAGAGTT	GCGGTAGATG	GGATTTTTGC	CTTTTCCCCA	GATGGTTGAA	GGTTAAGATT	240
TTTGGAAACC	CCCCCACCTC	CTTATTTCTA	TTATTATTTC	TGCNAGAAAA	GTATAAAGAG	300
AGTTGTAGTG	GAGGTGAGAT	TTGTGATCGG	GAAAGCCTTC	GACTCCCTCC	TTCTCCGTCT	360
TCCGCTTCTC	TCTCTCTGAT	TAGTTCCTAT	CCAGCAGCAG	ATTGAAGCAG	GAGATGATTC	420
TTCTCAAGGT	TTGTTCAGCA	GCTTCACTTC	TAGGCGAAGG	CTTCATGAAC	CAAGTGACGA	480
ACAACCTCGA	G					491

- (2) INFORMATION FOR SEQ ID NO:262:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 231 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

GAATTCGGCC	TTCATGGCCT	ACATTTTTCT	ATTGATATAA	AAATTGTTAG	AGAAATATAC	60
AGTTGTATAT	TTCCCCCCTT	TATACAGAAA	TTTTACAATA	ATTTCAGATT	TTTCTGAGTT	120
TTTTCAGATT	TTTGATTCTA	TAATATGAGA	TTATTCTTTC	TTCCTCTTAT	TTTTTTAGGT	180
TATTTATTTT	TTCTTTTCTT	TTTAATTTGC	TCATACAGGT	TTACTCTCGA	G	231

- (2) INFORMATION FOR SEQ ID NO:263:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 445 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

GAATTCGGCC TTCATGGCCT AGTAAAATTT AAAATACATA CTAACATATA ACCCAATTTC	60
AACATATTAA GTGAATATGT ATTCTTAAAA GATCCACTAC TTTACATTTA GATGCGTTAG	120
GATGTATTAG AAATAAAAAC AGAAGAAAAG ATTTAGAATC TAGTCTGTCT TTGCCACTCA	180
AGCTAGTTAC CCTCTCTGAG TTTTATACCC CCTTCATCTA TTAAAATGGG GGGTAACGCC	240
AACCTGACTC CTTTAAAATG AGTTTGAGAG TCAGGCAAAT TAGAAAGATA CATAGATGAA	300
AACTTTTTAA AAAGTATATA GTCTTTCATG ATTTGTAGAA CACTTTTATA CTTTTCAGAG	360
TACTTTCACA TTGATCATAT TGTTTGTACT TTATGAAAGT CTTCTACAAA TCAGAATTAT	420
GCTTATTATA CAGATGTGGC TCGAG	445
(2) INFORMATION FOR SEQ ID NO:264:	
(i) CENTENON GUANA CENTENA CO	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 343 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(b) Toronoot. Illieat	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:	
GAATTCGGCC AAAGAGGCCT AATTACTTTA TATTTTAAAA GCTCTGTGAC TTCAGTAGTG	60
CATTGAAATA AAATTTTTAT TCATTATGAG AGAGTCTGTG AGGAACAGAA TCATGGTTCC	120
TGTGTGTTTG AAGATATGGC GTGGGGTGAT AGTGCTGGCA GCAGCTCTGT TGCTCTTGTG	180
CCCATGGCAT ACAGACTGGA TCTGCTGGTC CACGGCTCCT GAGGTTAATG TCCAAGCCCT	240
CTGCAATGCT GACAGTCTTC CTCATCCTCA CACCCTACCT CTCAGTTTCT ACCTGCCACC	300
TCCCCAGTAA TATTAGCCTC TTGAGTCCCC AACAACACTC GAG	343
(2) INFORMATION FOR SEQ ID NO:265:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 349 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:	
CANDOCCCC ANADOCCCO ADDINANTO ADDINOCCO ACCADENTE TOTAL	
GAATTCGGCC AAAGAGGCCT ATTAAAATTC ATTTATCAGT AGGATCATTC TGTTCTAGAC AAGTTGGCTA TATTATAAAA CATTAAGCAA GCAGGCACTA AGTTAAATAT TGTAGCAGTT	60 120
GAAATTTAAT GCTAATCTTA CAGTTTTACA CAGTTAACAA TCTAGGCCAA ATCTATTGAT	180
ACCTTTGGAA CTACCCTTTA AATTCCATCC TATGCTTGTG AAAAGGTTGC ATATAATTTC	240
TTTTCCTTTT TCTCTCTCT CTTCCTCTC TTTTTTCTT TTCTTTTCT ATTTCCTTT	300
- ILLICOLLI CICICICI CIICCICIIC IIIIIICIII IICIIIITCI AIIICCIII	300

- (2) INFORMATION FOR SEQ ID NO:266:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 335 base pairs

TCTTCCTTTT TCTTTCACAG AGTCTTGGTA TATCACCCAC ACTCTCGAG

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

349

GAATTCGGCC AAAGAGGCCT AGAATAAAAA TGCTTGTGTC AAAAATTCAA ACATTTGTCT	60
CTTTCCTTTC CATTCCAGTT CTAGGTCTCG TTCCAGATCA TATTCTCCAG CTCATAACAG	120
AGAAAGAAAC CACCCAAGAG TATATCAGAA TCGGGATTTC CGAGGTCACA ACAGAGGCTA	180
TAGAAGGCCC TATTATTTCC GTGGGCGTAA CAGAGGCTTT TATCCATGGG GCCAATATAA	240
CCGAGGAGGC TATGGAAACT ACCGCTCAAA TTGGCAGAAT TACCGGCAAG CATACAGTCC	300
TCGTCGAGGC CGTTCAAGAT CCCGGCTCCC TCGAG	335
(2) INDODUMENOU DOD GEO ID NO ACC	
(2) INFORMATION FOR SEQ ID NO:267:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 380 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(II) MOLECULE IIPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:	
GAATTCGGCC AAAGAGGCCT AGTGGAAATT TGTGGCTAGT GTGATTTTTG TTTGTTTCCT	<b>5</b> 0
TTTAAGTACT GTTGATCAGT TGTGACACTT ACTGGTTAAA CTTACGTTGC TAAAGATTTC	60 120
CTATAATAA GCCACACATT ATATTTAGAC TATATTAAGG GACCTTGGTT TTCTTCTAGA	120
PAGCAGCTGT CCCAAAGAAA ATATTTCTTC TTTGTCTGTT AAGATTTAGC TATTATCTGC	240
CAGTTGTTAA GAGGTTTTGG TTCCAAACTC AACCAGCAAT GTTGAGAGCT GAACTTAAGA	300
PAGCIGITGT ACTITITGCT TICCATCIGT TACTGTCCTT CATTCTTGGC TCCCTACTAT	360
CTATAAACAG CAAGCTCGAG	380
	380
(2) INFORMATION FOR SEQ ID NO:268:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 283 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
· · · · · · · · · · · · · · · · · · ·	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:	
GAATTCGGCC AAAGAGGCCT ATCTAGACCT GCCTCGAGTC AGCAACAACA ATTTTTAAAA	60
PTTCTTTCTG GATTCTAGAG TGAGTTTTTT TCATAACACA AGAGGATAAG AGTGAGGACA	120
ACAGGAGGTA TTGATGATCT GCTGAGCACC AGGCATTATG CTAAGTGCAT TCACACACAT	180
CTCAGTGCCT ATTGCCTCGT TGTGGACTTC TCTATCCCAG CTCGTCCCCC TGGCAAATTC	240
TTTCTCATCC TTCAACTCTC AGACACCTCC CCCGCGCCTC GAG	283
(2) INFORMATION FOR SEQ ID NO:269:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 157 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:	
GAATTCGGCC AAAGAGGCCT AACCAGGCAT TTTTCATTAG GGTTCTAGGT CCAGGTGAAT	60
ICTTGAGTTG GTTCGTTGTG TCATGTATTG GCCTTTAATA ATGCTCTTAT TTTGGCCCAC	120

GCCTGTGGTC CCAGCACTTT GGGAGGCTGG TCTCGAG

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(2) INFORMATION FOR SEQ ID NO:270:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 157 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:	
GAATTCGGCC AAAGAGGCCT AACCAGGCAT TTTTCATTAG GGTTCTAGGT CCAGGTGAAT	60
TCTTGAGTTG GTTCGTTGTG TCATGTATTG GCCTTTAATA ATGCTCTTAT TTTGGCCCAC	120
GCCTGTGGTC CCAGCACTTT GGGAGGCTGG TCTCGAG	157
(2) INFORMATION FOR SEQ ID NO:271:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 368 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:	
GAATTCGGCC AAAGAGGCCT ACCCAAATAA AATCAGAGTC AGAAATGGAA ACAGACAGTG	60
GAGTACCTCA AAACACTGGA ATGAAAAATG AAAAAAUAGC CAACAGGGAA GAGTGTCGCA	120
CCCAGGAGAA AGTTAATGCA ACAGGACCAC AGTTCGTGAG TGGAGTGATT GTGAAGATCA	180
TTAGCACAGA GCCTCTACCT GGCAGGAAAC AAGTCCGGGA TACTTTGGCA GCAATCTCAG	240
AAGTTCTTTA TGTTGATTTG CTAGAAGGGG ATACAGAATG CCATGCTAGA TTTAAAACTC	300
CTGAGGATGC TCAAGCAGTA ATAAATGCCT ATACAGAAAT TAACAAGAAA CACTGCTGGA	360
AACTCGAG	368
(2) INFORMATION FOR SEQ ID NO:272:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 367 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:	
GAATTCGGCC AAAGAGGCCT ACAACGAACG GCTTGGGNGC GGACTGGTAT CCGGGGACTG	60
TGACTTGCAG GGTCCGCCAT GGAGCCAGAG CAGATGCTGG AGGGACAAAC GCAGGTTGCA	120
GAAAATCCTC ACTCTGAGTA CGGTCTCACA GACAACGTTG AGAGAATAGT AGAAAATGAG	180
AAGATTAATG CAGAAAAGTC ATCAAAGCAG ANGGTAGATC TCCAGTCTTT GCCAACTCGT	240
GCCTACCTGG ATCAGACACT TGTGCCTATC TNATNACAGG GACTTGCTGT GCTTGCCAAG	300
GANAGACCAC CACATCCCAT TGAATTTCTA GCATCTTATC TTTTAAAAAA CAAGGCACAG	360
ACTCGAG	367
(2) INFORMATION FOR SEQ ID NO:273:	

(i) SEQUENCE CHARACTERISTICS:

(1) SEGMENT CHARACTERISTICS;	
(A) LENGTH: 250 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:	
GAATTTGGGT CCTAGGATAT AAATATTTTT CCCTTTATAA GATATTTATA GGATATTGCA AACAATTTCT GTTTTTCAT ATCCTTGCCA GCAGTTAGGG TTATCAAATT CTTTGATTTC	60 120
TTACTGATTT GTAAGTTTTT TTGTTTGTTT TTAGGTATTT TCAGGATAGT TACAAATGTT AGGAAAACTT ATTTTTATTT GGCTTTTGAA GTTTCCAGAT TTCTTGAACA GTGACCAATA TGGACTCGAG	180 240
	250
(2) INFORMATION FOR SEQ ID NO:274:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 133 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:	
GAATTCGGCC AAAGAGGCCT ATCTTTTTTC CTCTTTTTTT GTTGCAGAAA TGATAACCTA	60
CTATTCACTA TTCTGTGCCT TGCTTTGTTT GCATACTGAA AATTATCCAT GGAAGGATAC	120
AGCACCACTC GAG	133
(2) INFORMATION FOR SEQ ID NO:275:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 396 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(wi) CRAITENCE RECORDITION, CRAITE NO. 275.	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:	
GAATTCGGCC AAAGAGGCCT AATGAAACAT TTCTGTAACC TGCTTTGTAT CTTGATGTTC	60
TGTAATCAGC AAAGTGTATG TGACCCGCCT TCACAAAATA ATGCAGCAAA TATTTCCATG	120
GTTCAAGCTG CTTCAGCAGG ACCCCCATCT CTGAGAAAAG ATTCGACTCC AGTTATAGCC	180
AATGTAGTAT CATTGGCAAG TGCCCCTGCT GCTCAGCCTA CAGTGAATTC TAACAGTGTC	240
TTACAAGGTG CAGTTCCAAC AGTAACAGCG AAAATCATCG GTGATGCAAG TACTCAAACA	300
GATGCCCTGA AACTGCCACC TTCCCAACCT CCAAGGCTTT TGAAGAACAA AGCTTTATTA	360
TGCAAACCCA TCACACAGAC TAAAGCCACA CTCGAG	
TOCHANCECK TCACACAGAC TAAAGCCACA CTCGAG	396
(2) INFORMATION FOR SEQ ID NO:276:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 391 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

GAATTCGGCC	AAAGAGGCCT	ACCCCTCCCC	ATTTCTAGTT	TCATGAACTG	TGCACAGGGA	60
TATGGGGCTG	TTCGAGGTAC	TTTTGGGCTG	ACCAAGGCTC	AGAGGCTACT	GACAGCTTTG	120
CTGCAAGTAA	CTTCTAGGCC	TTGTGGGTCC	CAGTGCAGGG	AACCCATGTG	CGGTGACACT	180
GGAGAAGCCA	TCTGATCCAG	GTCTCTCACT	TGACAGATGG	GGAAACTGAG	GTCCAAAGAG	240
GTACAGCAGC	TTGGTTTAAG	AGATAGAGAT	GGAACTGGAA	CAAAAATAAT	AACCATTTGA	300
TAATATTTTA	ACATTTATTG	ATTTGTTTTT	ATATGCCAAG	ACCTTTTAAA	GCATTATCTC	360
CTTTAAACTC	TCATAACCAC	TCTTACTCGA	G			391

- (2) INFORMATION FOR SEQ ID NO:277:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 299 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

GAATTCGGCC	AAAGAGGCCT	ACTGCTTCCT	GATCATTTGT	CTTTTTAAAT	AAAAATATGA	60
TATTTGAGAT	TCTTTTATTC	TCTTTAAATA	TTTGAATACA	GAGTCTATTT	GAAGGACCAG	120
TATATTGAAT	AGCAGTAATA	TTTGAAGGAC	TAGTCAGCTG	TAGAAGCCTT	GACTTCAGAT	180
CTTCACCCAA	GAAACTCTGT	GTATTTGCTT	TTCCTGGGCC	ACTCAGATAG	ACAATTGTGT	240
TTTNGATACA	GTAAGAGTTT	GCAGCTTAGC	TTAACTAGAA	ATAATCCGGA	TGCCTCGAG	299

- (2) INFORMATION FOR SEQ ID NO:278:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 430 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

GAATTCGGCC	AAAGAGGCCT	ACTAGGATTT	GAGGAGGACG	CCTCTTTTGC	AGGAGGATGC	60
AGTGAACAGC	CAAAGTCATC	TGACATCCTT	TTCCATCTTT	TTCCTTCTAG	TATCCCAGTT	120
TCAAGGCCCA	GGAAAGGCAG	<b>GGACTAACAT</b>	ATGGAGCAGT	TACCCCAGAG	TTCAAAGGGT	180
TAATCTCTAA	GAATTCATTC	TCTGACACCA	GCCACAGCTC	TTGTCCCCAT	CTCTGGGACC	240
GTCCCCTCTG	AGCCCCAGGT	TGGCAGCTTC	CCTGAATTCC	TTCTATGATA	TAATTTGTAA	300
TTCGGCAGGG	CTCTGGGACC	CAGGCTCAGA	GACCCAGGCT	CTGCTCTCTC	CTCAGTTTCC	36C
AGGAGTCAGG	GCTTGCTCTA	AGGGAGGAAG	TAAACAGGCC	TTTCCCTTGC	TCCCTCTCCT	420
TTTCCTCGAG						430

- (2) INFORMATION FOR SEQ ID NO:279:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 392 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

GAATTCGGCC	AAAGAGGCCT	AGTGGGAGTT	AGATGTATTA	TATAAAAATG	TCCCCAGCAT	60
CAAAATGACT	CAGAGTATGA	CTGTATTTTT	AAATTAAATA	TCAAGACCTA	TCATCTGACA	120
AAACATATGA	ATGACAATGA	GATATAATAT	TTGAAATTAG	ATCCGTTCTG	GGGAATCAAA	180
GATATTTTGT	AACAGTATAC	ACAGTAGGCA	TTGGTAAGTA	AATGAGAACT	CTATGAGCTG	240
TTTTCTGGAA	AAGTTTAAAA	TGAAATTTGT	CAAATATCAA	ATGATTGTTA	TAAGAAAATC	300
AGTGGAGGCA	GTATCCTTGG	AAAAATCCAG	AAACAGTTTT	GTNTGTTTGT	TGTTTTTTAC	360
ATCAAGGCAG	ATCAGCAGGT	GAACAGCTCG	AG			392

- (2) INFORMATION FOR SEQ ID NO:280:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 354 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

GAATTCGGCC	AAAGAGGCCT	AGAAGAAACT	TTTTCTTGGG	AGCAAGGTAG	TTATTTCAAA	60
GCACAGAAAA	AGGCGGCGGG	GGGCACAGAG	AAGCACAGAG	AAGCGGGGGC	AGTTGCTCAG	120
GTAAAACATT	CATCTTGGCT	TTTCTTTTTA	AAAGATAAAC	TTTGTCCCAC	GTAAAGAGGA	180
AAACTGCATA	GATATTCATT	GAGATTATCT	GATTTGTCAC	TGTTGCCAAA	GAAAAAACAA	240
AGGTAAAATA	CACGAGTTTC	TGCATTCAGA	AGAAAGTATT	TCAGGTAAAA	ATTAACTATT	300
AAGCAACTTT	TCTCAGCAGA	AGAAATGCCC	AAATTCTTAA	GGACAGTACT	CGAG	354

- (2) INFORMATION FOR SEQ ID NO:281:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 308 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

GAATTCGGCC	AAAGAGGCCT	ACTTTGAGAT	${\tt TTTTTTGTTG}$	TTGTTTCCTT	TTTGTATTTT	60
ACTGATATCA	CCAGGATAGT	TTACTCTCCT	TCTAGCTTTC	TGCTTACCGC	ACACTGGATG	120
ACACACACAT	ACACACCCGC	AAAAATGCTC	ATGAACCCAA	TCCGGAGAAG	GTTCCAGCAG	180
GTCCCCCACC	CTCCCCTCCT	CGTCCTACTT	CTCCTCTTGA	CAGCGAGGAC	AGGAGGGGA	240
CAAGGGGACA	CCTGGGCAGA	CCCGCCGGGT	CTCCCCCCAC	CCCACCCGGC	CCTCANATCA	300
TACTCGAG						308

- (2) INFORMATION FOR SEQ ID NO:282:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 462 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

GAATTCGGCC	AAAGAGGCCT	AGACCTGCCT	TGTGTTTTCC	ACCCTGAAAG	AATGTTGTGG	60
CTGCTCTTTT	TTCTGGTGAC	TGCCATTCAT	GCTGAACTCT	GTCAACCAGG	TGCAGAAAAT	120
GCTTTTAAAG	TGAGACTTAG	TATCAGAACA	GCTCTGGGAG	ATAAAGCATA	TGCCTGGGAT	180
ACCAATGAAG	AATACCTCTT	CAAAGCGATG	GTAGCTTTCT	CCATGAGAAA	AGTTCCCAAC	240
AGAGAAGCAA	CAGAAATTTC	CCATGTCCTA	CTTTGCAATG	TAACCCAGAG	GGTATCATTC	300
TGGTTTGTGG	TTACAGACCC	TTCANAAAAT	CACACCCTTC	CTGCTGTTGA	GGTGCAATCA	360
GCCATAAGAA	TGAACAAGAA	CCGGATCAAC	AATGCCTTCT	TTGTAAANGA	CCAAACTCTG	420
GAATTTTTAN	AAATCCCTTC	CACACTTGCA	CCACATCTCG	AG		462

- (2) INFORMATION FOR SEQ ID NO:283:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 240 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

GAATTCGGCC	AAAGAGGCCT	AGCAGATTCT	TAATTTCCCT	GTCCATATTT	TCCCCTTTCC	60
TTTCTCCCTG	CCCGTTCCAT	GGTCTTATCT	GGCTGCTTTC	TCAATTTATT	CTTGGTTGCT	12Ô
TGTGGATTCC	CTTCTATTAA	TCTTGAAGTC	GTTACTGACA	TGTTTGGCCC	TATACCAGCT	180
AGACCATTGC	CTGAAGACTT	TTTGATGAAC	<b>AATCTGTGTA</b>	AAGAAAAAGG	GAATCTCGAG	240

- (2) INFORMATION FOR SEQ ID NO:284:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 349 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

GAATTCGGCC	AAAGAGGCNT	ACCAGGANTT	TCTATTCAAT	TGAGAAGAAC	CCAGCAAAAT	60
GGGGATCTCC	ACAGTCATCC	TTGAAATGTG	TCTTTTATGG	GGACAAGTTC	TATCTACAGG	120
TGGGTGGATC	CCAAGGACTA	CAGACTACGC	TTCACTGATT	CCCTCGGAGG	TGCCCTTGGA	180
TACAACTGTA	GCAGAAGGTT	CTCCATTTCC	CTCGGAGTTG	ACCCTGGAGT	CAACTGTAGC	240
AGAAGGTTCT	CCGATTTCCT	TGGAGTCAAC	CCTGGAGTCA	ACTGTAGCAG	AAGGTTCTCT	300
GATTCCCTCA	GAGTCAACCC	TGGAGTCAAC	TGTAGCAGAA	GGACTCGAG		349

- (2) INFORMATION FOR SEQ ID NO:285:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 307 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

GAATTCGGCC AAAGAGGCCT AAAAAAATAA GAAATAATCT ATTCCACATT TAATAATTTG AATCTTCCTG CTATAGATAT TTGGTTATCT TGACTTTTTA ANATAACATA TTTCTACAGG ATTTTGAGTC TGAGAAGAGA AAGGTAANAT GCAAGACACT TCGATTTGTT GCACATTATT ATGGAGCATC ATTAATGGTT TGNACATTC TTGTCCTTTG GGCTTGAATG GACAGTACCA AATTTGGGGT AATCAGCAAC TTGATGCACA GCTACGAGGA ATAAATGCTT TTGCTAATGC ACTCGAG	60 120 180 240 300 307
(2) INFORMATION FOR SEQ ID NO:286:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 324 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:	
GAATTCGGCC AAAGAGGCCT AAAAGATTAA AAAAAAATTT GTGTGATTTG ACTATATATT	60
AAAATCTCTT TCATAATTAG TCAACAATTT AAGCAACAAT TAAATTATTA GTGCTGTGGA AAATATAGAA GAAAGATAAT TTCTTATTCC CCTCCTGAGG AAAGCATTG ATACACCTGG	120 180
AAAGGAGCTG CTATGAAGCC AATTTATCTG TTCTTTTTAT CAATTCAGCA GCATTTAAGA	240
TCAGATTTTT TCTCTAGTGG TCCAGCAGAG GGAGCCCTAG CACATGAATT GTTTTCATTT	300
CGTGCTTGCA CCCAGGATCT CGAG	324
(2) INFORMATION FOR SEQ ID NO:287:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 311 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:	
GAATTCGGCC AAAGAGGCCT AAGAGAGATC AGTAAAACCA CTGGNAAAGA AAAGATGGAG	60
AAAATGTTGG AAAACCAGAA CTGTNTGCTG TCAAGNTCAT GTGGAATGTT CAAGAAAGAA	120
TCTGACTCTA TTATCTAATA TCTTACATAC NTCCACCAGA CTGGACTTGC TATTTGAATT	180
TTAAGCAAGT TTCCTTTCCT TTTATACAAA TTGCAAATTT CATATTTTTA TAATCACATC	240
CTAGGAATAG CACAATAATT GGGAAATAGA ACCCTTATCA CTAGNAGAAC CATTTTCCTG CCACTCTCGA G	300 311
(2) INFORMATION FOR SEQ ID NO:288:	
A CONTRACT CONTRACTOR OF CONTRACT CONTR	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 307 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:	
GAATTCGGCC AAAGAGGCCT ATGCCCCATA AAAGGGCTCC TGAAGCTCTT TGTGAAGGGG	60
TCTGAAAAGG GCAGATGAGG GTGTCCTTTG GGGCGGATGT GGGGTTTGGG ACAATTGCAT	120

GTGATTGTCA TTCTTTAGCT GTCTGCATCC CACAGAAACT TTTTTCTGAG TCTTCCAGCT GGCCCAAGTC CTGGGTCTCT TTTACTGTTC TTGTAGCTGA CTACAGTAGG CAGATGAGGA ACTCTTAGTC AATCTGGAAA AACTCGACTG ACTATAAACA ATCCTAAATT GAAAGAAAGG TCTCGAG	180 240 300 307
(2) INFORMATION FOR SEQ ID NO:289:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 477 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:	
GAATTCGGCC AAAGAGGCCT AGCCGGTGTG GGGAGGATTG GCTCAGCCAC CCGCTGGGAA TCGTGCAGGG ATTCTTCGCC CAAAATGGAG TTAATCCTGA CTGGGAGAAG AAAGTAATTG AGTATTTAA GGAAAAGCTG AAGGAAAATA ATGCTCCTAA GTGGGTACCA TCACTGAACG AAGTTCCCCT TCATTATTTG AAACCTAATA GTTTTGTGAA ATTTCGTTGC ATGATTCAGG ATATGTTTGA CCCTGAGTTT TACATGGGAG TTTATGAAAC GGTTAACCAA AACACAAAAG CACATGTTCT TCATTTTGGA AAATATAGAG ATGTAGCAGA GTGTGGGCCT CAACAAGAAC TTGATTTAAA CTCTCCACGA AATACCACTT TGGAAAGACA GACTTTCTAT TGTGTTCCGG TGCCTGGGGA ATCTACGTGG GTAAAAGAAG CCTATGTTAA TGCAAACCAA GCTCGAG	60 120 180 240 300 360 420 477
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 318 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:	
GAATTCGGCC AAAGAGGCCT AAAAAAATCT TCTGGAAATA ATTCTTAGCT GTGTAAGAAA TTTGATACTT AAGGAGACAG CAGTGGAGTC ACTTAACTAA TTTGTGTTGG TTTTTGACCT GCATAGTGAC TGCCATTTAC TTTTATGTTT TGGTCAATTA GATACTAAGT AAAAAGATAG TTGGTATTTT GGCTTCAGAT CAGGTCTATT TCTCCAACTT CTATATATCC TTTCTGTGAT TAAAACAAAT AAACAATCCT CAGTATCATC ATTTAACACC TCTAACTGAT AGAAAAAATG AGGTTGTGGG TCCTCGAG	60 120 180 240 300 318
(2) INFORMATION FOR SEQ ID NO:291:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 213 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:	

120

GAATTCGGCC AAAGAGGCCT AACCTTGGGA TTTTCTATAT ATATGATGGT CTCATTTGTG
NATAAACACA ATTTTATTC TTCCTTTCCA ATCTGGATGC TTTTTTTTT TNCCTATTGC

ACTGCCTATT GCATTCCTAA AAACTCCATT CCAATGTTCA ATAGAAATGG TGAAAGTGGA

CATTGGAATG GAGTTTTTAG GAATGCACTC GAG

(2) INFORMATION FOR SEQ ID NO:292:

180

213

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 644 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:	
GAATTCGGCC AAAGAGGCCT AAAAAGAATT AACCAGCTCT TCAGTCAAGC AAATCCTCTA CTCACCATGC TTCCTCCTGC CATTCATTC TATCTCCTTC CCCTTGCATG CATCCTAATG AAAAGCTGTT TGGCTTTTAA AAATGATGCC ACAGAAATCC TTTATTCACA TGTGGTTAAA CCTGTTCCAG CACACCCCAG CAGCAACAGN ACGTTGAATC AAGCCAGAAA TGGTTGCAGG CATTTCAGTA ACACTGGACT GGATCGGAAC ACTCGGGTTC AAGTGGGTTG CCGGGAANKG CGNTCCCACC AAATACATCT CTGATGGCCA GTGCACCAGC ATCAGCCNTA NGAAGGAGNT GGTGTGTGCT GGCGAGTGAC TTGCCCCCTGC CAGTGCTCCN TAATTGGNTT GGAGGAGGCT GTGGAACAAN GTANTGGAGC AGGAGGAGCT CCCAGGGNTG GCGGTGTTCC AATGACAAAA CCNGTACCCA GAGAATCCAG NTGCAGTTCC AAGATGGCNG CACACGCACG TACAAAATCA CAGTAGTCGG TGCCNGCAAG TGCAAGAGGT ACACCCGGCA GCACANNGAG TCCAGTCACG ANTTTGAGAG CATNTCACGT GCCAAGCCAC CGAG	60 120 180 240 300 360 420 480 540 600
(2) INFORMATION FOR SEQ ID NO:293:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 299 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:	
GAATTCGGCC AAAGAGGCCT ATTTNTGGAT GGTGCTAGCG AANTAGAGGC TAATCCCCAA CATGAGGTTC TTCTAATTTC ANGGTTGTGA TTTTCCAGTG AAAGAAATNA ANAAGAATTT GCAGATTCGT GGAGACTTGG GAAGGATATN AAGCTGTCTT ACAACCCCAG ATTCACCCAA AATTCAGCAA ATCACTGAAT ATTCNNAATA AAAATTGAAG TATTTTCNAA CTTCAGTTTT TATCTCCAGA GGTTNACGTC CNATGTAATC CGAAATCCTC ACGANGACAT AACCTCGAG  (2) INFORMATION FOR SEQ ID NO:294:	60 120 180 240 299
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 310 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:	
GAATTCGGCC AAAGAGGCCT ACAACAACAA CAAAAGAAGA ATACTAATTA GAATTTGAGT TCTAGGGGTT TTTCCTAGGT TTTTCATTCT AGACTTAGCT TTTATTCAAA CCTGTTGATC	60 120
192	

TTCAATCAGA GTAGGGAGCA GTTTTATTGA ACAGCACATT TTCAAATTCT TCAGTTGTGT TTTGTTTTTC AGCTACGTGT CTCTCTGTGA TAATGAAAAG ACAGGTTGCA AAGCCCGGGA TTCGCTCGAG	180 240 300 310
(2) INFORMATION FOR SEQ ID NO:295:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 351 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:	
GAATTCGGCC AAAGAGGCCT ACATCTATTG AGGAAAACCA CAAAAAACTT CAAAACAGCT ACAACGGGAA AAAGAGAGTT TTGTCCCACA GTCAGCAGGC CACTAGTTTA TTAACTTCCA GTCACCTTGA TTTTTGCTAA AATGAAGACT CTGCAGTCTA CACTTCTCCT GTTACTGCTT GTGCCTCTGA TAAAGCCAGC ACCACCAACC CAGCAGGACT CACGCATTAT CTATGATTAT GGAACAGATA ATTTTGAAGA ATCCATATTT AGCCAAGATT ATGAGGATAA ATACCTGGAT GGAAAAAAATA TTAAGGAAAA AGAAACTGTG ATAATACCCA ATGAGCTCGA G	60 120 180 240 300 351
(2) INFORMATION FOR SEQ ID NO:296:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 330 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:	
GAATTCGGCC AAAGAGGCCT AGAGTGAGAC CTTATCTTAA AAAAAAAAAA	60 120 180 240 300 330
(2) INFORMATION FOR SEQ ID NO:297:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 439 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:	
GAATTCGGCC AAAGAGGCCT AAAAAAATAT AAGTAACAGA GGNAGAAATA ACTGTTATTT GTCAAGTGAC AAGCTTTTAA TGTCAGAATG GCTCACCTAA AGCGACTAGT AAAANTACAC ATTAAAAGAC ATTACCATAA AAAGTTCTGG NAGCTTGGTG CAGTAATTTT TTTCTTTATA ATAGTTTTGG TTTTAATGCA AAGAGAAGTA AGTGTTCAAT ATTCCAAAGA GGAATCAAGG	60 120 180 240

ATGGAAAGGG ACATGAAAAA CCAAAACAAG ATGTTGGATT TAATGCTAGA AGCTGTAAAC AATATTAAGG ATGCCATGCC AAAAATGCAA ATAGGAGNCA CCTGTCAGGC AAAACATTGA TGCTGGTGAG AGACCTTGTT TGCAAGGATA TTATACAGCA GCAGAATTGA AGCCTGTCCT TGACCGTCCA CGTCTCGAG	300 360 420 439
(2) INFORMATION FOR SEQ ID NO:298:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 428 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:	
GAATTCGGCC AAAGAGGCCT AATTATTCT TGTCTCTCCC CAAATGAAAT CTGGGACATT ATGACAATTT ATTTTCTAA GGATGATCTT GGTTCTGCCT ATTGAAATGT CCTCACTCAC CTCCAAGAGG AAGGGGGATG GCTTCAGAAA ATGTCTTTAA GTGTTTTTAT TTTTCACGAG TTATTTATTG CAACACTAGC TCTTCCCTGC AGGAAGCTAT ATAATTGTGT GCTTAATTGG TAACATAGAA GAATTCCTAG CTACTTCCTA GAGAATATAC TGTTGAATTC CTTGTCACTC AAGTATCTGT TAAAAACTCA ACCGTGGGAA ACAATGTCTA TGGATGCCTT TGGGAAAATA CACATTTTAC CTATTATTTC ATCTTTTTTC TCACTTTGTC AAGTAGTAGG TACCCCACTG	60 120 180 240 300 360 420 428
(2) INFORMATION FOR SEQ ID NO:299:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 300 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:	
GAATTCGGCC AAAGAGGCCT AACATTATCG ATTCCATTTT TTTACTGTTG TAATTCTGCT TCTTATTGCC TGTGTAAATT TCTGCTCTAT ATTAGTTTCC TGATACCCTA TCATTAATTC AGTCTGCCCT TTTTTCATAT CATTCTACTG TTTTGTCTCA TCTTCCTTAT ACTTTATTCA GAGACTGTGT TTTCATGAAG TTTGTGAAAA ACATTTTAAA AATTGTTTAA AATGTACTCT TTGTCTATTT CTTGCTATTT TTTCTTTTTG ATATTCTGGA ATATATCCAC AGCGCTCGAG	60 120 180 240 300
(2) INFORMATION FOR SEQ ID NO:300:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 311 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:	
GAATTCGGCC AAAGAGGCCT ATAGATTGTT ACATTTGTTC TGTGCATTCC ATGAAGTTTC TTACCCTTAG AGTTATTTCT GTCTTAGTAA CAGCAACAAG TGGGAATGGA GACTTTGGTG ACTGGAGTGC CTTCAACCAA GCCCCATCAG GCCCTGTTGC TTCCAGTGGC GAGTTCTTTG	60 120 180

GCAGTGCCTC ACAGCCAGCG GTAGAACTTG TTAGTGGCTC ACAATCAGCT CTAGGCCCAC CTCCTGCTGC CTCAAATTCT TCAGACCTGT TTGATCTTAT GGGCTCGTCC CAGGCAACCA TGACACTCGA G	240 300 311
(2) INFORMATION FOR SEQ ID NO:301:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 392 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:	
GAATTCGGCC AAAGAGGCCT AGCGCGGTGT GTCGTGGTGT GGCGCGTGT GGCATGGCGT GGTGTCCCAG CTTGCTACAC ATTTGTGGTT TTTAAATGTT TGTTGGATAC AGTAACACTT TGTTAATTTT AATTATATGC AAGATAACTT GATTGCCCTA AAACAGCCAT TTGGGTCAAG ATAAAGCCAT CGCCCTCTGA AGGGGCNTGA GCTGGGTGTC TCCTCCATCA GTCGNTGTGA TAACTCTATG CCAGTTCGA TTTCCAAAGT CAGAAGTGCA AAGCAGGGCT GGTTATTAAT CNTGTCAAAT CGTCCAGGTC CTGTGTNGTC GNACTCCATT ANTTATNTAG GTCCATANGA	60 120 180 240 300 360
TGTGTCTTAC NACGNAACAA ACCCCTCTCG AG	392
(2) INFORMATION FOR SEQ ID NO:302:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 387 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:	
GAATTCGGCC TTCATGGCCT AATGGAATTT GAGTCCAAAG GTAAATATAT TAAACATATA GATAAGAAGA AAAGAAAAAC GTTATTTAAG TATCTGATCA GCTCTGCACC CCAGGGACCT CCACTTTTGC CCAGGTTTGA GAATTTGATC TATAGAATTA CCTGCATTCT TTCCCGCTCA TCCATCCAAT CAGCCACCTT TCTCCCTTCA AAGAAGTGTC TTCATTTTT TCCTTCTTTT GTTATTTTTA TTGACTGCCC ATCACTGTTA TTAAATCCTT CCCTCTTTTT TTGAATGAAG CAGCAGAGCC TTTTATTTTG TTTTCCTTGT TTTGTTTTTT GTTTTTTGTGT TTCAGAAATG ACAGGGCTGT ATCACAGCAG TCTCGAG	120 180 240
(2) INFORMATION FOR SEQ ID NO:303:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 338 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:	
GAATTCGGCC TTCATGGCCT AAAAATTAAG CAAGCAATAC CTAGCCAATA GTTCTGCTTA ACTTTTNGGT TAAGTATTTT GTTGGGATTC CTATAAATAA TTTTTCACAC AAAGTTTTAA ATTTCTGGTG TACTTTGACT CTCAACTGAG AGTGGATAGA GTTTTTCTTT TGAGGATTAC	120

ATCTTAAAAT GTCCATCGCC TGGCTGGTTA TAAGCATTTG TCACCTTTTG AAGGTAAAAT	240
ATACTCTGGC CCTTCTTGAC TCAGTTACAG GTCATTTTAG GTCCAGTAAT AAGAGTCAGG	300
TGTTTGGTTA TTGCTTTCAG AGTCAGACAA ATCTCGAG	338
(2) INFORMATION FOR SEQ ID NO:304:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 478 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:	
GAATTCGGCC TTCATGGCCT ACGAAGAAAA AATATTTTIIG AGAGAATTTC CCAGATTGAA	60
AGAAGATCTG AAAGGGAACA TTGACAAGCT CCGTGCCCTC GCAGACGATA TTGACAAAAC	120
CCACAAGAAA TTCACCAAGG CTAACATGGT GGCCACCTCT ACTGCTGTCA TCTCTGGAGT GATGAGCCTC CTGGGTTTAG CCCTTGCCCC AGCAACAGGA GGAGGAAGCC TGCTGCTCTC	180
CACCGCTGGT CAAGGTTTGG CAACAGCAGC TGGGGTCACC AGCATCGTGA GTGGTACGTT	240
GGAACGCTCC AAAAATAAAG AAGCCCAAGC ACGGGCGGAA GACATACTGC CCACNTACGA	300
CCAAGAGGAC AGGGAGGATG AGGAAGAGA GCAGACTAT GTCACAGCTG CTGGAAAGAT	360
TATCTATAAT CTTAGAAACA CCTTGAAGTA TGCCAAGAAA AACGTCGTG CTCTGGG	420
THICHMAN CITAMANA CCITAMANA TACCAAGAAA AACGTCCGTG CTCTCGAG	478
(2) INFORMATION FOR SEQ ID NO:305:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 568 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:	
GAATTCGGCC TTCATGGCCT AGACGAGCGG AGTAAAATCT CCACAAGCTG GGAACAAACC	60
TAGTCCCAAC TCCCACCCAC CGGCGTTTCT CCAGCTCGAT CTGGAGGCTG CTTCGCCAGT	120
GTGGGACGCA GCTGACGCCC GCTTATTAGC TCTCGCTGCG TCGCCCCGGC TCAGAAGCTC	180
CGTGGCGGCG GCGACCGTGA CGAGAAGCCC ACGGCCAGCT CAGTTCTCTT CTACTTTGGG	240
AGAGAGAGAA AGTCAGATGC CCCTTTTAAA CTCCCTCTTC AAAACTCATC TCCTGGGTGA	300
CTGAGTTAAT AGAGTGGATA CAACCTTGCT GAAGNTGAAG AATATACAAT ATTGAGGNTA	360
TTTTTTTCTT TTTTTTTCA AGTCTTGATT TGTGGCTTAC CTCAAGTTAC CATTTTTCAG	420
TCAAGTCTGT TTGTTTGCTT CTTCAGAAAT GTTTTTTACA ATCTCAAGAA AAAATATNTC	480
CCAGAAATTG AGTTTACTGT TGCTTGTATT TGGACTCATT TGGGGATTGA TGTTACTGCA CTATACTTTT CAACAACCAA GACTCGAG	540
CTATACTITI CAACAACCAA GACTCGAG	568
(2) INFORMATION FOR SEQ ID NO:306:	
(i) SEQUENCE CHARACTERISTICS:	

- - (A) LENGTH: 349 base pairs
  - (B) TYPE: nucleic acid (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

GAATTCGGCC	TTCATGGCCT	AATCAAAAAT	ACCTTACCTT	GTTCTGCCCT	GTGAAAGTAG	60
CCTAAGGCCT	GTCAAAAACA	CAAAGAGCCC	AAACATAATA	AAAAAGATTA	AAGAAGACAA	120
TATTAAANAA	GCATTGTCTC	AAAGATCTAC	TGCTATATTA	TATTTAAGTC	AGGAAGTAAA	180
TCATCTTAAA	ATAATGGTCA	CTTCTTCAAC	AGTGAGAGTT	AACACCCAAA	GTGAACGTAA	240
CACTTCAATC	<b>ATCAAGATTA</b>	CAATATATGG	ACTACTTCTG	GTAATAACTT	GGTTGCTGTT	300
TAGAACTTGT	ACCAAACTAA	CATCATGTGC	AGAGAGGAAA	GAACTCGAG		349

- (2) INFORMATION FOR SEQ ID NO:307:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 316 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

GAATTCGGCC	TTCATGGCCT	AGTGATGGGG	ATGTGATGTG	GGCATCTGCT	AATTCGTCTG	60
CAACTACATG	ACCTAAGATG	GCCTCATTAA	TCTAAGGGGC	CTCAGCTGGA	ACACTTGCCT	120
CTGCTGGATA	ACCCAGGTCT	AGTGTTATCC	TCCAGACTAG	ACCTGGCTTC	TTCTGTGGCA	180
GTCTCAGGGC	AGTGTTCCAA	GACGGTGAGA	GCAGAAGCCT	AGGTTTGGCC	ACATATCCCT	240
AACTCATAGG	ATGGTGACAT	AAACTCTACC	TCTTATGGAG	AAATAGCAAG	TTACACTGCA	300
TACGGGACGA	CTCGAG					316

- (2) INFORMATION FOR SEQ ID NO:308:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 445 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

GAATTCGGCC TTCATGGCCT	AGTGGCAACG	ACTTGGACAT	CTGAGCTGTC	ACTGCCGAAA	60
ACAGGCCGCA AGAGAGATAA	TCAATATGCA	TTTCCAAGCC	TTTTGGCTAT	GTTTGGGTCT	120
TCTGTTCATC TCAATTAATG	CAGAATTTAT	GGATGATGAT	GTTGAGACGG	AAGACTTTGA	180
AGAAAATTCA GAAGAAATTG	ATGTTAATGA	AAGTGAACTT	TCCTCAGAGA	TTAAATATAA	240
GACACCTCAA CCTATAGGAG	AAGTATATTT	TGCAGAAACT	TTTGATAGTG	GAAGGTTGGC	300
TGGATGGGTC TTATCAAAAG	CAAAGAAAGA	TGACATGGAT	GAGGAAATTT	CAATATACGA	360
TGGAAGATGG GAAATTGAAG	AGTTGAAAGA	AAACCAGGTA	CCTGGTGACA	GAGGACTGGT	420
ATTAAAATCT AGAACAAAAC	TCGAG				445

- (2) INFORMATION FOR SEQ ID NO:309:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 531 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

GAATTCGGCC	TTCATGGCCT	AGAAGTTCCT	TATGCTACTT	TCACTGAGCA	TCCTATGAAA	60
TACACCAGTG	AGAAATTCCT	TGAAATTTGC	AAGTTGTCTG	GGTTCATGTC	TAAGCTTGTT	120
CCAGCTATCC	AGAATGCCCA	CAAGAATTCA	ACTGGATCTG	GAAGAGGAAA	GAAACTGATG	180
GTGTTAACTG	AACCCATTTT	GATTGAGACC	TACACAGGGC	TGATGTCATT	CATTGGAAAC	240
CGCAACAAAC	TTGGCTATTC	CCTTGCCCGT	GGGAGTATTG	GTTTTTGAGA	GTCTTTTTGG	300
TACCATAAGC	ATATCATCCA	CAGATATGTC	ACTTTGAAAA	TTCCAGTTTG	ACCCACGCTA	360
TTTTTGGACT	NAAACAATTA	ATTATTTTTA	AATGACGCTT	TATGATTTAG	AAATTTAGTA	420
TTTCCGAAAA	TTTAAAAGCT	TGATTGGACT	GATAGATACA	CACTTTAGAC	CTCATACAAG	480
AATAATCAAA	TTTTCTTAAA	ACTAGAAAAT	AAATGCTGCT	GATACCTCGA	G	531

- (2) INFORMATION FOR SEQ ID NO:310:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 381 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

GAATTCGGCC	TTCATGGCCT	ACACTCATGC	TGCCAGTCCC	CAAAAGACTT	CATTCATTCA	60
ACATATATGT	GACCGCCTGC	TACGTGCCAG	GCGTGGGCCA	GGTCCTAGGG	ACAAAGGAGA	120
GGCCTCCGCA	CCCCACCCCA	TGACCCATAC	CTCCTCTTCC	CCACCTCCCT	GGGCCAGCCT	180
GCCTTCCTTC	TCCCTCCTCC	TCCTTCCTGG	GGGAAGGAAG	CCCCACCTTC	TGTGCGCAGT	240
CAGCTCCTAA	GCACGCTCCC	GCTTCCCCTG	GCCTCCCCAT	TTAAAAAGGG	AGGCAAAGGA	300
TGTCACCACT	GTCACTACAC	TCATGGCTTT	GCTCTGGGAA	GTCCTGCAAA	TAAAATGAAA	360
GTTCTCCAAC	CCGTACTCGA	G				381

- (2) INFORMATION FOR SEQ ID NO:311:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 339 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - •
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

GAATTCGGCT	TCATGGCCTA	CTTTGACGCA	CCAGGCACAA	CCCAGAAAGA	CGAGATTGTG	60
GAAATCCATG	AGGAGAATGA	GGTCGCATCT	GGTACCCAGT	CAGGGGGCAC	AGAAGCAGAC	120
GCAGTTCCTG	CACAGAAAGA	GAGGCCTCCA	GCACCTTCCA	GTTTTGTGTT	CCAGGAAGAA	180
ACTAAAGAAC	AATCAAAGAT	GGAAGACACT	CTAGAGCATA	CAGATTAAGA	GGTGTCAGTG	240
GAAACTGTAT	CCATTCTGTC	AAAGACTGAG	GGGACTCAAG	AGGCTGACCA	GTATGCTGAT	300
GAGAAAACCA	AAGACGTACC	ATTTTTCGAG	GGGCTCGAG			339

- (2) INFORMATION FOR SEQ ID NO:312:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 384 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

CCCTCCCTCC	1 CM CM CC 1 -					
GCCIGCCICG	AGTCTTGGAT	ACATCACACT	TGAGTCAAAT	CCTGGATACT	GCCAAAGGAA	60
CCTGAAAATC	CAGGAGACAA	CGCTAGCTAT	TCCTGTGAAC	CTCTAGAGGA	TTTGCGCCTG	120
CTCTTCAAAC	AACAACCAGG	AGGAAAGTAA	CTAAAATCAT	AAATCCCCAT	GGCCCTCCCT	180
TATCATATTT	TTCTCTTTAC	TGTTCTTTTA	CCCTCTTTCA	CTCTCACTGC	ACCCCCTCCA	240
TGCCGCTGTA	TGACCAGTAG	CTCCCCTTAC	CAAGAGTTTC	TATGGAGAAT	GCAGCGTCCC	300
GGAAATATTG	ATGCCCCATC	GTATAGGAGT	CTTTCTAAGG	GAACCCCCAC	CTTCACTGCC	360
CACACCCATA	TGCCCACACT	CGAG				384

- (2) INFORMATION FOR SEQ ID NO:313:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 547 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

GAATTCGGCC	TTCATGGCCT	AGGGGGGTGG	GCTGATGGAG	GGTAAGTAAA	ACCTCCTACT	60
GGAAGATGTT	CTCCTAAGAG	TTCCACTTCA	TTTTCTATCC	TTTGCAGAGG	CGATCGTGAT	120
TGCTGTGTTT	GGAAAGGGAC	AAACTGGCCT	GGTGGTGGCA	AATGAGGAGG	ATGATGGGGA	180
GAAAGGTGAG	GAGGATGTAT	AAGAAATGGA	TCACTAGAAA	TAAGGGGTGG	GAATGCAGCA	240
TATGGTACTG	GTAAGTGCTG	AACTGAACAT	GCCTGAAGCA	TTGGAGGAGG	CACACTACAG	300
ACAGGGAGGT	GCTGTCCACT	GAAAACCACA	GAGCATCCTG	GGACCTGCTG	TGTACTACAA	360
GCAGGGATGT	GCTGGCCTGT	GCAGAGTGGA	ATCCCATGTG	GTGCCACTGT	TGTTACTGTG	420
TAAGAAACAG	GGACTGTTCC	TTGATGGAGC	TGATCATGTA	TGTCAACCAT	GACTGCATTC	480
TGCTGGGGTG	GATGAGCAGC	AGGATGTAGC	AGACGGGGAG	ATACATTCGG	AGGGTGGAAG	540
GCTCGAG						547

- (2) INFORMATION FOR SEQ ID NO:314:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 490 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

GAATTCGGCC	TTCATGGCCT	AATTTGTGGC	TTACCTCAAG	TTACCATTTT	TCAGTCAAGT	60
CTGTTTGTTT	GCTTCTTCAG	AAATGTTTTT	TACAATCTCA	AGAAAAAATA	TGTCCCAGAA	120
ATTGAGTTTA	CTGTTGCTTG	TATTTGGACT	CATTTGGGGA	TTGATGTTAC	TGCACTATAC	180
TTTTCAACAA	CCAAGACATC	AAAGCAGTGT	CAAGTTACGT	GTGCAAATAC	TAGACTTAAG	240
CAAAAGATAT	GTTAAAGCTC	TAGCAGAGGA	AAATAAGAAC	ACAGTGGATG	TCGAGAACGG	300
TGCTTCTATG	GCAGGATATG	CGGATCTGAA	AAGAACAATT	GCTGTCCTTC	TGGATGACAT	360
TTTGCAACGA	TTGGTGAAGC	TGGAGAACAA	AGTTGACTAT	ATTGTTGTGA	ATGGCTCAGC	420
AGCCAACACC	ACCAATGGTA	CTAGTGGGAA	TTTGGTGCCA	GTAACCACAA	ATAAAAGAAC	480
CACACTCGAG						490

- (2) INFORMATION FOR SEQ ID NO:315:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 371 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

GAATTCGGCC	AAAGAGGCCT	AGGAAGTAAC	AGTGTATCAT	GTATGCCACT	GATTCCAGGG	60
GACACTCCCC	TGCTTTCCTC	CAACCTCAGA	ATGGAAATAG	TCGTCACCCA	TCTGGCTATG	120
TTCCAGGGAA	GGTTGTCCCA	TTGCGTCCCC	CTCCTCCTCC	AAAGAGTCAA	GCTTCAGCCA	180
AATTTACCTC	CATCAGACGA	GAAGACCGGG	CAACCTTCGC	ATTCTCACCT	GAAGAACAGC	240
AAGCCCAGAG	AGAAAGTCAA	AAGCAAAAGA	GACACAAAAA	TACTTTCATT	TGTTTTGCTA	300
TTACTAGTTT	CTCATTTTTT	ATAGCACTTG	CAATCATTTT	AGGAATATCC	TCAAAATATG	360
CTCCACTCGA	G					371

- (2) INFORMATION FOR SEQ ID NO:316:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 448 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

GAATTCGGCC	TTCATGGCCT	AATTTAAATG	TGGACAGATT	GGAGGGGAAA	GGTTTGCAGC	60
AAAAATCATA	AGTAGAAGGA	AACAGAATGG	TTAAGTACAC	AGTGTAGTAG	CCATTTAGGA	120
AAGTTATAAG	CCATTTAAAT	GCCATGTATA	AAGTGTTTTT	GATAAGAAAA	AATCAAAGTG	180
TAAAGGAGAA	TACAAAATTA	TATGTGTACT	GCGGACACAT	CTGTATTGTT	CTGTGTATGG	240
AAAACAGACT	GGGGAGAAAT	AGCTTTAAGT	CCTAATAGTA	ATTTTCTTTT	TCTCTCTTCT	300
TTTTTCTGCT	TTCTCTTTTC	CCTGTCTCCC	TCAATATTGC	ATATCTTTCC	CATTAAAAAG	360
TATTGTATTA	TATATCTACC	AACAAGACAT	TTGTTTCAGA	TTTTTTGGTT	TTGTCTTCAA	420
GGAACATTCT	TCTGCATACA	AACTCGAG	•			448

- (2) INFORMATION FOR SEQ ID NO:317:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 471 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

GAATTCGGCC	TTCATGGCCT	AGAGATGGGG	TTTTGCCACG	TTGCCCAGGC	TCATCTCCTC	60
GAACTCTTGG	ACTTAAATGA	TCCTCCCGTC	TTGGCCTCCG	AAAGTGCTGG	GATTACAGGC	120
ATGAGCCACA						180
CCATCCATAC	CTTATTTCTT	TCCTGGCTCT	TCTCCCATGT	GTCCTCGTGG	GTCCTGGTCA	240
CCCTCTTAGC						300
		GGGCTTCTTC				360
GTGTATGGGC						420
		CCACTTCCCT				471

- (2) INFORMATION FOR SEQ ID NO:318:
  - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 506 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

GAATTCGCCT TCAT	rggccta cagcatcgto	GGGACCAGAC	TCGTCTCAGG	CCAGTTGCAG	60
CCTTCTCAGC CAA	ACGCCGA CCAAGGAAA	CTCACTACCA	TGAGAATTGC	AGTGATTTGC	120
TTTTGCCTCC TAGG	CATCAC CTGTGCCAT	CCAGTTAAAC	AGCTGATTCT	GGAAGTTCTG	180
AGGAAAAGCA GCTT	TTACAAC AAATACCCA	ATGCTGTGGC	CACATGGCTA	AACCCTGACC	240
CATCTCAGAA GCAG	GAATCTC CTAGCCCCN	AGAATGCTGT	GTCCTCTGAA	GAAACCAATG	300
ACTTTAAACA AGAG	SACCOTT CCAAGTAAG	CCAACGAAAG	CCATGACCAC	ATGGATGATA	360
TGGATGATGA AGAT	rgatgac gaccatgtg	ACAGCCAGGA	CTCCATTGAC	TCGAACGACT	420
CTGATGATGT AGAT	GACACT GATGATTCT	ACCAGTCTGA	AGAGTCTCAC	CATTCTGATG	480
AATCTGATGA ACTO	GTCTCG CTCGAG				506

- (2) INFORMATION FOR SEQ ID NO:319:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 341 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

GAATTCGGCC	TTCATAATTT	TTCTTATCTT	CATTCTTTCG	GGTGCCCAAA	TAAGCTCATG	60
TTTTCCATGG	TCGGTTTAGT	TTTTACTAGT	CGTTGGCTAG	TTTCCTAATT	GCATGTGAGT	120
TAGCATGTGG	TGATGGCGGA	GTAATGTCAT	GTCTTGGAGA	GAACATTGCT	TGAGTTCCAA	180
ACTTAGCTTT	TCTACTTCTT	GGTGAGACTT	TGGACAAATT	ATTTTTGAGC	TTGTTTCCTC	240
ACTTAAAAAA	ATGGGGTTTG	TACCTTTAGT	TGTTTCAACT	GTTGTGAGGA	CTTGAATAAT	300
AAAGTATATA	GCTATAGATA	AGAAAACTTG	GGGGACTCGA	G		341

- (2) INFORMATION FOR SEQ ID NO:320:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 572 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

GAATTCGGCC	TTCATGGCCT	AATTTTTTC	AAAACCTTGA	AATGACATGT	TAAAATGCTG	60
CTTTGAACTG	GTTTTTCTTT	AGCCTGTAGA	AAAGAACTTT	GAGTTACTGG	TCAAGTAGTT	120
TTGACCATAC	TGGCTTAGGA	AAACAGCGCA	TCAGCTGTCT	GATTGCTATC	ATGTAAAAAT	180
CTGTGAACGA	CTTTGAGAAG	TCATTGGTGG	ATTATGTTGT	TCAGGAATAG	GAATGGAGCT	240
TTCTTCCTAT	CACTTGTATT	TTTTTTTTT	TTTGGAAGGG	GGGAGGAGGA	GGAATTATTT	300
CCNCCCTAAT	AAANGGNGGN	NTTAATCCTG	GGCCCCNNNA	AGGCTGGNNN	GGGTCCNGAT	360
KTGGGGGTNC	NNTTTATTGG	GAACTGACNG	GGNTTTAATT	TTCCGGTTTT	TTTTTTTTCT	420
TGAATGATCT	TGTGTTGTAG	AGTTGAATAC	AGTTCTAGGG	AAGTATGATC	ACAAAATGAA	480
TGTTGGCAGT	TCCTCCTATG	ATTAATATGT	CAGACATGTC	AAAATTCTCT	CATCATGTGT	540

572

ATTTGCCGGG TTTATTCAGT CCAGGACTCG AG

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 342 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:	
GAATTCGGCC TTCATGGCCT AGATAACTTT GAACAGAATG GGAGGCAGGT TTACCCTAAG CAGTTCCCCA CTTGAAGTTT TCCTTTAGTT TAGTGATTTG AGGGGCCCAA AATACTTTCA CATTTCCCCCC CTTTTCTTT TAAAAATCTG TTGGAGAACG CATTTTAGAA GAAAATGAGT CTCTGGCCTC AGGTTTCGTC TGATCTCTCA TGGCTAGGAT GGTTTATTCC TAGATAGATA GGTCCTGAGT TATTAGGAAA GCTCCTTTTT AGAAGGTTGT GAAGTCTCAT GTCCTGTGAA GAGAAAATAG GGGGGAGGACA ACAACAAACA AAAGAACTCG AG	60 120 180 240 300 342
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 391 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:	
GAATTCGGCC TTCATGCCTA CAATATTGTT TAATAATTAT TCAGAAATAT TCAAGTATAA TACTTAATAA AAATTTCTGC TATGTGCAAG GCATGGTGCT AGGTACTGAG ACTATAAGGA GGTAAAAGAT AGTTCCTGCC CTTAAAGACT TCTATAATTT AATCAGAAAG GAGAGTATAT GAAAATCATA CTGAATAAAA AGTGGCTCAT AATAAATGCC AAGGAATCAA CACAAAGTCC TTTCCCTGGT AGGGAAAGTT TTTTTGAGGA AATGGGACAT GAATTTGGCT TTGAAGGATG TGGAGGGTTT AGATAAGAGG GAGAAACTGT TGTGTTCTAG GTTAGAGGAA CAACATAAAC TCAAAAGAGA CTAAAGAAGA ACGGACTCGA G	60 120 180 240 300 360 391
(2) INFORMATION FOR SEQ ID NO:323:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 324 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:	
GAATTCGGCC TTCATGGCCT ACCCTGAGCA GTGCCTGGCC CATACTGGAT ACACAGTGTG CATTTTGTGG GGACTCAAGG AAGGAAGGTA ATATTCCAGC TCAGGGTTCT CTCTGACCCT GAATAGTGTT ATGGACTCTT TGGGAAGGAT AGAAGCTTTC TTAGTTTTCT GACAGAGGCC TGTAGGCTGC AAACGTTGTG TTTGTAGAAA GAGTTGTAAA GGTGTCATGA GCCTTTATTT AAAAGTGTCT TTAATGTATC TTAGGCATCT TTTTCTTTTC	60 120 180 240 300 324
·	

(2)	INFORMATION	FOR	SEQ	ID	NO:324:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 336 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

GAATTCGAGC	TCGACTGGAT	AGTTTTTCTT	TTTAAACTTA	AAATGCTTTT	TAGTTTGGCA	60
CTCCGTAGTA	AAGGAGGTTC	CAGAAGCCAG	TAAGAGAACC	TCTGCCAACT	ATGAAAGAGA	120
AGATATTTCT	ATCTACAAGT	TATTTCAGGA	TCAATTATTC	AATTAATATT	TTATATAATA	180
GAAAGGTTTT	ATTTGTTAGG	ACTTTATCTT	TAAGTTCCCC	AAGAGTAAAA	AGGTCTAGTC	240
ATTATTATAC	TGTGGGAGAA	TGATAGAAGA	TTGATTACAT	TAGAACTCCA	GAACTTCTAT	300
TTATTTAAAA	GATTTAAGAT	TTGACACACT	CTCGAG			336

- (2) INFORMATION FOR SEQ ID NO:325:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 409 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

GAATTCGGCC	GGCATGGCCT	AANCTAAAAA	TAAAATNAAC	CCAACGCATA	NAANACGGGT	60
TTATCTCTCC	TAAAAACANT	TNAGTTTNGA	CTTAAATGAA	ACANATCATN	NNACAACNTC	120
ATTTTNAAAT	GAAGATTTTA	CCTGGACCCT	AGGTGTGCTA	TTCTTCCTAC	TAGTGGACAC	180
TGGACATTGC	AGAGGTGGAC	AATTCAAAAT	GAAAAAAATA	AACCAGAGNA	GATACCNNCG	240
TGCCACAGAT	GGTAAAGAGG	AAGCAAAGAA	ATGTGCATAC	ACATTCCTGG	TACCTGAACA	300
AAGNATAACA	GGGCCAATCT	GTGTCAACAC	CAAGGGGCTA	GATGCAAGTA	CCATTAAAGA	360
CATGATCACC	AGGATGGACC	TTGAAAACCN	GNAGGAAGTG	CATCTCGAG		409

- (2) INFORMATION FOR SEQ ID NO:326:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 502 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

GAATTCGGC	TTCATGGCCT	AGGCGGCGGC	AGCCGAGGGC	GTACTGGCGA	CCCGGAGTGA	60
TGAGCCCGCC	CGAGACGATG	CCGCCGTGGA	GACAGCTGAG	GAAGCAAAGG	AGCCTGCTGA	120
AGCTGACTT	ACTGAGCTCT	GCCGGGACAT	GTTCTCCAAA	ATGGCCACTT	ACCTGACTGG	180
GGAACTGAC	GCCACCAGTG	AAGACTATAA	GCTCCTGGAA	AATATGAATA	AACTCACCAG	240
CTTGAAGTA	CTTGAAATGA	AAGATATTGC	TATAAACATT	AGTAGGAACT	TAAAGGACTT	300
AAACCAGAA	TATGCTGGAC	TGCAGCCTTA	TTTGGATCAG	ATCAATGTCA	TTGAAGAGCA	360
GGTAGCAGT	TTTGAGCAGG	CAGCTTACAA	GTTGGATGCA	TATTCAAAAA	AACTGGAANC	420
CAAGTACAA	AAGCTGGAGA	AGCGATGAGA	AACTTATTTC	TATGGGACAG	AGTCTTTTTT	480

502

TTTTAATGTG GAAGGACTCG AG

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 468 base pairs

(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(b) TOPOLOGI. TIMEAL	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:	
GAATTCGGCC TTCATGGCCT AGAATATTCC ATATCAGTAC ATATAGCACT GCCTCACTTT	60
TTAATGGCTA TATAAAATAG TACTATAATT TTTAACCAGT CACCTGATGG TGGGCTTAGT	120
AGTTATTCTG TGGCTGTAAC CAACATCACT GCCATGTGCA CTGGTACACA TACAGAAGTC	180
CACACAAGTA GGCCTGTATC TGTAAGGTAA ATACTGGTGG GATTACTGAG TGAAAGGAGA CGTGAATTTT TAGATTTTTA CTATGAAAGA CAAACTGCTC TTTATGGGGA TTTTATTAAT	240 300
CTACAACCCC ATCAACAATG TATGAGAGCC CATTTTTCAC ACACTTGCCA ACTCAGTAGG	360
TTATTAAACC TTTTGGTCTC TGCCACTTGT ATATCCCAGA TCAACTTCTA ATTCTGCTTC	420
ATATTGTTTG CTATCCTTTA GAATATTTCT GTCCCACCTT GTCTCGAG	468
(2) INFORMATION FOR SEQ ID NO:328:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 300 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:	
GAATTCGGCC TTCATGGCCT AGGGAAAGGA AGTGACATAG TGGTATAAAA ATTTGAAATT	60
TGTGATGTGG CTTAGAAGCT TGATATATAC GGGTATGATT GCAGCTGCTA CATTTAGCCT	120
TTTTTTCTTT CTTTTTGGAG AATGAACCGC ATTAAGAAAT ACATTTTACA TCACAATTTA GCAAGTATAT GTGCTAACAT ACTTCTGTTT CTACAAGGGA TGTATTGTGG TATTTTCTAT	180 240
TGCATTTTAC TCTAATTTAG TTCATTTAAA AAAATGCTGA TTCTAACCCA TGAACTCGAG	300
(2) INFORMATION FOR SEQ ID NO:329:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 306 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:	
GAATTCGGCC TTCATGGCCT ACCACCACAC CCGGCTAATT TTTTGTATTT TTAGTAGAGA	60
CGGGATTTCA CCATGTTAGC CAGGATGGTC TTGATCTCCT GACCTCGTGA TCCACCCGCC	
TCGGCCCCC AAAGTGCTGG GATTACAGGC ATGAGCCACC GTGCCTAGCC GACTCTTGAG TTTTGACAAG AGGTGATATC TGGGAGATTA ATAAGTATTT AGTTTAAGAA AACATTTAGT	180 240
AAGCCTGTCC TGTGTTCCCA CACAAAGGGT ATAACAGCAA TATATTCCAT AAGAGTAAAG	300
CTCGAG	306
204	
204	

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(2) INFORMATION FOR SEQ ID NO:330:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 523 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:
GAATTCGGCC TTCATGGCCT ACATTACCAT CAGATTGACA TATTTAATTA TCAGATATCT
                                                                        60
TTCTTTTGCC AAAAAGTTGT GGTTGAGTTG GCCCTGGGAT TTATAAATAC ATGCACACAG
                                                                      120
CACATTTCTG TCATTGTTCA CTGCAGTCTT TTAACACATC TTCTCAGCAA TATTCTTAAT
                                                                      180
GTTTCCAGCG GGAAAATTGT AAATTATTTA ACCACTGAAT TAGAGGTGTG TTGTTTTTTA
                                                                      240
GCTAATCAAT AGCCATTGAA TGCTTAAATG GGCTTTAAAG TAGACAAAAG TAAAAGACAG
                                                                      300
CAAAGAAAAT TAATCAGTAA GATTGCCCAT ACTCCATAGA CACTTGAGCA GCTACTTTAG
                                                                      360
TCATTTTGAA ATACACGCTT TATGTTTTCC CTTGGACTGG CATATTCCTG TCATTTATAA
                                                                      420
AAAGAATATA CATTTGTAAA TTTAAGGTGT GGACATTCAT TATTGAAGGT AGAAATAGTT
                                                                      480
ATAATCATCA GTGTCTAGAT ATATCTGAAG AGAGGTACTC GAG
                                                                      523
(2) INFORMATION FOR SEQ ID NO:331:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 423 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:
GAATTCGCCC TTCATGGCCT AAAGTAGGCA AGGGATAATA ACCAAAGAAG NAAATTTCAT
GAAGACTAGA CATCATAAAG CATAATTTTA ATAGTCACTC AACCAAGTAT TTTTTATTTT
TTATGGATAC TCTGAATGGC AATTAAATGT GAAACCCAGT TTCTTGGGCA AGTCAAATTC
                                                                      180
TGGAATCACA TCCACCTAAA TTAAAATGAC TAGCTCGTAT TTTCCCCATC TTCAAGTTTC
                                                                      240
ACATCCTGGT CATCAAAAGA CTCGACAGCA AGACTTAGAA TGAAAAAGGG TACTTGTTTA
                                                                      300
TATTAATATT TTTTACTTGA ACACGTGTAG CTTGCAGCAG GTTCTTGATG AATGTGCTTT
                                                                      360
GTGTCCAAAA TGCCTCCCCA TTGTACACAG GTGTACACCA TGCATGCACC AACACCACTC
                                                                       420
                                                                       423
(2) INFORMATION FOR SEQ ID NO:332:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 410 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
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- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

GAATTCGGCC	TTCATGGCCT	ACAAGCCACA	AAACTGTGGT	GAATGGAAAA	GAATGTATAA	60
ACTTCGCCTC	ATTTAATTTT	CTTGGATTGT	TGGATAACCC	TAGGGTTAAG	GCAGCAGCTT	120
TAGCATCTCT	AAAGAAGTAT	GGCGTGGGGA	CTTGTGGACC	CAGAGGATTT	TATGGCACAT	180
TTGATGTTCA	TTTGGATTTG	GAAGACCGCC	TGGCAAAATT	TATGAAGACA	GAAGAAGCCA	240

THATALACTE ALATGGATTT GCCACCATAG CCAGTGCTAT TCCTGCTTAC TCTAAAAGAG GGGACATTGT TTTTGTAGAT AGAGCTGCCT GCTTTGCTAT TCAGAAAGGA TTACAGGCAT CCCGTAGTGA CATTAAGTTA TTTAAGCATA ATGACATGGC TGACCTCGAG	300 360 410
(2) INFORMATION FOR SEQ ID NO:333:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 376 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:	
GAATTCGGCC TTCATGGNCT ACCTTAGCCT CAGCTCTTC TTCTGGGTTG TTTGTATTTT CTTTTCTGTC CCAAACAGTT TCCCCCACAA AAAGAACTTT ATGTCTTTCT CTGTCTTCCC TCAGTCCTTC CAGTCAGCAG CCTGTGATTG GGCTTTTCCC CTCAGAAACG AACAATCCAG AACCCACTGT TTAAAACAAC TGTATTTTGC CTTGGGAAGT CCCATTGCCT TCCCTGAAAA CATTAAACAT TCCTCCGATC CCCAGCCTGA GTCTCTCTGT CTCTGGGCCC CATCCTGCTC CACAGCAGGG CTGGTGTCT CAGCACAGAG TGACCCTCCG ATGCCCTTTC CCACCCGCCG CCNTGCCTCC CTCGAG	60 120 180 240 300 360 376
(2) INFORMATION FOR SEQ ID NO:334:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 307 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:	,
GAATTCGGCC TTCATGGCCT ACGGGTTGTT ACATATTTAT TCTTTTTTGA AGCCCATCAC TACATCGCCA TTACGTTTTA CACTGTGTAT GTAACAAATG TTACCACTTT GTTCTTTATT CCTTTTTGGA TCATCTTCAG TGGGGGTAAA ACAGTATCAA GCTCTAGAGC TCCCTCTGGT GGTTTTTGTG ACATATTTGA AGATGGCAGC TTGCTTTTTG AGAATTTCTG GCTCTGCTCT	60 120 180 240 300 307
(2) INFORMATION FOR SEQ ID NO:335:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 368 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:	
GAATTCGGCC TTCATGGCCT ACATTACTCA GCTTTCCTGA ACAACCAGGC ACGACCCTCT GCCTGCAGGC CAGGCACGTG CTGCTGCCCC TGGAGGCGGG TGGGGGTGCC TCCGCGCTGG AGGACACGGG GTGCACTGAG GCTTCCCATT GGTGATGGGG GAATGTGGTG ATGAGGGGAT GCGGTGCCCG CGGACCGCAC ACATGCCATG TGTGGACACT CAACAGGAAG CTTCGGTCAG	60 120 180 240

CATTTCAGCT GGAAATGCAG AGCCAGGGCC CTGGAAAGTC CCTCAGCAGC TGTGCACAGG CCTGCTCACC GTGCGTGTGC GGGCAGAGCC TCCCTGGGGA GGCAGAGGCC CCGCGTTCTG CACTCGAG	300 360 368
(2) INFORMATION FOR SEQ ID NO:336:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 437 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:	
GAATTCGGCC TTCATGGCCT AATTGAATTC TAGACCTGCC TTCCTGCTCT TCTAGGTAGT CACACTTCAC TAAAGTGTCA TCCACCAGTG TGTTGAATCC GAAGAATGAC AATTTTCTAC CACTGGTGTA AAAAACAAAC ATTTGAAGAC CCTTGTGCAT TGTGTGTCAC AAAGCTAAAT ACATGGAAAT CGTTAATATC GCTGATATTA AGTAATTTCC CCACTCTGAG TGAATACTTT GATGATTGCC AACAGTGGCT AATAAAATGA CGGCTACCAC ACTCATGGGT CACTGGGGCT GCGCAGGGCT CTTTGAGGTG GGTGGCTTCT TTTGGAAAGT ACTATGAACG TCTCGAAGCA GTATTCTAGT GATAAGAATT CTTAACATAG CCAAGCGCCC CACGTTTGTT CCCCACGTTT GTTCCCCTTA TCTCGAG	60 120 180 240 300 360 420
(2) INFORMATION FOR SEQ ID NO:337:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 430 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:	
GAATTCGGCC TTCATGGCCT ACCAAACCCA ATTTATTTAA AAANATACTT CTATATCATT ATATGTATTA CCAATTGTTT TAGCCTTATA CAGGATGCGG TGTNCTGTGC TCCTTNGTGA ATGTCNGTTG CTGGTAGCTG GTTATGCTCA TGATGATGAC TGGGTTGACC CCACAGACAT GCTTAACTAT GATGCGGCTT CAGGAACAAT GAGAAAATCT CAGGCAAAAT ATGGTATTTC AGGGGAAAAG GATGTCAGTC CTGACTTGTC ATGTGCTGAT GAAATATCAG AATGTTATCA CAAACTTGAT TCTTTAACTT ATAAGATTGA TGAGTGTGAA AAGAAAAAGA GGGAAGACTA TGAAAGTCAA AGCAATCCTG TTTTTAGGAG ATACTTAAAT AAGATTTTAA TTGAAGCTGG AAAGCTCGAG	60 120 180 240 300 360 420
(2) INFORMATION FOR SEQ ID NO:338:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 316 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:	

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TTTAAGATTT	CCTNGTCCTA	TCCCCACCCC	AGACGTTTCC	ATTTTGCTTT	TATTTTCTAT	120
					TCCATTATAC	180
					TAAGAAACAA	240
					TTGTCCACTT	300
ATGCAGGATA					•	316

- (2) INFORMATION FOR SEQ ID NO:339:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 306 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

GAATTCGGCC	TTCATGGCCT	AGCTGGCTGG	CACCTGGAGA	ATCCCTGAGC	TGGAAAAGCA	60
GCTTGGTCTG	CAGAACTGAG	TCACAAGACT	GAGGCACTGG	GGAGCCTCAG	CCCCATCTGG	120
TTGTTGNTCC	CTCTGTGACC	TTGAGCTTGT	CTTCCACTTG	GTGCCGTAGG	CCCTCATTTG	180
TCCATTGAAG	TTAGCACCTG	TCCCTCCCGT	CCTCCAGAGA	GGTCAGGAGG	ATAAGCATTA	240
GAAGACTCAC	TGTGGTTTAT	TGAGTGCTTA	CTGTGCAGGT	ACTGCTGTAG	TTTTGTGCAA	300
CTCGAG						306

- (2) INFORMATION FOR SEQ ID NO:340:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 580 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

CAAACTTTTG	AGTNNNACAG	TTAAGATATT	ATGTGAAGCT	CAGAATCATG	TTTCAGACCA	60
TTGAAATTAC	TGGTTAAAAT	ACAAATAGCT	GAAGACATGA	TGTAAAAGAT	TAAGTACTTG	120
GTTTTGTAAC	ATATTTACCA	ATTAAAGTCA	CAAAATATTT	CTCATTATTT	ATTCATGCAG	180
GTAACTGAGA	AAAAGATAGT	GCAGAAATCA	ACTTTAAATA	AAAAATTATT	CCTCCCCTTC	240
CTCCCACTCC	CCTATACTCT	ACAAAATGTT	TTCCCTGGGA	CTAGGCCTTG	AAAAGGCCAC	300
TACATATTAG	TGTGACATGC	ATTACTGTCT	GCAATTAAAA	AAGCTAACCT	TGTGGTGATT	360
GTAATTACAT	TATAAAAATG	TCCACATGCA	TAAATCTAAA	AAAGGTTGAA	AACCTACAGT	420
AAATCTACAA	TATAGTGTTT	ACATTTGACC	ACTGGTTTGT	GTTATGTAGA	AGTCATAGAT	480
TTGGTAAAGC	ATTGTAACAA	TTTAGGAAGG	CATCTAAATC	TTTAAGTTCT	GGACAAATTT	540
TATGTTTTAA	TCTACAAAAT	TGCATGAAGG	CTAACTCGAG			580

- (2) INFORMATION FOR SEQ ID NO:341:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 433 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

GAATTCAGAN	TTNTGCTATG	GTAGCACCAG	ATGTCCAAAT	TGAAGATGGG	AAAGGAACCC	60
TCCTAATATC	TTCCGAAGAG	GGAGAGACGG	AAGCTACTAA	NTCACAAGAA	GTTNTTCAGA	120
ATTTGGAATT	AGAANTGGCA	NCCGGCTTCA	AGCAGATGAC	TTCNTCCAGG	ACTATACTTT	180
ATTGATCAAC	ATCCTTCATA	GTGAAGACCT	AGGAAAGGAC	GTTGAATTTG	AAGTTGTTGG	240
TGATGCCCCG	GAAAAAGTGG	GGCCCAAACA	AGCTGAAGAT	GCTGCCAAAA	GCATAACCAA	300
TGGCAGTGAT	GATGGAGCTC	AGCCCTCCAC	CTCCACAGCT	CAAGAGCAAG	ATGACGTTCT	360
CATAGTTGAT	TCGGATGAAG	AAGATTCTTC	AAATAATGCC	GACGTCAGTG	<b>AAGAAGAG</b> ĞG	420
AAGCCAGCTC	GAG					433

- (2) INFORMATION FOR SEQ ID NO:342:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 301 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

GAATTCGGCC TTCATGGCCT	AAAACTCTAA	TAGTCTCTCT	TCAGCGGAGC	CACTGAAGGA	60
AGATAAGCCT GTCACTGGTC	CTAGGAACAA	GACTGAAAAT	GGACTGACTC	CAAAGAAAAA	120
AATTCAGGTG AATTCAAAAC	CTTCAATTCA	GCCCAAGCCT	TTATTGCTTC	CAGCAGCACC	180
CAAGACTCAA ACAAACTCCA	GTGTTCCAGC	AAAAACCATC	ATTATTCAGA	CAGTACCAAC	240
GCTTATGCCA TTGGCAAAGC	AGCAACCAAT	TATCAGTTTA	CAACCTGCAC	CCAAACTCGA	300
G					301

- (2) INFORMATION FOR SEQ ID NO:343:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 385 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

GATTCAGATG	GAGATGCCAA	GCAGGCCCTT	AGGTGAAGGA	GTCTGGAGTC	TGAAAGCATT	60
TGGGATGGGG	ATATAGACTT	GAGAGCCATC	AGCTTATAAA	TAGGACTTGG	TCAAGAATGG	120
GTGGCCTCCA	TCCTAGATGG	ATATAAATAA	GAAATAAATA	TCAATTTTTC	TTCTTATAAC	180
ATTCCTAGGT	TTTCATTTTT	ATGACTTTAA	GAAAAATATG	AATGACAAAA	ATAAAACATA	240
AAATCAAATA	TATCCGTATT	GCCCTTTGGG	GGACACCATC	TCTTGCTCAC	TTTACACAGT	300
AAGTGCCATT	TCCTTCACCT	CCATGGAAAA	CATTTCGTAA	ATTACTAAGT	TGAATAACTT	360
AAAATATAGG	ACGGGACATC	TCGAG				385

- (2) INFORMATION FOR SEQ ID NO:344:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 299 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

GCAGAAACCT TCAGGGAAAC CCCATGCTAG CGGCAACTGC ACCACACTTT GAGGAGAGGCT GGGGGCAGAG ATGTCGTCGA CTCAGGAAAA ATACAGGGAA TCAAAAAGCT CTAGACAGTG ATGCTGAGAG TTCCAAAAAGT CAAGCAGAAG AAAAAATCCT AGGTCAGACT TATGCAGTTC CCTATGAAGA CGATCATTAT GCAAAAGACC CAGACATTGA AGCACCCAGC AACCAGAAGT CAAGTGAAAC GAATGAAAAG CCCAACGACAG CTCTTGCCAA CACCTGTGGA GAGCTCGAG	60 120 180 240 299
(2) INFORMATION FOR SEQ ID NO:345:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 304 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:	
GCATTTGGTT CTTTTATAT CTTCTATTC TCTCACTATA TTCCTGTTT TCTTTAATG CTTGTACATC ATTAAACTCG CTGTTATCCT TGTCTGTGAG TCATCTGGTC ATTTCTGTGT GTTTTTATTA ACTGATTATT CTCCTTGTCC TGGCCACATT TCTGTGCTTT TNGGCGTTTC AGTAACTTCT GATTGGATGT TGGGTATTAT AAAGATTATA TTATTGAGTG TCTGGATTTG GGGTGGTAGT TACTTGTGGA TCAGTATGAT CCCTTTGAGG CCTATTTTTA AGCTTCAGCT CGAG	60 120 180 240 300 304
(2) INFORMATION FOR SEQ ID NO:346:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 291 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:	
GAATTCGGCC TTCATGGCCT AGATTACAAC ACGTGTGCCA CCACACCTGG CTAATTTTC TATTTTTAGT AGAGACGAGG TTCACCATG TTGACCAGGT TGGTGGTCTT GAATTCCTGG CCTCCAGCCT GGTGACAGAG CGAGACTCCA TTTCAAAAAA AAAAAACAAA CTTCATGCTG AGAACTCTGA AGAAAAAAAA GATTTTTAAG AGGAAAATGT GTAAGAAAAA TACTTCAGCT TCTGTTACAA AATCAAAATA GAAAAAAACA CAAAATTGGT GTTTCCTCGA G	60 120 180 240 291
(2) INFORMATION FOR SEQ ID NO:347:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 282 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	•
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:	
GTAACTTTAG CTGTACCTTG CAAACCAGAA CATATGGTCA CCCTACCCTC CGGTCACTTT TTCTTCTTTG TTTCCATTCT TTTAATTTTT TTCCCTTTTA AACACACAGC ATTATCTTTC CCTGAGCACC ATTGTCTTTG CAAATGCTCT TGCAATCGGG ATATTTTTGA CCTGGCAACA TGCATATTCA GTCTGAACAG TCTCTCTGAA CCTACCCCAA AACCTGGTTT TAGCTTCCAG	60 120 180 240

282

GCAGAAGACT CTGTTCCCTG GCTTGCAACC CCCAAACTCG AG

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 342 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:	
GAATTCGGCC TTCATGGCCT ATATCAATGC AATTTTTAAT TTTTGTTAAT ATCAACAGCA AAAGCCTAGT GCATTGGGAG ATGTGCAACC TCCCTGAAAA TCTTTTCTGT TTCTGGAGTA	60 120
CTTCAGGGGT GGCCTCTGGC CCCAGAGCCT TTGCCACAGT GCTCCCACCA GCCCCCACCT	180
CATCCGTCTG TTTGCAGAGC CTCATCTACA GGTCCCCACG CTGCCTTCTT TACTCACTCT	240
GCGCTTGGCC GTTTTGTTAT TTGGCTTAGT CTACATTGGG CGGAAGTCTG TGTGCACAGA	300
GTGGGTGTTC CTTCGAGCCC CTTCCACTCA GAGGGCCACA CG	342
(2) INFORMATION FOR SEQ ID NO:349:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 442 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(b) lorologi: lineal	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:	
GAATTCGGCC TCATGGCCTA CAAAGAGCTG GGATTACTGG TGTGAGCCAC CGTGCCCGGC	60
CTGGACATCT GGTTTTAACT AGATGGAAGG GAAGAACATT ATGAATCTTT AAAATACGGC	120
TGTTGCCATT TTTCTCTCTT CTTAACATGC AGCATAGGTG ACAAGCTTTT CTGTCATCAT	180
CATGGAGCAT TCTGAATCAT GACATTTTTG TTTGAGAGTT CATTCTTGAA TTTTCAGTTC	240
AAAATATTGT TTGAACTATT ATTCCACATT CAAAGATTAT ATAAGGTCCT GTGCTTTTGA	300
ATCTTTTCA AAAAATTTAT TTCTGCCTGC TTAAAAAAAA TACTTTTATT TCCCCACAGA	360
GAGTTCAGGA CTTCAGATTA GTTTGTGTTC AGCTCACTTA ACTGGATAGA CAATTTTGCG	420 442
TTTTGCAACA CCATAGCTCG AG	442
(2) INFORMATION FOR SEQ ID NO:350:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 314 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:	
GAATTCGGCC AAAGAGGCCT AAAAAAATGA AATTCCTTAT CTTCGCATTT TTCGGTGGTG	60
TTCACCTTTT ATCCCTGTGC TCTGGGAAAG CTATATGCAA GAATGGCATC TCTAAGAGGA	120
CTTTTGAAGA AATAAAAGAA GAAATAGCCA GCTGTGGAGA TGTTGCTAAA GCAATCATCA	180
ACCTAGCTGT TTATGGTAAA GCCCAGAACA GATCCTATGA GCGATTGGCA CTTCTGGTTG	240
ATACTGTTGG ACCCAGACTG AGTGGCTCCA AGAACCTAGA AAAAGCCATC CAAATTATGT	300
211	

314

ACCAAAACCT CGAG

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 301 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:	
GAATTCGGCC AAAGAGGCCT AGCTACCAGA GTGTGAGAGA CCATTGTCTC GTTGGCTGGC GCTCACGGAC ATGCAGTCAC GGTAGCGGA GCAATCACAA AACTGTAATT TACTTACCAA ATCTCTTCCT TTCCGTAGCC TCGCCTGCCT GACTTAGAGA AAGAAAAGCA ATAATTTTAC AGGCATTTTG AGGTGTCTCT TTGGGTTCTT TCTGTTTGAA AGGATATTG TCGAAAAAAA GAGCAAAACC GTTTTAAATA AACTCCCCCT GGAAAAAAAC CCAAAACACT TGCATCTCGA G	60 120 180 240 300 301
(2) INFORMATION FOR SEQ ID NO:352:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 443 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:	
GAATTCGGCC AAAGAGGCCT AGCAAATACA CATTAATAAG AATGCCTAGA AGAGGACTGA TTCTTCACAC CCGGACCCAC TGGTTGCTGT TGGGCCTTGC TTTGCTCTGC AGTTTGGTAT TATTTATGTA CCTCCTGGAA TGTGCCCCCC AGACTGATGG AAATGCATCT CTTCCTGGTG TTGTTGGGGA AAATTATGGT AAAGAGTATT ATCAAGCCCT CCTACAGGAA CAAGAAGAAC ATTATCAGAC CAGGGCAACC AGTCTGAAAC GCCAAATTGC CCAACTAAAA CAAGAATTAC AAGAAATGAC TGAGAAGATG CGGTCACTGC AAGAAAGAAG GAATGTAGGG GCTAATGGCA TAGGCTATCA GAGCAACAAA GAGCAAGCAC CTAGTGATCT TTTAGAGTTT CTTCATTCCC AAATTGACAA AGCTGAGCTC GAG	60 120 180 240 300 360 420 443
(2) INFORMATION FOR SEQ ID NO:353:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 335 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:	
GAATTCGGCC AAAGAGGCCT ATAGGCNTCT TTGGCCGGCC AAAGAGGCCT AAAAAAATCT CAGCTATGGT TCATTATTAC TAGCTCAGCT TTTAATTCTT TAAATTGGTT GAATTATTCT CTATGTCAGT TATTTTTATT GACCAGTTTT GGAATATTTT TGTTCATTTA TCAGGGAGTA TGCGGTTAAT GAAGTTGTGG CAGGGATAAA AGAATACTTC AACGTAATGT TGGGTACCCA GCTACTCTAT AAATTTGAGA GACCACAGTA TGCTGAAATT CTTGCAGATC ATCCCGATGC	60 120 180 240 300
212	

335

ACCCATGTCC CAGGTGTATG GAGCGCCAAC TCGAG

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 318 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:	
GAATTCGGCC AAAGAGGCCT ACAGAGATTA TATTGGGGTT NCCATTTTGT GAAGCCANAG ACATNTGGTC ATTGGGATGT GNGATTGCAG AATTATTTCT TGGANGCCCG NTNTACCCAG GAGCCTNGGA GTATGCTCAG ATTCGANACA TTTCTCAGAN TCAAGNTTTN CCAGGAGNAC AGTTGTTANA TNTGGGTACT AAATCCACAA GATTTTTTTG ACANAGAAAC AGATATGTCT CNTTCTGGTT GGAGATTAAA GACACCGGAA GAGCATGNGG CAGAGACTGG AATGNAGTNT TAAGAAAGCCG GACTCGAG	60 120 180 240 300 318
(2) INFORMATION FOR SEQ ID NO:355:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 435 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:	
GAATTCGGCC AAAGAGGCCT AGTGGGAATT TTAAATACAA GATCCTGTTG AAAATATTGA TATTCAAAGA AACAACAGC TTTGGATCCA TAGCCACAAT TTAGGTTTTC CTAGATTAAA ATCAGAAGTG ATTTTATTGT TGGAAGATAC ATTAATTCTT TGAAGTCAGA ATAAGAGGCT TGACAATTTA ATTTCTAATT AAGTGACTGA ATAGACAAAG GATCAAATAC AAACAGTAGT GCAGGAAGAA AATAAATTGG AAGAAATAAT TGTTCAACCA GTAGTAATAA TTAAGACCAC CATTTTAAAA TTTTCTATAC ACAAAGAATG AGAAAATATT GTTATTATTA TTATACTTCT TTCTTCTTCA GTATTAGTGG ACCCACATTA TCTCCTGTCA ATTCATTGTG TTTATNATGT GAACCATCTC TCGAG	60 120 180 240 300 360 420 439
(2) INFORMATION FOR SEQ ID NO:356:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 158 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:	
GAATTCGGCC AAAGAGGCCT ACAGGCTCAC ATTGACTACA CACGTTTATA CCAGGCGCCA TGTTCTTTGC CGAAACTCCC GCTCAGAGCC TGGATGATCT GCCCCTCACC TCTGCCCTCG TTCCCATCCA CTCTCCCCTC CTTGCTCTGT TCCTCGAG  (2) INFORMATION FOR SEQ ID NO:357:	60 120 150

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 303 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:	
GAATTCGGCC TTCAAGGCCT ACTCTTCTTG GCATATTATT TTCCTGAATT GCTGCCT TTGTTCAAAC CATCCCGGAT TAATGACAAA ACACTATCTT ATTCAAACCA AGAATTA ACAACCCTCC TTCTCAACTA GTTTNNGCAA GATCATTTCA GTTTTTCTTT TTGTGCT TCCTGGATTA ATTCTTCAGT TTNGTCTTCT CTGGAATCAC TACCTAAGGC TTATTCC TTTCAAGTTT TTTGTTTTTT GTTTTTTTTT ACTTTGATGA GTATGTTTAC CAACGCT GAG	TCT 120 ACA 180 ATG 240
(2) INFORMATION FOR SEQ ID NO:358:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 493 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:	
GAATTCGGCC TTCATGGCCT ACAAAGTGTT GGAATTACAG GCGTGAACTA CCGTGCC CCTTTTTTTT CATAGCAGTT TTATTAAGTT GTATTGCCA TACCACCCAA TGTATCC TAAGCACCTG ATTCAGTGGT TTTTCATGTA CTCATGGAGT TATGCAGCCA CAATCTT GCATTTTCAT TACCCCAGAA AGAAACTGTA CCCATTATGC ACCCCGTTCC CNTCNTC TCNTGGCAAC CACGAGTGTA CTGTCTGTCT TCATGGATTT GCCTATTCTC GACGTTT TGGGATGAAA TCACACAGTG TATGGCTTCC ACACTTTACT GTGCTGTTGT CAAGGTT CTATGTGTTG GGTGCAGCCA CCCCTTGGTA TCCACAGGGA TTGGACCCAG GAGCCTG CGATCCCTG CAGGGATGCC TGTGTCCCAC AGTGCCCCCT GCAAAACTCA CTGATAT	TATT 120 TAGC 180 TCGG 240 TCAT 300 TTAT 360 GCAC 420
(2) INFORMATION FOR SEQ ID NO:359:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 420 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:	
GAATTCGGCC TTCATGGCCT AGTTAACATG ACACAAAATC TTTACCTGCA GTTCTAY TTTGCAAGGC TGAAGTCCAT ATTTACAACT GTCTTAGATC ATCTCAATCT GATTATT CTATTCTCT TAACTGCTAG TCCAGCCCCT AAAACTGCAT TTCTCTGCTC CTCCAAY TAGTGGCTTA TTGAAGTCCA TATTTGCATT GTGACAGAGC CAACTCCCAA GAATGGG CCACTCAGTG TAATGCAATA GGAGCACTTT AATTTTATCT CCATTTTCTG GACCCAA ATCATTCTAG CCCTTTTTTC TTGGAATGAA GTCTGGCTGA GAATGATGAT CCATTAC GAATTACTTA ATAAATCAAC TCTTGGTTAT GAGTGGCAGA AAACTAAAGC CAGGCTC	TTAA 120 AGCT 180 ATTC 240 GTGC 300 GTAA 360

WO 98/45435

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PCT/US98/06954
(2) INFORMATION FOR SEQ ID NO: 360:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 356 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:
GAATTCGGCC TTCATGGCCT AATGTCACCA CTGTGGAAAA CCATATAGGT CGAAGGCTGG
ACTTGCATAT CACCTGAGGT CAGAGCATGG GCCTATATCC TTCTTTCCAG AGTCAGGACA
                                                                      120
GCCAGAGTGC TTAAAGGAGA TGAACCTAGA GTCAAAGAGT GGGGGCCGAG TTCAGAGACG
TTCTGCCAAG ATAGCTGTAT ACCACCTACA GGAGCTGGCC TCTGCTGAAC TGGCCAAGGA
                                                                      240
ATGGCCCAAG AGGAAGGTGC TTCAGGACCT GGTACCTGAT GATCGAAAGT TAAAATATAC
                                                                      300
TCGTCCAGGG CTCCCTACCT TCAGCCAGGA AGTACTACAT AAATGGAAGA CTCGAG
                                                                      356
(2) INFORMATION FOR SEQ ID NO:361:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 353 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: CDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:
GAATTCGGCC TTCATGGCCT ACATGATGAA ATGTTGGCTA AAAGAGTCAC CCTAATATTA
ATAAAATGTT TTATTCTTCA TGTGACTAAA TCAGTGTGCA TGCAAGAAAA AGAAAGAAAA
                                                                      120
AATGCTTAGA TTCCTTTTTT AAATTATCTC CAGAATTTCT AATTTTTATA AATTAAGGAC
                                                                      180
CAACAAATCC CATTTTGTTT TCACGTTTGA CATTTGTTCC TTTGACTTAA ATAACTTCTC
                                                                      240
CACTCTTTAT TTTCCTATTT GTGGTGATTT GAATAATTTT TCAGAAAATA TGTACTTTCT
                                                                      300
GATAAATTGT AGTGTCAG TAATGAAAAC TGCTCTATGG TGCTCCCCTC GAG
                                                                      353
(2) INFORMATION FOR SEQ ID NO:362:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 395 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:
GAATTCGGCC TTCATGGCCT ACGAACTACT CTAAGTAATG GGCCAAGTCA TGAGCTGCAC
```

AAAGGCCCCC AAGACCCAGA CGGGTTTAAT GTTAAGCAAA ATGCCGCCTG GTCTCAGGTA 120 GACACTCAGC CACCGCTAGC CCCAGTCAAC TGTCCCATGG GAAGGCAGAA GGCCCGGTGT TGCCAGGTCT TAAGTTTTCA GGAGGAAATC CTTAAACGAT GGTGTTTCAC TATAATGGAT 240 TCATTTTTAT GTTTTATAAA TCTCTATGTT CATGTACTGG TATTAGTACT TTTATGTGAT 300 AAAATCTTTT TTTTAAACAT TGGTAATTCA AAAACACAAC ACCCACATAC AGTGAGGACC 360 AAACAAAACC CGTCTGCAAG CAGGCTCTCT CCGAG 395

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 281 base pairs

(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii') MOLECULE TYPE: cDNA	
A IN GROUPING PROGRESSION CO. S. NO. 252	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:	
GAATTCGGCC AAAGAGGCCT ACAAAGGACA GCCCTGTCTG CACACTGAGT TACTGTGGAT	60
TTTTAAGAAA CTTCGCTAAA GAATTTAGGC ATTTCTGATT CAGTTAAAGG ATTGCCAATT	120
CATCAGTCCC TGAAACTAGA GCAATCTCAA CAGGACAAGA AAAGAAAATG GGCTTTTTAA	180
GTCCAATATA TGTCCTTTTC TTCTGTTTTG GAGTTAGAGT ATACTGCCAA TATGAAGCTT	240
ACCGATGGGA TGACGATTAT GACCAAGAGC AAAATGTCGA G	281
(2) INFORMATION FOR SEQ ID NO:364:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 357 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:	
(AI) begoence bescarrizon. beg is no.30%.	
GAATTCGGCC TTCATGGCCT AGTGCCACTG CACTCCAGCC TGGTGACAGA GTGAGNCTCC	60
GTCTCAAAAA AAAAAAAAA AACTCAGCTT CTTCAGAGAG ATAAAATTGG GGGAGGAGCC	120
CAGGGCCACA TACCAAGCTT TGGGACATGG TGCCTCATGC TCTCTGGGAT TGCAGACCAT	180
CCAGGTCTGT CTTCGCCCCT GTTAGTGCAC ATATATCCAC TCACATGTCT TCCCTCAGGC	240
TATCGGGCAG GGGGACTTCA CCAGGGGGTT TATGGATAGG CTTCAAGAGG GTCTGTGAGC CCCCAGAAAT TGTGTGTGAG ACTGAGTATG TGTTCTTTTT TCCAGGAAAT TCTCGAG	300 357
(a) Three Martin Don Cho To No 165	
(2) INFORMATION FOR SEQ ID NO:365:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 325 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:	
GAATTCGGCC TTCATGGCCT ATTACAATAT GCTTAAAGCT CAAAATGATC GAGAAACACA	60
AAGTTTGGAT GTCATATTTA CTGAAAGACA AGCGAAAGAA AAACAAATCA GAAGTGTCGA	120
AGAAGAAATT GAACAGGAAA AACAAGCAAC AGATGACATT ATCAAAAATA TGTCTTTTGA	180 240
AAACCAAGTC AAGTACCTAG AGATGAAAAC CACAAATGAG AAACTGTTAC AGGAATTAGA TACACTTCAA CAACAATTGG ATTCACAGAA CATGAAAAAA GAGAGCCTGG AAGCAGAAAT	300
AGCTCACTCC CAGGTGAAAC TCGAG	325
(2) INFORMATION FOR SEQ ID NO:366:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 549 base pairs	
(B) TYPE: nucleic acid	

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

GAATTCGGCC	TTCATGGCCT	AGTGAATTGA	GTTTTGTAAA	CCTCCTTAGC	ATATCACACA	60
ACACTAATTT	TCCACTCTCA	ATATGTGGCT	GTAGAGTGTT	TAATGTTTAC	TTTCATATCG	120
CTTTTCCATA	GTAGTGCAAG	ACCTCAGTTT	AGCTTGTTTA	CATTATTTGC	AGATTTACTT	180
ACAGTGTACT	ATTTATTTCT	GTTTTAAATA	GTGTTTGCAA	TAGGAGAAAA	TCATATGATC	240
TTAAGCATAT	ACACCAAAGG	TAAGAAAGGA	AGCCACTATT	GTATCTTTTT	GATGAATTCC	300
AGATGAGCTG	GGATCAAATT	GAACTGCTTA	GGCAGAAATT	TAAGAGACAA	GTAGAAGTGG	360
TGCAGAAAGA	CATTGTGACT	GCAATGTCCT	ATTTACAGCT	ACTGCCCAGA	GGAGAACACT	420
CCCAACATGA	CAAAGAGTTC	ATCAGCTTGA	ATGTTAACTT	TTGAAAACAA	TTAATTGAGC	480
CACTGCACCC	GGCCAATCTA	GTGAATTGAG	TTTTGTAAAC	CTCCTTAGCA	TATCACACAA	540
CTACTCGAG						549

- (2) INFORMATION FOR SEQ ID NO:367:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 481 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

GAATTCGGCC	TTCATGGCCT	AGGAGGCGGA	GGTTGCAGTG	AGCCGAGATC	ACGCCATTGC	60
ACTCCAGCCT	GGGCGACAAC	AGCAAGACTC	CATCTCAAAA	AAAAAAAGTG	AGATCCTGCC	120
GATGGGCCCT	TCCTGTCCAC	CTGTCAGGAA	AACCTGCAAA	AGGTTCTTGT	CGCACCATTA	180
GAGCCAGTTT	TTCCCAAATG	ACACCCATAC	CTGATTTTCC	TTGTTCTTCT	AAGACAGTTT	240
TAATTAGGAT	AATCTCATAA	GTGCTACATT	TTCAGTGAAT	TTTTCAATAT	AGTGGCCCAT	300
GTTCTTTCTT	TTTTTTTAAA	GTCTTTTTCC	TCTGGTAGCA	CATGTGATTT	AATGCTTGCT	360
TTCCTGAATT	GTAGAAATAA	AAGGAAATCA	CAAGTATTTT	CCAACAAAGT	GGAACTGAGG	420
CCGAAGGGTG	CAGAAAAAAA	CTATAGAAAT	TAGTTAAAAA	TTAGGAAGGG	GCAGTCTCGA	480
G						481

- (2) INFORMATION FOR SEQ ID NO:368:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 285 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

GAATTCGGCC	TTCATGGCCT	ACCAACTCAG	AAGGGAATGG	AATGTGGAAA	AAAAGAAAGA	60
AAACCTGAGT	AACTTTTCCT	AAAAAAGTCT	AGCTGTTCTC	AGTTTGTGGC	ACCAAATGGG	120
GAGCAGGGAA	TGTTCCAGTC	GCAACTGACT	AATTAGCCCA	ACCCTNATTT	ATTGATAATA	180
ATAATGATAA	ATAATAATGC	TAGCTAACAC	TTACTGAGCA	AATACTAGGT	ATTATGTGAA	240
ATCATTTTCT	TGTATTAACT	CACTTAATCT	ACACAGCAAC	TCGAG		285

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:

```
(A) LENGTH: 472 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:
GAATTGGCCT TCATGGCCTA NGTGTGGATA GTGGAGGCAT TGGTAGCCAG AACATGTCAC
TTTATGACAG CATATGGACA GCAATATGGA AGCCCAGCAT GGTTGGTAAA AAATGGGGCA
                                                                       120
GCCTAAGGTC AATGACTTTT GGCTGAGTCT GTGAAGATCT CAAAGCTTGG TGGTTTTTAG
                                                                       180
CATAGCCTTT ATACCATACT TAACTCCGGG TAAGGACCAG GACCACTGTA GCGACCAATT
                                                                       240
GATTGACAGA GTAAAGTATG TGGGTTTTTT TTTTCCCCCA ACTGGGCTGA TTCTCTTAGA
                                                                       300
ATAAAAATTG TATACCATTA TATTATGTTA ACTTGATCAC AAAGAACAAA ATGTTATTTA
TTAATAATAT AGCATTGTCA TCTGTTTGAT GAATTTTCTT GATTTAATGC TTGTTTAGAT
                                                                       420
TCAGTAAGCC ATTUTCAGGA ACTATAATAA ATGCTTCTTC CAACTTCTCG AG
                                                                       472
(2) INFORMATION FOR SEQ ID NO:370:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 307 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:
GAATTCGGCC TTCATGGCCT ACGAGTGCTT GCTGGAATCG TTTACCCTNG TTAATTTTTA
TCATNTCCTC TTTATGAGCA TGATATGGCT TCAGCTGTTC CACTTTGATC CAGGCATGAT
                                                                       120
CTTCTGTTCC AAAAAATTTC ACAAAGAAGC ATTTCTTTCC GCGAGGTTTC TTCAAGTCCT
                                                                       180
TTGGTGGATT AACAATCTTT CCTGGCCAAG GAGGATATCG GCCGAGTTTC CCCCACACCA
                                                                       240
AGTCGCCGAG CCGCAGACTC ACAGCCGCCA TCTTACCACC CAACCACCGC CGACGCACGG
                                                                       300
GCCGCCG
                                                                       307
(2) INFORMATION FOR SEQ ID NO:371:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 414 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:
GAATTCGGCC TTCATGGCCT ACAACGATCT TGTCTTCTTC TATCAGGTTT GCGAAGGTGT
TGCGAAGGCC AGCCATGCCT CCCACACAGC TGCCCAGGCT GGGCTTCCTG ACAAGCTTGT
                                                                       120
GGCTCGTGGC AAGGAGGTCT CAGACTTGAT CCGCAGTGGA AAACCCATCA AGCCTGTCAA
GGATTTGCTA AAGAAGAACC AAATGGAAAA TTGCCAGACA TTAGTGGATA AGTTTATGAA
                                                                       240
ACTGGATTTG GAAGATCCTA ACCTGGACTT GAACGTTTTC ATGAGCCAGG AAGTGCTGCC
                                                                       300
TGCTGCCACC AGCATCCTCT GAGAGTCCTT CCAGTGTCCT CCCCAGCCTC CTGAGACTCC
                                                                       360
GGTGGGCTGC CATGCCCTCT TTGTTTCCTT ATCTCCCTCA GACGCAAACT CGAG
                                                                       414
(2) INFORMATION FOR SEQ ID NO:372:
```

(i) SEQUENCE CHARACTERISTICS:

```
(A) LENGTH: 376 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:
GAATTCGGCC AAAGAGGCCT ACTGGATGGC ATCTACTTCG TATGACTATT GCAGAGTGCC
CATGGAAGAC GGGGATAAGC GCTGTAAGCT TCTGCTGGGG ATAGGAATTC TGGTGCTCCT
                                                                      120
GANCATCGTG ATTCTGGGGG TGCCCTTGAT TATTTTCACC ATCAAGGCCA ACANCGAGGC
                                                                      180
CTGCCGGGAC GGCCTTCGGG CANTGATGGA GTGTCGCAAT GTCACCCATT TCCTGCAACA
                                                                      240
AGAGCTGACC GAGGCCCAGA AGGGTTTTCA GGATGTGGAG GCCCAGGCCG CCACCTGCAA
                                                                      300
CCACACTGTG ATGGCCCNAA TGGCTTCCCN GGATGCAGAG GAGGCCCAAG GACAAAAGNA
                                                                      360
AGTGAGGNAG CTCGAG
                                                                      376
(2) INFORMATION FOR SEQ ID NO:373:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 345 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEO ID NO:373:
GAATTCGGCC AAAGAGGTCC TGTAAGTATG ACTATTTAAT TTATTTCTTT TCACAATATA
                                                                       60
AAAAGCACAT GCGATATTTT GAAAGACTAT TAAAGGTGGG GACAAGAGGT TATTTAAATC
                                                                      120
TATGTTTGGA TGCAACTTTT ATGGCTTAAA CTACAAAGAA TTATCCTTTT TATATATAA
                                                                      180
ATGATTGTAT AGTTCTTTTA ATACTGTTTT TTGATACAAG TGTGAAATNC TTAAAGAAAA
                                                                      240
TGGCAAACAT CACTAACAAC CATTACAATT CTAATAGCTA ACTTTTCTGA GCCATTACTT
                                                                      300
GGAACCATGC ACTGTTTAAA ATGCCTCACT TGGCCAATGC TCGAG
                                                                      345
(2) INFORMATION FOR SEQ ID NO:374:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 507 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:
GAATTCGGCC AAAGAGGCCT AAAATGCGGA GTTATAATCC AGAAGGGGAG TCTTCAGGGA
GATACCGAGA AGTAAGGGAT GAAGATGACG ATTGGTCCTC TGATGAATTC TGAAGATAAT
                                                                      120
CTCCTAAATC ACTGACGTTG AGATGTCATC ATCTTACATC AGACTTTCTA ACTAGTATCA
                                                                      180
AGATCAGTGT CAGATATTGT TGAGGGAAGT AATTTTATAA AGTTACACAA AGGTAGTTAT
                                                                      240
AAAAAAAGCC CAGTTTGTCT TTCAGAAGGT GACTTTCATG TGCTTGAAAA GTTTAATATT
TGAATATTGT GTTTAACCAC ATGGTATTAA AATTTTGCAA TATATTGTGT ATTGGTCTGA
TATTTTAGTA TATAGTAGAA CATACTTTTT TTTTCTTTAA GCCAAATGAA AAGAGGTAAC
                                                                      420
TTTGCTTTTT TCCTTTTTCT TACCTATCAA ATAGCATTTA TTACATGTCT TTCAGTGAAA
TACTTAGTTG TTCCAGGCAC GCTCGAG
                                                                      507
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(2) INFORMATION FOR SEQ ID NO:375: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 346 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:375: GGAACGAATA GAAGTGTTTG TATCTGTGGG TTNGACACAC TACTGAATCA CAAAGTCTTT GGAATAATTC TCAAAAGCCA TCACTTTTAG CCCACTTTCT CATTCATTAA TGCTCTATTC TTTTTCTAGC ATGTCTAGCA GAATTCTCTT GAATTCTTGC AGTGAATTGG TGCTCCTTAA ATACCTGCTA TTTTGGAATA GTTTTGACTT AAATACATTT TCCTTTTCTC CCAGTTGCAA AATGTCAGGG CTGACAACTG AAAGGGCTTC TGAAGATTGT CAGTGTTCTC ATATTCAGAT AGGTAGCAAA GAATCTGACA CATTTGGTAT AATAAACCCA CTCGAG (2) INFORMATION FOR SEQ ID NO:376:

120

180

240

300

346

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 371 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

GAATTCGGCC	TTCATGGCCT	AGGATGAATG	ACCTTAAAGA	TCGAACATGA	ATAAGAGACA	60
TCATTTACCC	TCAAAGAAAC	TAGAGTCTGA	TTGGGCAGGG	AGGAAAAGGT	ATTAAAATTA	120
TGTCTTTCTG	CATTGTGTGG	ATTTGAAGTT	TGTTTTTTGT	TGTTAAGAGT	CTTATTATTA	180
GGATAATGAC	ACTGTTTTTT	CTTTATTAAG	TTACTTGTGT	GGCAGTTAAG	ATGATTCTGG	240
TGGCTCTTAA	CATTTTTTT	TTCTCCAGTC	GGGAACATGC	CCTGTGTGCC	GCCGTCATTT	300
CCCACCTGCG	GTTATTGAAG	CATCTGCAGC	TCCTTCCTCT	GAGCCTGATC	CTGATGCCCC	360
ACGGTCTCGA	G					371

- (2) INFORMATION FOR SEQ ID NO:377:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 258 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

GAATTCGGCC	AAAGAGGCCT	AGGAACTGTT	CTGTTGAAAA	TACCCATCCA	ACAGTTTCTT	60
ACTATGCTCA	TCCCCAAGTG	GCATCCTACA	ATACCTACTA	CCATAGCCCT	CCTCACCTGC	120
CACCATATTC	TGCTTATGAC	TTTCAGCATT	CCGGTGTCTT	TCCATCCTCC	CCTCCCTCTG	180
GACTTTCTGA	TGAGCCCCAG	TCTGCCTCTC	CCTCACCCAG	CTACATGTGG	TCCTCAAGTG	240
CACCGCCCAA	AACTCGAG					258

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 436 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

```
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:
GAATTCGGCC AAAGNGGCCT AATATAACTT AGCTGCTATT TACAACACTA GAAATTTAGT
ACTITAAGTA ATTICACATC TATGATAACA TITGITACIT TATTITTAAT GATTITITA
                                                                      120
CAGTAGTTAT GACAGTAGGA TGGTTATGGA ATTGGAATTT AAACTCCCAA CTAATGAGCT
                                                                      180
TAAGCTGCTT GGAATATTAA TTATGTAGTT TTTACATTCC ATTTTAAAAC AAAAACTTAG
                                                                      240
NAAAGGTGCT GGCATTCTGA GGCCTGCAAT TAGGCCACAT AGCAGAAGCT TGCTCCTTCC
                                                                      300
TTATCTGGGT GAAATATTTT ATTTTTGCAC TTTGAGTCAT ATTCCCACCC CTGTATAAGC
TACATAGGAG CCTGAATGAA TTGGGTAGGA AAGGAAATTA TGCAAACAAG TCTCAGCTAG
                                                                      420
TGCTGAATGA CTCGAG
(2) INFORMATION FOR SEQ ID NO:379:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 535 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:
GAATTCGCC AAAGNNGCCT AGCACATGCG TCCCCGCAGT TGTCTCTTTC TCCTTTCCAA
                                                                      120
GTTCGTGNCT CTAAGGAGAT GGAAGTATTC TAAATTTTCC TACTTCTAAT TTTTACTATG
CAACCAGCAA AGGCGGGAAG GTTGCAGGGA AAATTGTCCG GTCTTTCACA ACTAAGNNGG
                                                                      180
AAATTACTTC TCCTATGTTT TTATTCAAGA GTTGTCTTTA AAACTGCCTG CCGGCTTTCC
                                                                      240
CTTTTAACTT TTAGGATTAT AGTTAAGGTT ATGGAAAGTA GTCATTCATT AGTTCAGTAC
                                                                      360
GTTCATATAA GTTCTCTAAC ATAGAAGAAA ACTCAGTCAC CAGACAGTGA AGTCATTTAG
CAGTGGTTAT TGGAAGATAA TCCACAGTGA TGGTAATGGA ATACTGGAAA CNCATCCTAA
ATAATCTGTA ATTATTATTA TTATTATTTT GGGACAGNGC GAGGCTCCGT CTCCAAAAAT
                                                                      480
AAATAAATAA AATAAATAAA TAAATAAATA AATAAAGGAT GGTGCACGTC TCGAG
(2) INFORMATION FOR SEQ ID NO:380:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 113 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:
GAATTCTAGN CCTGCCTCGN GTCGCACCCA TGTTCATTCG TTCCTTCCTT CCTTCCTACA
                                                                       60
TTCTTTTTT TTNCCTTCTT CTTCAGGGTC TCACTCTGTC ACCCTGGCTC GAG
                                                                       113
(2) INFORMATION FOR SEQ ID NO:381:
     (i) SEQUENCE CHARACTERISTICS:
```

- (A) LENGTH: 660 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

GAATTCGGCC	AAAGAGGCCT	ACACACATCG	TTCATGTACA	TGATCGCCGG	ACTCTGCATG	60
CTGAAGCTCT	ACCACAAGCG	GCACCCGGAC	ATCNACGCCA	GCGCCTACAG	TGCCTACGCC	120
TGCCTGGCCA	TTGTCATCTT	CTTCTCTGTG	CTGGGCGTGG	TCTTTGGCAA	AGGGAACACG	180
GCGTTCTGGA	TCGTCTTCTC	CATCATTCAC	ATCATCGCCA	CCCTGCTCCT	CAGCACGCAG	240
CTCTATTACA	TGGGCCGGTG	GAAACTGGAC	TCGGGGATCT	TCCGCCGCAT	CCTCCACGTG	300
CTCTACACAG	ACTGCATCCG	GCAGTGCAGC	GGGCCGCTCT	ACGTGGGACC	GATGGTGCTG	360
CTGGTCATGG	GCAACGTCAT	CAACTGGTCG	CTGGCTGCCT	ATGGGCTTAT	CATGCGCCCC	420
AATGATTTCG	CTTCNTACTT	GTTGGCCATT	GGCATCTGCA	ACCTGCTCCT	TTACTTCGCC	480
TTCTACATCA	TCATGAAGCT	CCGGAGTGGG	GAGAGGATCA	AGCTCATCCC	CCTGCTCTGC	540
ATCGTTTGCA	CCTCCGTGGT	CTGGGGCTTC	GCGCTCTTCT	TCTTCTTCCA	GGGACTCAGC	600
ACCTGGCAGA	AAACCCCTGC	AGAGTCGAGG	GAGCACAACC	GGGACTGCAT	ACCCCTCGAG	660

- (2) INFORMATION FOR SEQ ID NO:382:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 377 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

GAATTCGGCC	AAAGAGGCCT	AGTGTTGGGA	GCTGTGGGCT	GTGCCCTTCC	AGTCCCCCAC	60
AGCAGTGCTG	TTGCCCAAGA	ATCTCCTAGC	GAGAGACCAG	GGGCTACTGC	CAGGTGACAG	120
AAAAGGGAAC	ATCAGTTCCG	CTATACCCAC	AGCTCACCTG	GCGGCCTGGG	GCCTGCACAG	180
GGCCTGGTTG	AGGCAGTGGA	CCCCATTTTT	GGGCCGTCTG	TGGAGTTGAT	GTTCCTGCCA	240
					AGTTAAAATT	300
	ATAATTCACT					360
ACTTGGAGAG						377

- (2) INFORMATION FOR SEQ ID NO:383:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 304 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

ACTGGGCGGT	CTTTGCAGCA	ATAACAATAT	CTGCTCCATC	60
TAGCTTTGCC	AATGCCACGG	CTTGCACCTG	TGATAAAAAC	120
CGGTGTTGGG	TAACATGACT	TTCGTAGATC	AGAGGAGGCG	180
GCGGGGGAGC	GGCGCTGCCT	GTGGAGATCC	GCGGAGGCCG	240
				300
				304
	TAGCTTTGCC CGGTGTTGGG GCGGGGGAGC	TAGCTTTGCC AATGCCACGG CGGTGTTGGG TAACATGACT GCGGGGGAGC GGCGCTGCCT	TAGCTTTGCC AATGCCACGG CTTGCACCTG CGGTGTTGGG TAACATGACT TTCGTAGATC GCGGGGGAGC GGCGCTGCCT GTGGAGATCC	ACTGGGCGGT CTTTGCAGCA ATAACAATAT CTGCTCCATC TAGCTTTGCC AATGCCACGG CTTGCACCTG TGATAAAAAC CGGTGTTGGG TAACATGACT TTCGTAGATC AGAGGAGGCG GCGGGGGAGC GGCGCTGCCT GTGGAGATCC GCGGAGGCCG TCCCCGCTGC TGTGCATTGG GTTAAAAAACG ACAACCAACT

- (2) INFORMATION FOR SEQ ID NO:384:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 351 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

GAATTCGGCC	AAAGAGGCCT	ACTTATTTTA	CACAGCTTGA	TTAAGGTCTA	TGTCGGTATA	60
ATTTTTTTA	TGAGTCTNAC	ACGTGGGATT	TGTTGAGCTT	CTTGAATTTG	TATGTTTATA	120
CAAATTTAGG	AATTTTTTTC	ATCCATTATT	TATTTGAATA	TATTCTCTGT	CTTCACTGTC	180
CTTTGAGGAC	TCCAATTACG	CATATACCTA	ATTGCCTGGA	GTTGTCCCAT	AGCTTACTGA	240
TGCTTTGTTC	ATTTTTTTCT	TTCTTTTTTT	CTCACCATGC	TTTAGTTAGG	ATAGTTTTTA	300
TTACTGTTTT	TTTAAGTTTG	CTAATCTTTT	CTTNCAGCAT	GCCAGCTCGA	G	351

- (2) INFORMATION FOR SEQ ID NO:385:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 359 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

GAATTCGGCC	AAAGAGGCCT	AGCGTCTTGG	ACATGCCAGG	AATAAAAAGG	ATACTCACTG	60
TTACCATTCT	GGCTCTCTGT	CTTCCAAGCC	CTGGGAATGC	ACAGGCACAG	TGCACGAATG	120
GCTTTGACCT	GGATCGCCAG	TCAGGACAGT	GTTTAGATAT	TGATGAATGC	CGAACCATCC	180
CCGAGGCCTG	CCGAGGAGAC	ATGATGTGTG	TTAACCAAAA	TGGCGGGTAT	TTATGCATTC	240
CCCGGACAAA	CCCTGTGTAT	CGAGGGCCCT	ACTCGAACCC	CTACTCGACC	CCCTACTCAG	300
GTCCGTACCC	AGCAGCTGCC	CCACCACTCT	CAGCTCCAAA	CTATCCCACA	TATCTCGAG	359

- (2) INFORMATION FOR SEQ ID NO:386:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 320 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

GAATTCGGCC	AAAGAGGCCT	ACTACATGTA	AAACACTTTT	ATTCATTAAA	AAGAAAACTG	60
ACTGGCTTGG	ACCTACAAAT	TAGTTTCATT	ATTTGTTAAT	GTTTGAAAGC	CATTAAAAGA	120
TGAATATTAA	GGTTTCTTTA	TACTCAATAC	TTGTAGTTTT	GTTTGGGGGA	ATGAGAGGAT	180
GCCCTTGGTA	CCTTTGTGAG	GCCTCTCCAC	TGAGGGTCAA	TCATGACTTC	TGTTTTAAAC	240
CAGCCCATCC	CATCTTCTCC	AGCTGCTCTC	CTTATGTCTT	GCTTCTCTCC	CCTCCAACCT	300
TCTCAGCACC	AGGACTCGAG					320

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 279 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:	
GAATTCGGCC TTCATGGCCT AGTGGGAGCT ATTTTCTTT TTGTGCATAT AGATATTTCT TAAATGAAGC TGCTTTCTTG TCTTTTATTT CTAAAAGCCC CCTTATACCC CACTTTGTGC AGCAAAGATC CCCGTGCAGG TCACAGCCTG ATTTGTGGCC AGGCTGGACA AATTCCTGAG GCACAACTTG GCTTCAGTTC AGATTTCAAG CTGTGTTGGT GTTGGGACCA GCAGAAGGCA AACGTCCAGC CAACACACAG GACTGCAAGA GGTCTCGAG	60 120 180 240 279
(2) INFORMATION FOR SEQ ID NO:388:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 255 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:	
GGTAGAAGCA GGAGGTTTTC AACCTAGTCA CAGAGCAGCA CCTACCCCCT CCTCCTTTCC ACACCTGCAA ACTCTTTTAC TTGGGCTGAA TATTTAGTGT AATTACATCT CAGCTTTGAG GGCTCCTGTG GCAAATTCCC GGATTAAAAG GTTCCCTGGT TGINAAAATA CATGAGATAA ATCATGAAGG CCACTATCAT CCTCCTTCTG CTTGCACAAG TTTCCTGGGC TGGACCGTTT CAACAGAGGC TCGAG	60 120 180 240 255
(2) INFORMATION FOR SEQ ID NO:389:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 282 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:	
GAATTCGGCC TTCATGGCCT AGGCCCACAT AGAAGAAATG AATGAAAAGA CTTTAGAAAA GCTTGATGTG AAGCAAACAG AACTAGAATC ATTATCTTCT GAACTGTCAG AAGTATTAAA AGCCCGTCAC AAACTAGAAG AGGAACTTTC TGTTCTGAAA GATCAAACAG ATAAAATGAA GCAGGAATTA GAGGCCAAGA TGGATGAACA GAAAAATCAT CACCAGCAGC AAGTTGACAG TATCATTAAA GAACACGAGG TATCTATCAA GAGGAACTCG AG	60 120 180 240 282
(2) INFORMATION FOR SEQ ID NO:390:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 458 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

GAATTCGGCC	TTCATGGCCT	AGATAGAGCT	CAAAAACATG	GCATGGATGA	ATTTATCTCT	60
				TGGTACAACG		120
GATCACAGAC	TTAATGATTC	CTATTCTTGC	CTGGGCTGGT	TCAGTCCTGG	CCAGGTGTTT	180
GTACTAGACG	AGTATTGCGC	CCGAAATGGA	GTCCGGGGGT	GTCACCGACA	TCTCTGCTAC	240
				TCGACCCCAC		300
				GTCAACAAAT		360
				TATAGTGAGT	CGTATTAATT	420
TCAGAGGAGT	ATTTAGAAGA	GAAGCTGAAG	CTGTCGAG			458

- (2) INFORMATION FOR SEQ ID NO:391:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 366 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

GAATGGGACT	CCAAGCCTGC	CTCCTAGGGC	TCTTTGCCCT	CATCCTCTCT	GGCAAATGCA	60
GTTACAGCCC	GGAGCCAGAG	GAGCGGAGGA	CGCTGCCCCC	AGGCTGGGTG	TCCCTGGGCC	120
GTGCGGACCC	TGAGGAAGAG	CTGAGTCTCA	CCTTTGCCCT	GAGACAGCAG	AATGTGGAAA	180
GACTCTCGGA	GCTGGTGCAG	GCTGTGTCGG	ATCCCAGCTC	TCCTCAATAC	GGAAAATACC	240
TGACCCTAGA	GAATGTGGCT	GATCTGGTGA	GGCCATCCCC	ACTGACCCTC	CACCTCGAGG	300
TTCTCCCTAT	AGTGAGTCGT	ATTAATTTTC	AGAGGAGTAT	TTAGAAGAGA	AGCTGAAGCT	360
GTCGAG						366

- (2) INFORMATION FOR SEQ ID NO:392:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 523 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

GGCGGGTGGG	GGTTAATTAT	CTGAAACCTA	CTAAAACGGA	CTACAGTTAT	CTCTAGGCAA	60
TGCTGTTGGA	GTGTTTCCTG	CAAATGCATT	TCACTCATTT	TTTTGTGATT	ATTTTATAAG	120
TATACTGGGG	CAAAAATTTT	ACATTCTAAA	TTGTTCTTAT	TTATTATTTT	TATTATAGAT	180
ATATGAGGAT	ATTACTTACT	CTATTACACA	TATAATTTAT	CTTTTAAATT	TTCAAGTGAG	240
TTCTACAATT	AACTTTATCA	TCTAAATTCT	CATTACAGAT	AGCATTTTAA	TGTCCAGAAA	300
GAAAAAAAGG	TTTTTTATTG	TTATATGTGA	AACCATAAAA	ATATTACCAG	CTTGTGGCCG	360
GGCGTGGTGG	CTCACGCCTA	TAATCCCAGC	ACTTTGGGAG	GCCGAATCAC	CTGAGGTCAG	420
GAGTTCAAGA	CCAGCCTGGC	CAACATGCGG	AAACCCCGTC	TCTACAAAAA	TGGAAAAATT	480
AGCCCGGCAT	GATGGCAGGT	GCCTGTAATC	CCAGCTACTC	GAG		523

- (2) INFORMATION FOR SEQ ID NO:393:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 548 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

GAATTCGGCC	TTCATGGCCT	ACCCAGATGA	AACTTTTGGG	GGGAGAGTGC	CCAGACCAGC	60
CTTTGTCCAC	TATGACAAGG	AGGAGGCATC	TGATGTGGAG	ATCTCCTTGG	AAAGTGACTC	120
TGATGACAGC	GTGGTGATCG	TGCCCGAGGG	GCTTCCCCCC	CTGCCACCCC	CACCACCCTC	180
AGGTGCCACA	CCACCCCCTA	TAGCCCCCAC	TGGGCCACCA	ACAGCCTCCC	CTCCTGTGCC	240
AGCGAAGGAG	GAGCCTGAAG	AACTTCCTGC	AGCCCCAGGG	CCTCTCCCGC	CACCCCCACC	300
TCCGCCGCCG	CCTGTTCCTG	GTCCTGTGAC	GCTCCCTCCA	CCCCAGTTGG	TCCCTGAAGG	360
GACTCCTGGT	GGGGGAGGAC	CCCCAGCCCT	GGAAGAGGAT	TTGACAGTTA	TTAATATCAA	420
CAGCAGTGAT	GAAGAGGAGG	AGGAAGAGGA	AGAAGAGGAA	GAAGAAGAAG	AGGAAGAAGA	480
GGAAGAGGAG	GAAGACTTTG	AGGAAGAGGA	AGAGGATGAA	GAGGAATATT	TTGAAGGGGT	540
TACTCGAG						548

- (2) INFORMATION FOR SEQ ID NO:394:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 577 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

GAATTO	GGCC	TTCATGGCCT	ACTTACTAGG	AATTAAAAGA	CGGATTTCGA	AGGAGATTCA	60
GAGGCA	GCAA	GCACTACAGA	AGTCAGAACT	CCAGCACCAT	CTGCTCCGTT	TCTTGAAGTT	120
TGCTGA	ACGA	GGACTCACAG	CTGCAACGTG	GGGTGATTGT	ATTGATCAAA	ACCCACTGGG	180
AAGGAC	AAAG	AGTTTGCCGC	CTTTCGGGGA	TCCAAGGGAC	TGTGGCGACC	GTGCCTCTGT	240
GCCAGC	GTCC	CAGGAAGGAA	GCCAACCCTG	AGCGAGCCTG	TCCTCTGTGG	CAGGTCCACA	300
CGGTGT	GGGT	GGGCAGGGCT	TGGACCCCCG	TCTCCATGGC	AGGTCCATAC	AGCATGGGTG	360
GCAGGG	TTTG	GACCCGCCCA	GCAGCACCAC	GGACCCCAGC	CACTCTCGGG	GGCAGACGTC	420
AGAATO	CGTT	CCTGAGCAGC	TCCCGTGCCC	TGGGGGCAGT	CACAGAGCCC	CCCAACACCC	480
CCGTGC	TCTG	CACCAGCCTC	TCCCTCCACA	CCCGAAGCAG	GCGTCCATCT	GTGTCCTCCT	540
GGCAGC	CCCT	CAAACACACA	CCACCCCATA	TCTCGAG			577

- (2) INFORMATION FOR SEQ ID NO:395:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 415 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (11) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

GAA?	TCGGCC	TTCATGGCCT	ACATCTTCAT	TGCTGAGGTT	GCAGCTGCTG	TGGTCGCCTT	60
GGT	TACACC	ACAATGGCTG	AGCACTTCCT	GACGTTGCTG	GTAGTGCCTG	CCATCAAGAA	120
AGA?	TATGGT	TCCCAGGAAG	ACTTCACTCA	AGTGTGGAAC	ACCACCATGA	AAGGGCTCAA	180
GTG	TGTGGC	TTCACCAACT	ATACGGATTT	TGAGGACTCA	CCCTACTTCA	AAGAGAACAG	240
TGC	TTTCCC	CCATTCTGTT	GCAATGACAA	CGTCACCAAC	ACAGCCAATG	AAACCTGCAC	300

CAAGCAAAAG GCTCACGACC AAAAAGTAGA GGGTTGCTTC AATCAGCTTT TGTATGACAT CCGAACTAAT GCAGTCACCG TGGGTGGTGT GGCAGCTGGA ATTGGGGGCC TCGAG	360 415
(2) INFORMATION FOR SEQ ID NO:396:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 286 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:	
GAATTCGGCC TTCATGGCCT ACTAAAAGAT ACTTCAAAGT GACAAAAACG TGTTCCTTCC CCACTTAGAG ACAATGATTA ACAGGGCCCT ATATGTTCTT ACCACATACA GAGGATGCAT TTATTTTTGC TCTATGACAC TTGCAAAAAAT CTCTACTGTA ATTAATTTGG GTCTATTATT AACTCTCTGT TCCATCATAG AATGTGGCCA GGCCTTACAA TGGAGAGCCA GAGTTAAAAC TTCAAGTTGC ATCTGTTTTT GGGCTGAGTC ACCACCGGAC CTCGAG	60 120 180 240 286
(2) INFORMATION FOR SEQ ID NO:397:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 208 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:	
GAATTCGGCC AAAGAGGCCT AAAAATGAAA ACCTCTGCAC TTTAATTTTT TTCAGTAATT TCCAGCTATT TCTAGGTATA AAGAGCAGCT CGTTTCTCTT ATTTATTTTA GTCTCATGTG TCAATACTTT CCGATGCTTT GCTTAATTCA TGTATGTGTG CAGTGCTGCA ATGCCCAGAC AAACGTGAGC ACACCCACCA ATCTCGAG	60 120 180 208
(2) INFORMATION FOR SEQ ID NO:398:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 452 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:	
GAATTCGGCC AAAGAGGCCT ATGATGAAGC TGGGCATTTA TAACTAGATT CATTAAGGAA TACAAAGAAA ATACTTAAAG GGATCAATAA TGGTGTCTTC TGGTTGCAGA ATGCGAAGTC TGTGGTTTAT CATTGTAATC AGCTTCTTAC CAAATACAGA AGGTTTCAGC AGAGCAGCTT TACCATTTGG GCTGGTGAGG CGAGAATTAT CCTGTGAAGG TTATTCTATA GATCTGCGAT GCCCGGGCAG TGATGTCATC ATGATTGAGA GCGCTAACTA TGGTCGGACG GATGACAAGA TTTGTGATGC TGACCCATTT CAGATGGAGA ATACAGACTG CTACCTCCCC GATGCCTTCA AAATTATGAC TCAAAGGTGC AACAATCGAA CACAGTGTAT AGTAGTTACT GGGTCAGATG	60 120 180 240 300 360 420
TGTTTCCTGA TCCATGTCCT GGAACGCTCG AG	452

WO 98/45435

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PCT/US98/06954
(2) INFORMATION FOR SEQ ID NO:399:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 330 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:
GAATTCGGCC AAAGAGGCCT ATCTTCCTGA AGAGCAATGG AGCCGCTTTT ACTTGGAAGA
                                                                       60
GGACTAATCG TATATCTAAT GTTCCTCCTG TTAAAATTCT CAAAAGCAAT TGAAATACCA
                                                                      120
TCTTCAGTTC AACAGGTTCC AACAATCATA AAACAGTCAA AAGTCCAAGT TGCCTTTCCC
                                                                      180
TTCGATGAGT ATTTTCAAAT TGAATGTGAA GCTAAAGGAA ATCCAGAACC AACATTTTCG
                                                                       240
TGGACTAAGG ATGGCAACCC TTTTTATTTC ACTGACCATC GGATAATTCC ATCGAACAAT
                                                                       300
TCAGGAACAT TCAGGATTCA CAAACTCGAG
                                                                       330
(2) INFORMATION FOR SEQ ID NO:400:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 377 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:
GAATTCGGCC TTCATGGCCT AAGCAAACCC AGAGGTGGAT GTTATGAACA GCTGTGTCTG
CCAAACACAT TTACCCTTTG GCCCCACTTT GAAGGGCAAG AAATGGCGTC TGCTCTGGTG
                                                                      120
GCTTAAGTGA GCAGAACAGG TAGTATTACA CCACCGGCCC CCTCCCCCCA GACTCTTTTT
                                                                       180
TTGAGTGACA GCTTTCTGGG ATGTCACAGT CCAACCAGAA ACACCCCTCT GTCTAGGACT
                                                                       240
GCAGTGTGGA GTTCACCTTG GAAGGGCGTT CTAGGTAGGA AGAGCCCGCA GGGCCATGCA
                                                                       300
GACCTCATGC CCAGCTCTCT GACGCTTGTG ACAGTGCCTC TTCCAGTGAA CATTCCCAGC
                                                                      360
CCAGCCCCAT CCTCGAG
                                                                       377
(2) INFORMATION FOR SEQ ID NO:401:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 311 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
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- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

GAATTCGGCC	TTCATGGCCT	AGGCAAGGTC	TTCGGCTCGT	GCCGTTCTAA	GCCGGAGAAT	60
TCTCGCGGGA	GCAGGGTTAC	GTCCTCGTGG	GATTCGTTGG	CGGTGGCTGA	GGTCCTCCAG	120
CAGCCTGACC	TGAGTGGGTT	AGTGATCCAG	AGAAACCAGC	AGGCCAACTT	GGTCAGGAAG	180
GTTCGGGAAG	CTGTTGGAGC	AGTGTGGGGA	ATTTCCCACC	AGGATGAGTA	TGATTGGCTG	240
TGATTTTAGA	TCGTAAAGCT	GAAAATTGAA	ATCATGAAAG	TAGACAGGAC	TAAACTGAAG	300
AAGAACTCGA	G					311

(2) INFORMATION FOR SEQ ID NO:402:

```
(i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 357 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:
GCATTGATGG AAAAGCATAA TGTCTTAGAA AAAGGCTTTC TAAAAGAAAA AGAGCAAGAG
GCCATTTCTT TTCAAGATAG ATACAAAGAA CTTCAGGAAA AACATAAACA AGAATTGGAA
                                                                      120
GACATGAGGA AAGCTGGTCA CGAAGCCCTC AGCATTATTG TGGATGAATA TAAGGCACTA
                                                                      180
CTGCAGTCTT CAGTTAAGCA ACAAGTAGAA GCTATTGAAA AACAGTACAT TTCTGCAATT
                                                                      240
GAGAAACAGG CACACAAGTG TGAGGAGTTG CTAAATGCTC AGCATCAGAG GCTCCTTGAA
                                                                      300
GTGCTAGATA CAGAGAAGGA ACTGTTAAAA GAAAAAATAA AGGAAGCCCA TCTCGAG
                                                                      357
(2) INFORMATION FOR SEQ ID NO:403:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 492 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:
GTTCTAGACC TGCCTCGAGC GTTAATGGTA TAAATCACTT GTTTGTAAAG TATTGTTTTT
                                                                       60
AAATATTGCC AGATTTGATA TCTTAGTATT GTATTTTTAT ATTTGTCTTC ATGTGTTTTT
GTTTTCTCAT AAGTGTCTGT ACCCCCCTTT TTTTTTCTTT AAAGAGAAAT AATGAGAGAG
                                                                      180
ATTGTCTGTC TTGAAGTTCT CAGTGCCTGT GCATTGCTGC CACTACACAG CTAGTATCAT
                                                                      240
GACAGCAGCT TCAGAACCAG AGCTGGCTTC CAGGCAAGGC TGGGTGGGGA AGAAAGAGAA
                                                                      300
AAACAAAGA ATTATTCTC TATGCCGAGA CCAGCTCGGT CAGGGAGACC CTAACCTAGC
                                                                      360
GGTGCTAGAG GAATTAAAGA CATAGACACA GAAATATAGA GGTGTGAAGT GGGAAATCAG
                                                                      420
GGGTCTCACA GCCTTCAGAG CTCAGCCACG AACAGAGATT TACCCACGTA TTTATTAACA
                                                                      480
GCAAGACTCG AG
                                                                      492
(2) INFORMATION FOR SEQ ID NO:404:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 395 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:
GAATTCGGCC TTCATGGCCT ACTTCCCTCT AAGGTCCCCA AATGCCTCTC ACGTGCCTAG
CATTTAGCTG CTGCACCGAG CATGCTCACT GACAAACTTT TGGCCAAGAA GAGCCTTTTG
                                                                       120
GTCTCTCTG GTCAGATCTA GGAGGGCTTC AGGACTCTCC AAAACTCACC CACTCAGAGA
GCCTGCCAGG AACACTCAGC TGAGCGATGG CATTGTGGAG CCTGGGTTTT CAGAAGGGAG
                                                                       240
CCCATAGTGA GTGGTAGCAT AACCTTGTTA AGGTTGTATT TTCCTTAGAT ATAGAAACAA
ATCAAATGCT GCTAAATTGG TAAGGGATGG AGTTTTCATA TCACGTCACA TTTTGCTGAG
                                                                       360
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CCGTAACCAG ACAGGGAAAA AGCAGAGACC TCGAG

(2) INFORMATION FOR SEQ ID NO:405:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 262 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(b) IOPOLOGI: IIIlear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:	
GAATTCGGCC TTCATGGCCT ACCAAGTTCT AACTGTAAAA TGGGGACATT TTACCTTTCT	60
TTCTTTGGAT AGGATCAGTT CTTAAGAGCA GCCCCGGTAA CTGGAGGAAT GGGAGCCGTT	120
TTGATGAGAA AAATGGGCTG GAGAGAAGGA GAAGGATTAG GAAAAAACAA AGAAGGCAAT	180
AAGGAACCCA TCCTAGTTGA TTTTAAGACA GACCGAAAAG GTCTTGTTGC AGTAGGAGAA AGAGCACAAA AGAGGCCTCG AG	240
AGAGCACAAA AGAGGCCICG AG	262
(2) INFORMATION FOR SEQ ID NO: 406:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 289 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:	
GAATTCGGCC TTCATGGCCT ACCCATTTGT CAATTTTTGC TTTGTTGCAA TTGCTTTTGG	6
TGCCTTTGTC ATGAAACCTT TGCCTACAGG TGCTGTTTAT TTACACCCCT GTCCCAACCT	120
CACCCCACTC CCTTTCTTTT GCTGGTGGGA AGTCAGTAAG AACTGTGGGT GGGGTTCTGA GGTAATCAAT ACAAAGAAGA AGGTAAGAAA TTGGAGGGGA CTCAGGGGAG ATGGCAATGC	186 246
TGACAAGGGG TTGGATGGAA TTTGTTCTGT AAACTGGAAG CAGCTCGAG	28:
(2) INFORMATION FOR SEQ ID NO:407:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 329 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:	

- GCTCCTTCTG TATCCTTCCT TTCCCATCTG TCTGCTTCTA ACAAATAAGA CAAGCTAAGA 60
  AGCAGCTTGT TTCATGATTC TATACTCACT TCCAAGCTTT CTCTGCATAG ACTTTCCTAG 120
  TTTGCCACTT TATCTTTTCT CCATCCCTCC AGCCAGTCAT GAGATTCTAC TCCCCATTCA 180
  TACATGCATT TATTTATCCA GACTTTACTG AAGGCTTACT CTTTGAACTT TGCAAAATGC 240
  CAGTGAGGCA AAGCATGCAT CCTGTACAGG AAAAACTCAG TCTAGAGGGG AGAGATAAGC 300
  AAACAAGTGA TTACCACACC AGGCTCGAG 329
- (2) INFORMATION FOR SEQ ID NO:408:
  - (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 222 base pairs

- (B) TYPE: nucleic acid (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

ATTGAATTCT	AGACCTGCCT	CGAGAGCTTT	TGAGATTGTC	TATTTTGTCT	GAGTGAGTTT	60
TGGTACTTTA	TTGTTTTCGA	TTGGTCCATT	TCTTCTACGT	TGTCAGATCT	CTGAGTGTCA	120
AGTTGTTCAT	AGTACTCCGT	TATTATCTTT	TTCATGACTG	TAGGATCTGT	GGTGATATTG	180
ATGATTTGTG	TCTTCACTCC	TTTTTGTTGG	CCTACACTCG	AG		222

- (2) INFORMATION FOR SEQ ID NO:409:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 505 base pairs
    - (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

GAATTCGGCC	TTCATGGCCT	AAACTTGCAG	AAATGAAGAC	TAGAGTACAC	AGCACACTCA	60
GAGCCCAGAC	AGACTTCGTC	CCAGGACATC	ATCTGTTCTT	GATGCCCATT	CTTCTCTCCT	120
AAACATCATT	TACTTTTTCC	TCTAAAAGTG	CCTGCAGACC	CCCACTACTC	TCTCCCATGG	180
AGAAGGGCAT	ATAAGCTTCG	AATCTCACGG	GGTTATTGGG	CACTCTGTCT	CTTGTGATGC	240
TCCTATGCAT	GTAATAAATT	TATGTGTCCT	TTCTCCTATT	AATTGGTCTA	ATGTCCATTT	300
ATTCCATAGA	TTCAATTATC	AAACTCTCAG	AGGGCAGAGG	GAAAATTTTC	ACTCCCTTAT	360
ATCATCAGAA	ATATAAATAA	AAATAGCACA	ACACTCAGTA	AATGATTATG	TTATTATTGT	420
TATGTTTGTA	ATATCTTGGT	GTCTGGTTAT	TTTAAATCAT	ATCACTTAAA	GAAACAGTGT	480
TCCTTAGGCC	ATGAAGGCCG	AATTG				505

- (2) INFORMATION FOR SEQ ID NO:410:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 650 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

GTATGAACAT	TGAGGGCCCA	GATCTCAATG	TGGAAGGTCC	GGAGGGAGGC	TTGAAAGGTC	60
CCAAATTCAA	GATGCCTGAC	ATGAATATCA	AAGCTCCCAA	GATCTCCATG	CCTGACATTG	120
ACTTAAACTT	GAAAGGCCCC	AAGGTGAAAG	GTGATGTGGA	TATTTCTCTT	CCCAAACTTG	180
AAGGGGATCT	GAAAGGGCCA	GAGGTTGATA	TCAAAGGCCC	TAAAGTGGAC	ATCAATGCCC	240
CAGATGTGGA	TGTTCATGGT	CCAGACTGGC	ATCTGAAGAT	GCCCAAAGTG	AAAATGCCCA	300
AGTTCAGCAT	GCCTGGCTTC	AAAGGAGAAG	GCCCTGAAGT	CGATGTTACC	CTCCCTAAAG	360
CTGACATTGA	CATTTCTGGT	CCCAATGTAG	ACGTTGATGT	TCCAGACGTG	AATATTGAAG	420
GTCCAGATGC	AAAGCTGAAG	GGCCCCAAGT	TCAAGATGCC	TGAGATGAAC	ATCAAAGCCC	480
CCAAGATCTC	CATGCCTGAC	TTTGACCTGA	ACTTGAAGGG	ACCCAAAATG	AAGGGTGATG	540
TGGTTGTGTC	TTTGCCCAAA	GTGGAAGGTG	ATCTAAAAGG	CCCTGAGGTG	GACATCAAGG	600
GCCCCAAAGT	GGACATTGAC	ACTCCTGACA	TTAACATCAA	GAGGCTCGAG		650

## (2) INFORMATION FOR SEQ ID NO:411:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 445 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

GAATTCGGCC	TTCATGGCCT	AGGGGCTGGA	GGGTGGCCCG	AAGCAGATGG	GGCCGGCCTT	60
GCAGGCACTT	CTAAGGCCTT	GGGGTTTGCT	TCCGAGGGAG	TAGGGAAGGA	GAGCGATGTC	120
ACCCTGTGAG	GCTTGGTCAC	ATACCCCAAT	GGATTTGGTA	GCACACGCCA	CAGTGAAGGT	180
ATAAGCTACT	GTCATCACAC	GTAATTATTT	CATGAAACAG	AAAATTTTAA	AATAAAAGAA	240
AATAGAAGTT	TCCCTATTTT	CTTCTCCTGC	ACTATTGGAT	CATCCTGTTT	AGCCCTCTTT	300
TAAGACAAAT	GGACTTAGCA	AACGAGTGTA	AATAGGAATG	AATGGTTTTG	TGGGGTTTAT	360
TTTATTTTAT	TTTATTTTAT	TTTATTTTAT	TTTATTTATT	TTATTGAGAC	AGAGTTTCAC	420
TCTTGTTGCC	CAGGCTGGGC	TCGAG				445

- (2) INFORMATION FOR SEQ ID NO:412:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 290 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

GCCTGCCTCC	AGGCCTTTGC	TCCCACTGTT	GNCTCCACTT	AGAATAACAT	TCCACCCCAT	60
CTCTATAAAT	ATCCTACAGA	CAAATACTAC	CTTCCCCTTA	AGGCCAGTTC	TAACCCTAAC	120
TGACAACAAA	TCATCTCTAC	ATGATCTTTT	CCTTCTGGGA	ATGCCTGCAG	CACTGTTTAA	180
TCCTGCCCCA	CCACCATCCC	CTCACCCAGC	ACCCTCTCCC	AGACCAGACA	GGGTGGCTCA	240
TGCCTGCAAT	CCCAGCACCT	TGGGAGGCTG	AGGCAGGAGG	ATTGCTCGAG		290

- (2) INFORMATION FOR SEQ ID NO:413:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 421 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

GAATTTGACA	TCTTAGAACA	TTCTGCAACC	TTTTGCCTGG	GAAATGGAAA	CAGATCTAAT	60
CTTTACCACC	CTCATGGCTC	AAGGACCTCA	TCTGGCAGCC	TGGCTCATGT	TTTTCAGCCA	120
AGTAGCTTCC	AGCTTACAGC	AGCCCTCAAA	TTTGGACCTG	CCACCAGCTC	CAGAGCTTGA	180
CTGGATGGAG	ACAGGACCAT	CTCTGACATT	CATTGGCCAT	CAGGATATAC	CAGGAGTTGG	240
TAACATCCAC	TCAGGTGCCA	CACCTCCCTG	GATGATCCAA	GATGAAGAAT	ACATTGCTGG	300
GAACCAAGAA	ATAGGACCAT	CCTATGAAGA	ATTTCTTAAA	GAAAAGGAAA	AACAGAAGTT	360
GAAAAAACTC	CCCCCAGACC	GAGTTGGGGC	CAACTTTGAT	CACAGCTCCA	AGGACCTCGA	420
G						421

(2) INFORMATION FOR SEQ ID NO:414:

```
(i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 254 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:
GAATTCGGCC TTCATGGCCT AAGCCAGTCA ACCAGCAGTA TTAGTGCTGT TTTCAAAGAT
TTAAGCTCTA TAAAATTGGG AAATTATCTA AGATCATTTT CCCTAAGCAT TGACACATAG
                                                                    120
CTTCATCTGA GGTGAGATAT GGCAGCTGTT TGTATCTGCA CTGTGTCTGT CTACAAAAAG
                                                                    180
TGAAAAATAC AGTGTTTACT TGAAATTTTA ACTTTGTAAC TGCAAGAATT CCAGTTCAGC
                                                                    240
CGAGCCACTT CGAG
                                                                    254
(2) INFORMATION FOR SEQ ID NO:415:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 313 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:
GCAAACAGAC AAGGCTTACA GGTTAGTTCA GGATCTGCGC CTTATCAAGC AAATTGTTTT
                                                                     60
120
AACCCCTCCA TAACCCATTA TTCGGTTCTG GATCTCAAAC ATGCTTTCTT TGCTATTCCT
                                                                    180
TTGCATCCTT CATCCCAGCC TCTCTTTGCT TTCACTTGGG CTGGCCCTGA CACCCATCAG
                                                                    240
CCTCAGCAAC TTACCTGGGC TGTACTGCCA CAAGCCTTCA CGGACAGCCC CCATTACTTC
                                                                    300
AGTAGCCCTC GAG
                                                                    313
(2) INFORMATION FOR SEQ ID NO:416:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 347 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:
GCCTGCCCC ACCTTACAGG TCTGGGATGT ACCTTTCCAT CTGTTGCTGC TTTCTTCTAT
                                                                     60
GGGCCCCTGC CCTCACTCTC AAGAACCTCA ACTACTCCGT GCCGGAGGAG CAAGGGGCCG
GCACGGTGAT CGGGAACATC GGCAGGGATG CTCGACTGCA GCCTGGGCTT CCGCCTGCAG
                                                                    180
AGCGCGGCGG CGGAGGGCGC AGCAAGTCGG GTAGCTACCG GGTGCTGGAG AACTCCGCAC
                                                                    240
CGCACCTGCT GGACGTGGAC GCAGACAGCG GGCTCCTCTA CACCAAGCAG CGCATCGACC
                                                                    300
GCGAGTCCCT GTGCCGCCAC AATGCCAAGT GCCAGCTGTC CCTCGAG
                                                                    347
(2) INFORMATION FOR SEQ ID NO:417:
```

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 452 base pairs

(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:	
CLAMMONO OR MINISTER AND AND AND MORE MORE MORE MORE MORE MORE MORE MORE	
GAATTCGGCC TTCATGGCCT AGCAGATGAT TGACATTGCT ATCGATGGTT TCCTTTTGAC	60
TCCAGTGCAG AAGATCTGCA AGTATCCCTT ACAGTTGGCT GAGCTCCTAA AGTATACTGC	120
CCAAGACCAC AGTGACTACA GGTATGTGGC AGCTGCTTTG GCTGTCATGA GAAATGTGAC	180
TCAGCAGATC AACGAACGCA AGCGACGTTT AGAGAATATT GACAAGATTG CTCAGTGGCA	240
GGCTTCTGTC CTAGACTGGG AGGGCGAGGA CATCCTAGAC AGGAGCTCGG AGCTGATCTA	300
CACTGGGGAG ATGGCCTGGA TCTACCAGCC CTACGGCCGC AACCAGCAGC GGGTCTTCTT	360
CCTGTTTGAC CACCAGATGG TCCTCTGCAA GAAGGACCTA ATCCGGAGAG ACATCCTGTA	420
CTACAAAGGC CGCATTGACA TGGATGCTCG AG	452
(2) INFORMATION FOR SEQ ID NO:418:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 259 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:	
GATAACTTGA GATCAAATCA GTCATATTTG ACTCTTCTCT TTTTCACTCC TTTTATATCT	60
GATCAGTCAG CAGTTTTTTG AAACCCTGTT CGAAGCAGTT CTCAACACTT GTGCACCCAT	120
TCTTTCTCCT ACACCACTCA ATCTAGACCC TCACATGTGG CTGTCCTGCT TTCCTTCTCT	180
CCTACTTCTA AGCTATTCTG TGGAGAGATG TCAAAGTAAT CTTCACAAAA AATCTGATTG	240
CATCACTTCA CATCTCGAG	259
(2) INFORMATION FOR SEQ ID NO:419:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 331 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:	
GAATTCGGCC AAAGAGGCCT AATTAGAAAT GGCTACTCCC CAGTCAATTT TCATCTTTGC	60
AATCTGCATT TTAATGATAA CAGAATTAAT TCTGGCCTCA AAAAGCTACT ATGATATCTT	120
AGGTGTGCCA AAATCGGCAT CAGAGCGCCA AATCAAGAAG GCCTTTCACA AGTTGGCCAT	180
GAAGTACCAC CCTGACAAAA ATAAGAGCCC AGATGCTGAA GCAAAATTCA GAGAGATTGC	240
AGAAGCATAT GAAACACTCT CAGATGCTAA TAGACGAAAA GAGTATGATA CACTTGGACA	300
CAGTGCTTTT ACTAGTGGTA ACGGGCTCGA G	331
(2) INFORMATION FOR SEQ ID NO:420:	
(i) SEQUENCE CHARACTERISTICS:	
(I) JEQUENCE CHEMOTOLINIZATION.	

(A) LENGTH: 269 base pairs

(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:	
TACCACATTT TTCCATTTGA CTGTTTATTT TTATGTCCTT TCTTTCTTTT AGATTAAGTC TTTTTTCTTC TCACCCCCTC ACCCCTCCCC CCTGGTTATA CATTCTTTTA CTATTCTTTT	60 120 180 240 269
(2) INFORMATION FOR SEQ ID NO:421:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 405 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:	
AGCTGTTCCT GTATCGACTC CGTGTCAACT CCAGAGCAGG GGGTATCCTC CTGTAGTGCA CCTTCTCTCT TGGCCTGGAG GCAGCACTTT CTGTGCCTGG GCAGCAGAAA TGGGGAATGT TCTTTGGTCC GTTGGAAAAA CGGGCCCCAA CATCTAGCCC TGTTGCATAA GGCATGGAAT TGCCCAGTTG GGGAGGACCT GTGCTGGAAA GGGATCATCA AACTCCATCT GCCCCATCAG	60 120 180 240 300 40!
(2) INFORMATION FOR SEQ ID NO:422:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 327 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:	
CCATATGTGT TATTGCACCT GAAGACCTTT CACCTGGACA AGATGCCGAG GTGGAAGACA GTGATACAGA TGATCCTGAG TATCTTAGTT TTTTTGTTTT TGTTGAGACG AAATCTCACT CTTGCCCCCA GGCTGGAGTG CAATGGCACG ACCTCGGCTC ACTGCAACCT CTGCCTCCCG	60 12 18 24 30 32
(2) INFORMATION FOR SEQ ID NO:423:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 315 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li></ul>	

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

GAATTCGGCC	AAAGAGGCCT	AGAATAATAC	ACTAGTAAAA	AAAAATGTAT	GTCAGGCACT	60
GGGAAGGGCA	GTAGGAATAT	AGAAATGAGA	AGCCGTGGAT	TAGAGACTCA	CAGTCTACTG	120
GGTAAAAGAA						180
ATAGAAAAGT						240
GAAGGGTTTT	GGGGCTGGAT	TTTGAAGGCT	CAATAGGCTC	CTACCATATA	GAGAACTAGG	300
AAGCGAGTCC	TCGAG					315

- (2) INFORMATION FOR SEQ ID NO:424:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 326 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS; double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

GAATTCGGCC	AAAGAGGCCT	ACTATCCAGG	TTTACATTTT	AAGGCAGTCG	AGACCTTATT	60
CACGTGGTAT	ATAAACAACC	ACATTTCTCT	TTTATATGGA	ACAACACTTT	TCATTTGCGG	120
CTGGCCTTCT	CACTAGCTTA	TGCTTTTTTT	TTTTAAGACC	TTTCTTAGCA	CTCGCTGAAC	180
TCCTCCCCCT	CACAATCAAT	CTCAGCAACT	CAGCAGAGTC	GCTTCAGTTC	ACAGCTCTTA	240
ATCCTTCACT	CCAGACTAAA	GCTAATCTTA	TGTCCTCAAA	CAGCTACAAC	TCACTGTTAT	300
CACAGTTCCG	ACAGCAGAGA	CTCGAG				326

- (2) INFORMATION FOR SEQ ID NO:425:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 385 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

GAATTCGCCA AAGAGCCTAT	AGAAATAATA	CCACGACCTG	CGCATTCAAA	GCTGTTGTAT	60
CTGGATTGTG ACTGCGTGGA	AGGTCGAGGC	GGGAAGACAG	GGGCTGTTGC	TTTTCGTTAT	120
AAACTCTGCA TTACTTGATT	TTTGCACTAC	GTACATTTAC	TTTGATAACA	CTGGAAAGAA	180
TAAATTGGCC ATGTAGTGTA	GCTTCCAAAA	AAAACTATTG	CTTGGGTTTC	AAGGTCAAGG	240
AAATTTCATT CTCATCAGTT	TCTTGGGAAA	GAGGAAGTGG	AATGATGTTG	TCAGAAAGTG	300
AAACCATGGG TCATTTTCAG	<b>AACTACTCAG</b>	AGTAATAAAT	ATTTTTTGTC	AGTTTTGTTC	360
TTACAAGTGA AATGGTCCCC	TCGAG				385

- (2) INFORMATION FOR SEQ ID NO:426:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 460 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

```
GAATTCGGCC AAAGAGGCCT AAGAGATTT TATTATGATT TTGATTCTT TACTACAACA 60
TTGCATGTGT CTGGAGTATA GCCATTACAC TTTATGAAAA AGGCAAAATG GTCATTTGGG 120
GTGTTTTAGG AAGTTTGCCA AAAGGCTCCT TTGTCATTAT AATCCTTCCT AAGCTGCCAT 180
CCACGGGTTT AGGTCATGGA TATGAAAAGT GAAAGGGTTT AGAGATGAAG TAGTGTCCCC 240
TGAGTGCTTA CCAACCTGTT AATCTTTTTG AGATGTAAT TTTTTCATAT AGAGCCCCCT 300
AAAAATCTTGA TGGCTCTAGA TCAGTCAAGC CTAAGAGAAG ACGTATTTAT GGAAAAAAAA 3AAACCTTGC TGGATTGCTA GTAATATCTA CTTCTTGGAA ATTAATACTT 420
CATATTTTTT AAAAAAAATTA TTGATGCATT AGGACTCGAG 460
```

- (2) INFORMATION FOR SEQ ID NO:427:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 522 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

GAATTCGGCC AAAGNGGCCT	AGGAAAAACA	TGAAATACAT	AAATGGATTA	ATTTTGCAAA	60
TTAATCTNGC AAATTAATCT	ATAGCTCTTA	ATGTTTCTTC	CAAATTAAAG	GAAAAATGGA	120
TAAGGAAGTA CTTTCTTGGC	AAACTGTAGA	TGAATACTGA	ATAAAAGTCA	TTCTTTCCTA	180
AAGAAGAAAA GTGCATTTTA	GTTTTTTAGA	AAAAATGTAA	TTTTAGAAAG	TCTCTTCTAT	240
GCAGATTTTA GAAAGTCTTT	TCTATTTTTA	GAAAGTCTTC	TTGTATGCAG	ATTTTGTTCA	300
ACTTCCCCAT CTGTACTTAC	CAAAGGAAAA	ATAAACAGTT	TATAGAATAT	TAATAGAATA	360
ATTATGTGCN ATGTAAAATA	TGTTGAATCT	CCCTAATTTA	TATTTACTAT	GTGAATATAA	420
ACTACAGAAT AAAGAAACTG	TTCCTCCTTT	TATCCATTAT	TTTGTTGAAA	ACAACTAAAG	480
AAATCTTACA GATTAATGTT	CATATTAAAA	GGACTCCTCG	AG		522

- (2) INFORMATION FOR SEQ ID NO:428:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 582 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

```
GAATTCGGCC AAAGAGGCCT AGGTAGTTAT CAAGAGATTT TAAAACTTCA ACCCTTTTTC
TCTTATAGTT AGTGAAGAGA GTAGAATATC TCCAGTTTTG GCTGACATCT CTACAACCTG
                                                                      120
AACAATTGGC TTAAACTTCA CTTGGGATTC CCGGTTGCTT GTTTTAGCAT GGCNAAATTT
                                                                      180
GGCGTTCACA GAATCCTTCT TCTGGCTATT TCTCTGACAA AGTGTCTGGA GAGTACAAAA
                                                                      240
CTGCTGGCAG ACCTTAAAAA ATGTGGTGAC TTGGAATGTG AAGCTTTAAT AAACAGAGTC
                                                                      300
TCAGCCATGA GAGATTATAG AGGACCTGAC TGCCGATACC TGAACTTCAC TAAGGGAGAA
                                                                      360
GAGATATCTG TTTATGTTAA ACTTGCAGGA GAAAGGGAAG ATTTGTGGGC AGGAAGTAAA
                                                                      420
GGAAAGGAGT TTGGATATTT TCCCAGAGAT GCAGTCCAGA TTGAAGAGGT GTTCATATCT
                                                                      480
GAGGAAATTC AGATGTCAAC GAAAGAATCT GACTTTCTTT GTCTTCTTGG AGTAAGTTAC
                                                                      540
ACATTTGACA ATGAAGATAG TGAATTAAAC GGTGAACTCG AG
                                                                      582
```

(2) INFORMATION FOR SEQ ID NO:429:

(i) SEQUENCE CHARACTERISTICS:

```
(A) LENGTH: 314 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA .
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:
GAATTCGGCC AAAGAGGCCT ACTGATCAAG TGACCCATTA CTGCGGGAAA AAACCACACA
                                                                       60
TACAAAAGCC TTTGACCCCA GTAATTTTGT ATTGGTATAT TTACCCTGAT CTTAAACTGC
AAGGAATGTC CGCAATTAGA GTTTTTCTTT GTTTTCTAAG TCTGAAACTT GATAATCCAT
                                                                      180
TTCTGCCTTC CCATGACGAG TGGACATTCC TCCAGCCAGT GGTGAGTTCC TCTTTCCTTC
                                                                      240
GCTCTCAGCA AGAGCATGGG TTGCCCTCCC ATCTCGTAAG CAGAGCCTAC CACAAACGCA
                                                                      300
GCTCAAATCT CGAG
                                                                      314
(2) INFORMATION FOR SEQ ID NO:430:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 556 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:
GAATTCGGCC AAAGAGGCCT ATTGGGTCCT ATTTACAACT TTAAGAATGG AGGCATACTT
                                                                       60
CAGGAAAGAA AGCACCAGTG CAGTTCCAAT TTATTATTGT ATCTGCTGTC TTGAGAGTAC
                                                                      120
AGGGTGTATG AGAGTGCACA GTGGTTTAGA ATCACTATGG AATTTAAAAA GACCCAGAGA
                                                                      180
CATTAACAAG AATCCACATT CTAAGTCGTC AGAATCCACA TTTCTGACCT TGTCTGCTGG
GGCCTGCTCT GTTTTTGATG GCTCAAAATA TAATTCTTTT ATTGAAATAC ATGTTCCTCA
                                                                      300
TCCTGTTTCA GGGCTTCTGC CTGGAATGTT CCTCCCCCTA GCATTTGTAG GGCTGGCTCC
                                                                      360
TTCCTGTCAT GCAGGTCTCA GCTCAGATGA CCCCATCTCA GAGAGGGCTT CCCTGACCAA
                                                                      420
CCAATCTACA GCCCTTCCTA GTCACTTTTT TCCACATCAC CCTCTTTATG CATGGAGGCA
                                                                      480
GATAGGTGTT TTACCCTGTT TATTTATTAT TATTATTTT TTGAGACAAA GTCTTGCTCT
                                                                      540
GGCACCCAGG CTCGAG
                                                                      556
(2) INFORMATION FOR SEQ ID NO:431:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 424 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:
GAATTCGCC AAAGAGCCT AGAAGTAACG GAAGCTACCT TGTATAAAGA CCTCAACACT
                                                                       60
GCTGACCATG ATCAGCGCAG CCTGGAGCAT CTTCCTCATC GGGACTAAAA TTGGGCTGTT
                                                                       120
CCTTCAAGTA GCACCTCTAT CAGTTATGGC TAAATCCTGT CCATCTGTGT GTCGCTGCGA
                                                                       180
TGCGGGTTTC ATTTACTGTA ATGATCGCTT TCTGACATCC ATTCCAACAG GAATACCAGA
                                                                       240
GGATGCTACA ACTCTCTACC TTCAGAACAA CCAAATAAAT AATGCTGGGA TTCCTTCAGA
                                                                       300
TTTGAAAAC TTGCTGAAAG TAGAAAGAAT ATACCTATAC CACAACAGTT TAGATGAATT
                                                                       360
TCCTACCAAC CTCCCAAAGT ATGTAAAAGA GTTACATTTG CAAGAAAATA ACATAAGGCT
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•	
CGAG	424
(2) INFORMATION FOR SEQ ID NO:432:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 418 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:	
GAATTCGGCC TAAGNGGCCT ACATAAAAGT AAGAAAATAT CTTACTAAAA TCTCTTTTCT TATAACATTT AGNTTACGTA TATATTTTAT CTCCCTTTTT TTGNAATATA TATAAATCAA ATAACAGCTG AATAAACCTT TGGTCTTTTT TTTTTTTTTT	60 120 180
CTGGGACCCG AGATTAATTG CTTCGTTTTT GCTTTGGCAA AAGATTGTTC TTACAATTTT	240
TAGTCTTTTA AAGTTGACAC AGATTTGTTC AGTCTTGCTC ATTCTAAAAG CACACAAAAG	300
TTGAGCATAA AAATAGGATT AAATTTAGCA ATAAAGAATT ATAAAGACTA AAAGATACTG	360
AGTAAGTTGT TTGACAGAAA CCTGATTATC CATGATGATT ATTTGCAGGC TTCTCGAG	418
(2) INFORMATION FOR SEQ ID NO:433:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 157 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:	
GAATTCGGCC AAAGAGGCCT AGAACTCCAG AGGCAAGTGT TATATGAATT ATGCATTTGA TTCTACATGT TTATTAGACA TGTATGGCAG ATACATTTAT ATTTTACTAA TGGTTATGAT GACTTTAATA ACTTTCAAAG GATTATGGGG ACTCGAG	60 120 157
(2) INFORMATION FOR SEQ ID NO:434:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 440 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:	
GAATTCGGCC AAAGAGGCCT ATGTTTTTAC TACTATTATT TTTTTTTTACC CAAGGGAGAA	60
AGACAAAAAA ACGGTGGGAT TTATTTAACA TGATCTTGGC AAACGTCTTC TGCCTCTTCT	120
TCTTTCTAGA CGAGACCCTC CGCTCTTTGG CCAGCCCTTC CTCCCTGCAG GGCCCCGAGC	180
TCCACGGCTG GCGCCCCCA GTGGACTGTG TCCGGGCCAA TGAGCTGTGT GCCGCCGAAT	240

300

360

420

440

CCAACTGCAG CTCTCGCTAC CGCACTCTGC GGCAGTGCCT GGCAGGCCGC GACCGCAACA

CCATGCTGGC CAACAAGGAG TGCCAGGCGG CCTTGGAGGT CTTGCAGGAG AGCCCGCTGT

ACGACTGCCG CTGCAAGCGG GGCATGAAGA AGGAGCTGCA GTGTCTGCAG ATCTACTGGA

GCATCCACCT GGGTCTCGAG

(2) INFORMATION FOR SEQ ID NO:435:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 345 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (x1) SEQUENCE DESCRIPTION: SEQ ID NO:435:

GAATTCGGCC	AAAGAGGCAT	AAACATAGAG	AAATTGGTGA	TGTTAAACCT	TCTGAATTTT	60
GTTTTAAGTG	CACTGGGAAG	TGATGGAAGG	GTTTGTAGCA	TAGCAGTAAT	CTGATCTGAT	120
CTGATCCGGT	GTGAATGTCT	TTTTAGCAGA	TGATTTCATT	TTACCAGCTC	TCTNGAAAGT	180
TTAATCAATG	TGATAGCCAT	GACAGTTTAT	TAAACTACTT	ATTTGAGAAA	GTAACTGCCT	240
					CCCTTGTTTA	300
ATATTTGTTT						345

- (2) INFORMATION FOR SEQ ID NO:436:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 321 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

GAATTCGGCC	AAAGAGGCCT	AAGAACTCAC	AATAAAGTAT	CATATTCCTC	TCTTTTGACC	60
TAGAATTCAT	AGCCCTAGTA	ATCTCGTTTT	GATTAGATGC	TTTGATTGGC	AGTTATACAT	120
CTTTGATAAC	ATTTTCAATG	TGAAATGAAT	TATTCTTTCG	TTAAAGCCAT	TTTAAGCAGA	180
ATGTCTATAA	ATGAGGGCCC	ACGAGAAGGA	ATAACAAAGC	AGGGGTGTTG	GGGATGGTGG	240
CTGGGGAGCT	TTGGTGTATT	TATTAACCTG	TGGTTGAGTT	TTGCGATGTG	TGCAAGTACA	300
CACAGCCCCG	AACAACTCGA	G				321

- (2) INFORMATION FOR SEQ ID NO:437:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 431 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

GAATTCGGCC	AAAGAGGCCT	AGTTTTAAAA	CGTATTGTTT	AATTTTCNAA	CATTTAGGGA	60
TTTCCCAGAT	ATCTTNGTTG	TNGGTTTCTA	ATTTGATTCC	ATTATGGTTA	GAGACCATAC	120
TTGGTATGAT	GAATTAAAAA	AAAAAATNTA	GAGGTTTGTA	TATGGCCTGA	AACATTTTTT	180
AGGTGAGTGT	TCAGTTTGTA	ATAGGAAAGA	TGTGTCCTGC	TGCCGTTAGG	TAAAGTGTTT	240
CATAAGTAAT	AATTAGGTCA	AGTTGGTTGA	TCGTGNTAAG	GTCTGCTCTA	TCCTTGCTGA	300
TTTCCTGTCT	GCTTGTTCTA	GTGATTACTG	AGAAAGGAGT	GTTGAAGTCN	ACAACGATTG	360
TTATGGGTTT	GTTCTCTTTC	TCCNTGAAAT	TCTGTCTGNN	TATGCGTCCT	GTATTTTGAG	420
GACCCCTCGA	G					431

## (2) INFORMATION FOR SEQ ID NO:438:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 392 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

GAATTCGGGC 1	TTCATGGCAT	ANGCAGAGGT	TCCGGGNCCA	GNNCANGCNC	GGGACAAGNT	60
CAGAGATGAN (						120
CTCTTGTGGN A	ACATGGGGAN	NTNTGGANTC	CAGCTCCCAG	NACTGGAGTG	CTATTCAANT	180
GATCNAGGAN (						240
GGGGATCNGA A	AGNAGATGAA	TGCCCTCAAA	GGCCATGNAT	GTACTTCAAA	NGAAGTGGNT	300
NNTGAAAACA (	GNTNNAANAA	TGTAAANCGA	NAGTNAAAAT	NNATGTTGNG	GANGAAGGAA	360
NTTGGTGGNN A	AGTNAAAAAA	GAAGTAANCC	GA			392

- (2) INFORMATION FOR SEQ ID NO:439:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 304 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

GAATTCGGCC	TTCATGGCCT	AGGTGTGCTT	CCCTTTCCCC	ATTTCCCATT	ATTCCCAGCT	60
GTATAGTAGT	GTAGTGAAAA	TCACTTGAGA	TGTGGAAGAG	TAGTCTGGTC	TAGGAAGAGA	120
GAGGGAAAAG	TAAGTTTCCC	AGGATAAGAG	GGGGAAAAA	GGCCCCAAAG	CCTTCTCAAT	180
GAGGAATGGG	GAAGGAGGTT	TTGCTGCCAG	GTTTTACTAA	GTGCATTTGA	ATGAACCCTG	240
CTATTGTAGT	CCTCTTTTAT	TAATGCTTTC	CTGACATTTA	CCCTGTTAGT	TGAGGCTACT	300
CGAG						3.04

- (2) INFORMATION FOR SEQ ID NO:440:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 579 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

GAATTCGGCC	TTCATGGCCT	AATCACNGNA	GTGACTGACA	TTATATATTA	NGGATCAAAT	60
TATGTCCACA	AGCAATATTA	TATAATCTAC	GTAGAAGTGT	AATAACAAAC	AAGAGTACAC	120
TTAAAATTAC	TTTAAAAGAT	GTCTTTAGTT	CATTCCAATA	TAATTCTTGA	TTAAAATTAG	180
GATTATTTCT	ACATTTTAGG	ANNTACAAAG	GATCACGGGT	AACATGGATT	GGGNCCANAT	240
ATTTTTTTAA	AGTTTCGAAT	TGGTATCTGT	AGTAGTGGAA	TGTTATAGAT	TTGAAGTAAC	300
TCTCCACGGA	CAGTGCTGCT	TTCGTGTAGA	GCAATTTAAT	TGGAGAAGTG	GCCATTCTTA	360
CTTCAGGGAT	GCAAAGATGG	TCTCATACCA	TTTGGATAAA	TGTCGTGGTA	TCCATGCTTT	420
TTTTCAACTA	ATAACATCAT	CTCTCTTCAT	GACCAGTTAA	TTGGGCTATT	TGGCAGCCCA	480

STGAACCTAT GTACTAATGG CAAGTTAGGG GCAAATGGAA ATGGACACAT CCGATAAAGT TGAAATGTAT GTTTTAATCT TTCACAGAAG TCCCTCGAG 579 (2) INFORMATION FOR SEQ ID NO:441: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 556 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:441: GAATTCGGCC TTTATGGCCT ACCTACGGTA CCTGAAAACA ACGATGGCAT GGAAAACACC TCCCATTTAC CTGTTGTTGC TGCTGTCTGT TTTCGTGATT CACCAAGTTT CNTCTCAAGA 120 TTTATCHNCC TGTGCAGGGA GATGTGGGGA AGGGTATTCT ANAGATGCCA CCTGCAACTG TGATTATAAC TGTCAACACT ACATGGAGTG CTGCCCTGAT TTCAAGAGAG TCTGCACTGC 240 GGAGCTTTCC TGTAAAGGCC GCTGCTTTGA GTCCTTCGAG AGAGGGAGGG AGTGTGACTG CGACGCCCAA TGTAAGAAGT ATGACAAGTG CTGTCCCGAT TATGAGAGTT TCTGTGCAGA 360 AGTAAAAGAT AACAAGAAGA ACAGAACTAA AAAGATACCT ACCCCCAAAC CACCAGTTGT AGATGAAGCT GGAAGTGGAT TGGACAATGG TGACTTCAAG GTCACAACTC CTGACACGTC 480 TACCACCCAA CACAATAAAG TCAGCACATC TCCCAAGATC ACNACAGCAA AACCAATAAA 540 TCCCAGGACC CTCGAG 556 (2) INFORMATION FOR SEQ ID NO:442: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 528 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:442: GAATTCGGCC TTCATGGCCT ATTATTTTGG CACCAGCGTC AAGACAAATA ATATCCTCTC 60 CCATTATTTT CATAAGTAAC ACAGATTCCC TGATTTTTAA AAACTAAAAA TACAGCTAAA 120 CCTTTCTTAT GTATAAAGTA TGCCTATCAT ATACAGGGAG AGGTGGGTAA TAAACTTCCT 180 GTAATGACAG TGTTTGGCAT TTCTTTATGG ATGGAATTGG AACATGAACA AGACCATGTC CAGCGTTTTT ACTGTGAATG TAAATGGAAC AGCAGCCCAA AGCTGTTGTC TGTGCCCCAG AGGTGCTACC TGTAGACAGG GACCAACTCC ATGTGTGTGT GTTAAGTGTT TGACTCCAAT 360 TAAGACTCCC AAGCAAATCC TGCATATTCC AAATGTAAAG AGTACTCAGT GGGAAAAAGG 420 TTGTTACCTC AAAGTCATTG CTTCTTTCCT GGCTGGGTCA CAGGGTGAAG AGATGAAGGT 480 GTCTGATGTA TATAGACAAT TAGGGAAAAA TGAGCGGCTT TCCTCGAG 528 (2) INFORMATION FOR SEQ ID NO:443: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 304 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

GAATTCGGCC TTCATGGCCT ACTGGAATCT GCAGCCCCCA CATGCATCTG TCTAACGCAT GCCTCGTGTT CGTTTTGCAA ACATGCCTGT GGTGGAGGGT GGTCAGTTGT AGCCCTGTGC GTCTCAAGGC TGCCTTGTGA GGCCATTCCC AGTGCGTGCC CTTGAGCTCC TTACCACCCC TTTTCCTGCT CGGCCCTTTA ATCCCTGACA GACCTGGACT GTGTGGCTGA AGGGGGACCT GCAGCACTGC AGAAATGCCT CTGCGTGGTG CCATGAAGGA AAGAAACCTT GGCCTGGTCT CGAG	60 120 180 240 300 304
(2) INFORMATION FOR SEQ ID NO:444:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 275 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:	
GAATTCGGCC TTCATGGCCT AGGGCAGGGG GAGGGGTGCA NAGTGGGACC CTCACCACAG GGTACTGAGA CAGGTCATTG TAGGTCCGCC CCGCAATGGT GTTGAGTTGC ATCAAGTACT CGAAGTTGGA TATCTCACGC TGTACCCATT TCTGGGTAAG GCCTGAGGCA CGCACCATCT CCTGGGGGGA GCGGCTGCTT AGGTAGCCAA GAGAGGGGGG CCGTAGGCGC AGGANCCACG AGTACACCTG GCCCCATCCC ACCCCATCCC TCGAG  (2) INFORMATION FOR SEQ ID NO:445:	60 120 180 240 275
•	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 418 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:	
GAATTCGGCC TTCATGGCCT AACCAGCTTT AATTTCAATT GAGGAATAAT AACAACCCTA GAGATTCATA GGAAAGAGCA TTGAAATACA TTTTTTTGCAT AAAGATACCT AAAACCATCT ACCCAGCTTA GGGTTGAACT GAATTTCTGT GAAATAAATT TGTTTTAAAAT ACTAATTATT TTAAAACTAC TTAATTCTTA AAAACAATGT CATCAGTTTC AAAAGTTTCA CTTTGGGAGG ATATTCCTTA AAAGGCATAC ATAGATGGTA AAGTATAAAA TATTTCTGAC AGAATTATTC AGTATTATTC AACATTTACT TTCATGTTTG TTATTGTACC ACAAAGATAG TGTCATTGTT GGGTTAAAAAT GTTGGCTGTT TTTGTTAATA TACTTAAAAC TGTAACCAGT GGCTCGAG	60 120 180 240 300 360 418
(2) INFORMATION FOR SEQ ID NO:446:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 304 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(x1) SEQUENCE DESCRIPTION: SEQ ID NO:446:	
GAATTCGGCC TTCATGGCCT ACTACATCAA GCACCAGAAC CGCCAGCTGC GCGCCCTGTT GCTCAGCCAC CAGTTCAAGC GCCCCGAGGC CCACCAGACC CACCAGACC ACTTCAGGCC	60

CGCCGTGAAG TCCCCGGTCC AGGTCATCCT GCTCCGTGCC CTCGCCTTCC TGGCNTGCGC CTTCCTACTG ACCACCGCGC TGTATGGGGC CAGCGGACAC TTCGCCCCAG GCACCACTGT GCCCCTGGCC CTGCCACCTG GTGGCAATGG CTCAGCCACA CCTGACAATG GCACCAGGCT CGAG	180 240 300 304
(2) INFORMATION FOR SEQ ID NO:447:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 380 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:	
GAATTCGGCC TTCATGGCCT ACAGAGATGG ATTATCCTAC TTTACTTTTG GCTCTTCTTC ATGTATACAG AGCTCTATGT GAAGAGGTGC TTTGGCATAC ATCAGTTCCC TTTGCCGAGA ACATGTCTCT AGAATGTGTG TATCCATCAA TGGGCATCTT AACACAGGTG GAGTGGTTCA AGATCGGGAC CCAGCAGGAT TCCATAGCCA TTTTCAGCCC TACTCATGGC ATGGTCATAA GGAAGCCCTA TGCTGAGAGG GTTTACTTTT TGAATTCAAC GATGGCTTCC AATAACATGA CTCTTTTCTT TCGGAATGCC TCTGAAGATG ATGTTGGCTA CTATTCCTGC TCTCTTTACA	60 120 180 240 300 360 380
(2) INFORMATION FOR SEQ ID NO:448:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 144 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:	
GAATTCGGCC AAAGAGGCCT AAACAAATGA GGGTAGTAAT TTTTTATCTG CTAAAACTTA TATTTATATC ACATACTTGT TGCAATGATT TCAGTGTCTA CATAAATGGT GGCTTAGCTG AGGCAGGTCT AGAATTCAAT CGAG	60 120 144
(2) INFORMATION FOR SEQ ID NO:449:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 351 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:	
GAATTCGGCC AAAGAGGCCT ACTAGACGTT TGTACAAACT ATTCCCTTGA GTTATTTCT CTGGCTCTTC AGCTCCTTCC TCCCACCCCC TCCCCTGCAC CACCAATCCA TTCTTTTGCT TAATTTCTCT CCATCCTTCA GGTTTCAGCT TTAAGAGGTC ACTTCTTTTA GGACACATTC CCTGAATCCT CTCACCTCCA CCCACAAAAA AGGCCTCTCC AGATGCCCTT CTTTTCTGCT CAAACCTCAT CTGCTTCCTT TATCATATGC TTATCGTTTT GGATTGTAAT TATTTATTTA ATTGCATGTC TTTCTGCTAG TTTTTTGTGTT AGCAACAACA AGGATCTCGA G	60 120 180 240 300 351

(2) INFORMATION FOR SEQ ID NO:450:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 505 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

GAATTCGGCC	AAAGAGGCCT	AGATGATGGC	AGGAATGAAA	ATCCAGCTTG	TATGCATGCT	60
ACTCCTGGCT	TTCAGCTCCT	GGAGTCTGTG	CTCAGATTCA	GAAGAGGAAA	TGAAAGCATT	120
AGAAGCAGAT	TTCTTGACCA	ATATGCATAC	ATCAAAGATT	AGTAAAGCAC	ATGTTCCCTC	180
TTGGAAGATG	ACTCTGCTAA	ATGTTTGCAG	TCTTGTAAAT	AATTTGAACA	GCCCAGCTGA	240
GGAAACAGGA	GAAGTTCATG	AAGAGGAGCT	TGTTGCAAGA	AGGAAACTTC	CTACTGCTTT	300
AGATGGCTTT	AGCTTGGAAG	CAATGTTGAC	AATATACCAG	CTCCACAAAA	TCTGTCACAG	360
CAGGGCTTTT	CAACACTGGG	AGTTAATCCA	GGAAGATATT	CTTGATACTG	GAAATGACAA	420
AAATGGAAAG	GAAGAAGTCA	TAAAGAGAAA	AATTCCTTAT	ATTCTGAAAC	GGCAGCTGTA	480
TGAGAATAAA	CCCAGAAGTC	TCGAG				505

- (2) INFORMATION FOR SEQ ID NO:451:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 347 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

GAATTCGGCC	AAAGAGGCCT	AGTCGTAAGT	TACCATAATA	GGTGCTTGCA	GTCATTGATA	60
TAATCCAGAA	AGCTAACGAA	ATGCAAATGA	TCAGGCTCAG	TATAACTATA	TTAGTTATCA	120
TCTTTATATA	TCTTTTGCAT	ATATTGTCGT	TAAGATCTGT	CATGGAAAAT	AAGGATATGA	180
GCTCCTGCGG	GAAAGAATAT	TTAGCGTTTC	GGAGAGAAAG	TCATTTACGA	TGTGAGCAAG	240
ACACTTGTTC	AGAGGCAAAC	ATAAATCCCA	ACATATTCCA	CCGACCAAAC	AAGCATAAAA	300
ATCACAAAAA	TTCAAACTCC	TTCCGGAAAC	TCCTACTGGC	CCTCGAG		347

- (2) INFORMATION FOR SEQ ID NO:452:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 394 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

GAATTCGGCC	AAAGAGGCCT	ATCTTACTAT	TTTTATGTCA	TIGGITITIT	CTTCTTTCTT	60
TCTTTCTTTT	TTTTTTTTT	TTTTTGAGGC	AGAGTCTCGC	TCTGTGGGGA	CACTGTTCCG	120
TTCAGAGGCC	CCTCCCAGCC	ATGGGGTGGG	GGACAGTGGT	GGGCGTGGGA	ATCCCAGCGA	180
GCATCCTGGA	GGGTGCGTCG	TCTCCATGTA	TTTTGCTCTT	CCCCATCTTT	TCCATGGGGT	240
CCCCTGCCAG	GGTCAAGCAC	TAATATGTGG	TGAAGGCAGC	AAACAGCGTC	GGCGTCCCTT	300
TAGGGGTGGG	GAGAGGGCTG	TAGCACCAAG	AACCCCCTCC	CCCGCCCACG	ACATCCCTGA	360

AAAGGAGACT AAAATAAAGC CCCGGCGCCT CGAG	394
(2) INFORMATION FOR SEQ ID NO:453:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 325 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:	
GAATTCGGCC AAAGAGGCCT AGGAAAAACA GAGTAAAAAA TTGGAAAAGA AGAAGGAAAC AATAACAGAG TCAGCTGGTC GACAACAGAA AAAGAAAATA GAGAGACAAG AAGAGAAACT GAAGAATAAC AACAGAGA: TATCAATGGT TCGAATGAAA TCCATGTTTG CTATTGGCTT TTGTTTTACT GCCCTAATGG GAATGTTCAA TTCCATATTT GATGGTAGAG TGGTGGCAAA GCTTCCTTTT ACCCCTCTTT CTTACATCCA AGGACTGTCT CATCGAAATC TGCTGGGAGA TGACACCACA GACTGTTCCC TCGAG	60 120 180 240 300 325
(2) INFORMATION FOR SEQ ID NO:454:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 422 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:	
GAATTCGGCC AAAGAGGCCN AGGGTCACAG GGTGGTTATC TCACTTCGCA GCTTTTCCTT TCTGAGGCCA GAAAAGGAAG GGGTTTGCCT TCCTCTAGTA TTTATTCTTC TGGACTACAT CAAGTACTCT AAGCCTGATG TTAGGCAATA ACTGCCCATT AGCCATTGGC TACATTTGCC TCTTTCTTGT TCCAACAATA TTAGTGATCT GTGGNACAGG ACACACTCTT TGTTTGCTAG CTACAAAATTC TAACAAAGCT AAGTTTTATT CATGTAGNTA TTCACAAAATT AANACAACAC ACACACCACA CACACACACA CACACACACA	60 120 180 240 300 360 420 422
(2) INFORMATION FOR SEQ ID NO:455:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 316 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:	
GAATTCGGCC AAAGAGGCCT AGACGTCCAA GAAAAAACAT TTGGTGAAAG TCAGGATTTA CCTTTGAAAT CCGACTTGGG CACCAGGGAA GATAGTAGTG TTGCATCTAG TGATAGGAGT AGTGTGGAGC GAGAAGTGGC AGAACACCTA GCAAAAGGCT TCTGGAGTGA CATTGGCAGC ACGGACACTC CTTGCCAAAT GCAGTTATCA CCTGCTGTGG CCAAAGATGG CTCAGAACAG ATCTCACAGA AACGGTCTGA GTGTCCGTGG TTAGGTNTCA GGATTAGTGA GAGCCCAGAA	60 120 180 240 300

CCAGGTCTCA CTCGAG

316

(2) INFORMATION FOR SEQ ID NO:456:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 458 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:	
GAATTCGGCC AAAGAGGCCT AGTCAGTCTG AGTTAGAAAA TCGACTCCAT CATCTAACAG AGACTCTCAT CCAGAAACAG ACCATGCTGG AGAGTCTCAG CACAGAAAAG AACTCCCTGG TCTTTCAACT GGAGCGCCTC GAACAGCAGA TGAACTCCGC CTCTGGAAGT AGTAGTAATG CTGTTCTTTT TAATGACACA GAAACTAATC TGGCAGGAAT GTACGGAAAAA GTTCGCAAAG CTGCTAGTTC TAATGACACA GAAACTAATC TGGCAGGAAT GTACGGAAAA GTTCGCAAAG CTGCTAGTTC AATTGATCAG TTTAGTATTC GCCTGGGAAT TTTTCTCCGA AGATACCCCA TAGCGCGAGT TTTTGTAATT ATATATATG CTTTGCTTCA CCTCTGGGTC ATGATTGTTC TGTTGACTTA CACACCAGAA ATGCACCACG GCCTCGAG	60 120 180 240 300 360 420 458
(2) INFORMATION FOR SEQ ID NO:457:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 186 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:	
GAATTCGGCC AAAGAGGCCT ATCGAGGTTT GGTTGACTGA TGGAAGCTTT TATTTCTTTA ACCATTTATG CATTTCTCA ATTTGCTACA ATAAACATAG ATTGCACAGG GGTGAATACT AAGGAACTCG GAGGGTTAGG GTTAATTTCT GTGAAAGACC AAATATGTTT CTCTGGTTCT CTCGAG	6) 12( 18)
(2) INFORMATION FOR SEQ ID NO:458:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 308 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:	
GAATTCGGCC AAAGAGGCCT AGCATTATGG TATATTTTAA ATTCATCAAG CTCATCTGTA TGTGTCTTTT TGTCCTTTTA CTACTGAGAG GATTGGGGCT GGGATCATGG CAGCCTGCTC TGATGTATTT CTCTCCACTC TATTTTATTA TTTTTTTAAA GAGTTCTAAC TTAAATACGT GGACCAGCTA TTGGATAACT TTAAATCCTA TATTTATCAT TCTTTCTATT CACTTTGCCA CATACACACC ATGTGATGAT TTTAAACCCG ATTTCTGTAT AGAGAATGTT AAAAGGATAG CACTCGAG	6 12 18 24 30
CACICGAG	30

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(2) INFORMATION FOR SEQ ID NO:459:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 303 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:
GACATGCTGT GGTTCCACCG CGCACTCACC CTGCTCATCA TCCTCCGCCA CCTCACCAGG
                                                                       60
AAGGACCCAC AGGGGCTGGG CGTGACGAGT GACGCCATCG CCGATGCCTG CCAGGCCCTG
                                                                      120
GTGGGCCCCA CCGCCCACAG CCGTTGCTGG TGATCTCCGG GATCCCCACC CACCTGGACG
                                                                      180
AGGGCGTAGT CAGAGGCGCC ATCCGCAAGG CCTGCAACGC CCACGGCGGG GTCTTCAAAG
                                                                      240
ACGAGATCTA CATCCCGCTG CAGGAAGAAG ACACCAAGAA GCCAAAAGAC AAGGCCGAGG
                                                                      300
CCG
                                                                      303
(2) INFORMATION FOR SEQ ID NO:460:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 250 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:
GAATTCGGCC TTCATGGCCT ACACTTTAAT TGCTGTTATC ATGGGCCTAA TTACAGTCAC
                                                                       60
TGCAGTGGCC ACCACTGCCG GAATGGCATT ACACCAGTCC ATTCAAGCGG CTCATTTTGT
                                                                       120
TAATGGTTGG CAAGCCAATT CCATCCAAAT GTGGAATTCT CAACAAGGCA TCGATCGAAA
                                                                      180
ATTGGCAAAT CAAATTAGTG ATTTAAGACA GTCTGTTATT TGGCTTGGAG ATCAGGTAGT
                                                                       240
                                                                       250
GAGTCTCGAG
(2) INFORMATION FOR SEQ ID NO:461:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 309 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:
GGTGACGCCT GCTTCACATC TCTAATGAAC ACCCTCATGA CGTCGCTACC AGCACTAGTG
                                                                        60
CAGCAACAGG GAAGGCTGCT TCTGGCTGCT AATGTGGCCA CCCTGGGGCT CCTCATGGCC
                                                                       120
CGGCTCCTTA GCACCTCTCC AGCTCTTCAG GGAACACCAG CATCCCGAGG GTTCTTCGCA
                                                                       180
GCTGCCATCC TCTTCCTATC ACAGTCCCAC GTGGCGCGGG CCACCCCGGG CTCAGACCAG
                                                                       240
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(2) INFORMATION FOR SEQ ID NO:462:

TTCCTCGAG

(i) SEQUENCE CHARACTERISTICS:

300

309

GCAGTGCTAG CCCTGTCCCC TGAGTATGAG GGCATCTGGG CCGACCTGCA GGAGCTCTGG

(A) LENGTH: 251 base pairs

(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:462: GAATTCGGCC TTCATGGCCT AATGAAGAAA AGCAGAATTC CAAATTCAAA CTGTTGGAGT GAGCCAAGTG GACAGACCCT CCATGAGTGC ACTTTCTTCC AAGAAATCCC CAGATTTACC 120 CCATAGAGGT CTGGGATTAC CTGGAATATA ATATGAAAAA CATTTTTTAG GCTGGGTGTG 180 GGGCTCACAC CTGTAATCCC AGCACTTTGG GAGGCTGAGG CGGGCGGATC ACCTGAGGTT 240 GGGAGCTCGA G 251 (2) INFORMATION FOR SEQ ID NO:463: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 225 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:463: GAATTCGGAA CAATGGGGGT TTCAAAACAT AAAAGTGAAA GTCCTTGTGA ATCTCCTTAT CCAAATGAGA AAGACAAGGA AAAAAATAAG TCAAAATCTT CAGGCAAAGA AAAAGGCAGT 120 GATTCATTTA AATCTGAGAA GATGGATAAA ATCTCCTCCG GTGGCAAAAA GGAGTCCAGG 180 CATGATAAAG AAAAGATAGA AAAGAAAGAG AAACGGGACC TCGAG 225 (2) INFORMATION FOR SEQ ID NO:464: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 527 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: CDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:464: CTCGAGGCGT GTGGGATCAT GAGGCAAAGA AAGTCCAACG AGGGAGAGAG GAGAGTGAGG 60 GATGAGAGGG GACACTTGCT CCATCCTAGT CCCCACGCGG CCCAGCTGGC TTCCTTTTCC 120 AGAATATCTC CTTGCTATAA CCTGGCAGCA GGGGAGCCAA GGTCCTTCTC CATCCTTACA 180 GGCACTGAAC CAGGATGTAG GCGCACACTG CTGTGTTCTC TCTGGCCCAT CCTCTCTAAT 240 TGTCTTTCCC TTCCCAGGTC ACAGGATGCT TATTCTCATC TCCAGGCCTT TGCACGGGCC 300 GGGCCTGCTG CCAATCCCCG CACTCTCCCC TTCTTAGGGC CAGGCTAACT CTTCCCCATC 360 CCCGGGGCTC AAGCGTTCAG GTCTCTTCCA AAAGCAGTCT TGGTGGTCCC TGCCACGCGT 420 TACCCTCCTC TCAAGTCACC CGGGAGGTGG AGGTTGCTGT AAGCCAAGAT CGCAGTGAGC 480 TGAGATTGCA CCATTGCACT CCAGCCTAGG CCATGAAGGC CGAATTC (2) INFORMATION FOR SEO ID NO:465: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 317 base pairs (B) TYPE: nucleic acid

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WO 98/45435
                                                                  PCT/US98/06954
                  (C) STRANDEDNESS: double
                  (D) TOPOLOGY: linear
             (ii) MOLECULE TYPE: cDNA
             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:
       GCACTCATAA AAATCTTACT CAGAAATCTT CAGAGGTTTG CTAAGGATAC AATTTGATTC
                                                                              50
       TTACACATTT AATGCTCACC AGCTGCTTAG GCCCACACCA TTTATCCACC CTGATTTGCT
       ACTGCTCTTT GAAATACAAC CAGTGTTTCA GCCAGACTGT TTTCCTGCTT CTGCTCCCCT
                                                                              180
       TCTCCTCCTC CCAGCACATC TGTGAATTCT TTGACTGGTT TACCACTCCC AAACTCCTCC
                                                                              240
       CCAGCAATGC AGATCTTCTA CACCCTTTAG GATCTAAGCT AAGTCTGCTT CCCAGATATC
                                                                              300
       CTCCCGAACA GCTCGAG
                                                                              317
        (2) INFORMATION FOR SEQ ID NO:466:
             (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 348 base pairs
                 (B) TYPE: nucleic acid
                 (C) STRANDEDNESS: double
                 (D) TOPOLOGY: linear
            (ii) MOLECULE TYPE: cDNA
             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:
       GGTCATTCTT TCCATCGCTG CGGACACGGG AGTCAGAAGT GAAACAGTCC TGTCCTCGTG
                                                                               60
       GGGCTTACGT TCCAGGCGCA AGAGCCACAG GTAGTCGAAT TGGGAAACCG CCTCGGATGT
                                                                              120
       CACATAAGCG CCCAGGGAGG ACAGGGCAGG ACAGGGCCTC CCTGGGGAGG TGACTTGAGT
                                                                              180
       CAAGACTCAA AAGAGGGAAG CGAGGGAACA AGCCATGCGA GGAACTAACG AAGGAACATT
                                                                              240
       CCAGAAAGAT TTCACATCCC AAGCCTAAGG TCCAGGGGCA GCAGGCATTG AGGCGGATGT
                                                                              300
       GGCTGGAGTG GAGAGAAAGA GGAATTAAAA GGATGGCATG AGCTCGAG
                                                                              348
        (2) INFORMATION FOR SEQ ID NO:467:
             (i) SEQUENCE CHARACTERISTICS:
                  (A) LENGTH: 293 base pairs
                  (B) TYPE: nucleic acid
                  (C) STRANDEDNESS: double
                 (D) TOPOLOGY: linear
             (ii) MOLECULE TYPE: cDNA
             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:
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GAATTCGGCC	TTCATGGCCT	ACGAGGAAAG	ATCTAATTAT	CATGGACCTG	CGACAGTTTC	60
TTATGTGCCT	GTCCCTGTGC	ACAGCCTTTG	CCTTGAGCAA	ACCCACAGAA	AAGAAGGACC	120
GTGTACATCA	TGAGCCTCAG	CTCAGTGACA	AGGTTCACAA	TGATGCTCAG	AGTTTTGATT	180
ATGACCATGA	TGCCTTCTTG	GGTGCTGAAG	AAGCAAAGAC	CTTTGATCAG	CTGACACCAG	240
AAGAGAGCAA	GGAAAGGCTT	GGAAAGATTG	TAAGTAAAAT	AGGCTGGCTC	GAG	293

- (2) INFORMATION FOR SEQ ID NO:468:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 279 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

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GAATTCGGCC	TTCATGGCCT	AATAAATTGC	CAGCATANTA	AAAAACTGCC	TTACACTCAA	60
						• •
TIGCTACACC	TTTTCACAGG	CAAAAGGTTT	TATTCTCTCC	TAAATTAATT	TTATCCCGTT	120
						120
TTTTTTTACC	ACCTAACTTT	TGCCTTTTAT	TCAGAACTAA	TOTATOTOTO	TCTTATTGTC	180
						100
GTTTTTTTT	TCAAAATTCC	CTCCTCGGTG	CANACTANAC	CACTACCAAC	ATACTATTAT	242
				GAG I AGGAAC	MINCIALIAL	240
TCAACCAACA	TOCACCAACC	CTTACCTACC	CTCCTCCAC			
LCIBICCIBICA	IGCNGCMACC	CITACGIACG	GICCICGAG			279

- (2) INFORMATION FOR SEQ ID NO:469:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 296 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

GAATTCGGCC	TTCATGGCCT	AAGTTTTGAA	AAAAAAAATC	TTTAAGTGGA	TTGTGAGTAG	60
ATTTTTTAA	GGAGCATTTT	TATAATATTT	TTCCTGAATC	CTTGCATATT	TGACAGTGTC	120
TTTCTATTGT	GTTTATGTGT	GGCAGCAATT	TACTTTATAT	CAAAGTTTTT	TGTTTTTGTT	180
TTTGTTTTGT	GAGACACAGT	CTCACCCTAT	CACCCAGGCT	GGAGTGCACT	GGCACTATCT	240
CGGCTTACTG	CAGCCTTGAC	CTCCCAGACT	CAAGTGATCC	TCCCACCTGC	CTCGAG	296

- (2) INFORMATION FOR SEQ ID NO:470:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 376 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

GAATTCGGCC	TNCATGGCCT	ATGTTTTTTA	TATATGGATT	TATTTTTGCT	TTTTTAGGCT	60
GATTCAGTGT	GAAAATGAGG	TAGGGAAATT	GTTGTTTATC	ACAGAAATCC	CAGAATTAAT	120
ACTGGAAGAC	CCCAGTGAAG	CCAAAGAGAA	CCTCATTCTG	CAAGAAACAT	CTGTGATAGA	180
GTCGCTGGCT	GCAGATGGGA	GCCCAGGGCT	AAAATCAGTG	CTATCTACAA	GCCGAAATTT	240
AAGCAACAAC	TGTGACACAG	GAGAGAAGCC	AGTGGTTACC	TTCAAAGAAA	ACATTAAGAC	300
ACGAGAAGTG	AACAGAGACC	AAGGAAGAAG	TTTTCCTCCC	AAAGAGGTGA	GAAGGGACTA	360
TAGCAAAGGA	CTCGAG					376

- (2) INFORMATION FOR SEQ ID NO:471:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 280 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

GAATTCGGCC	TTCATGGCCT	ACAAGATTGG	CAAGATGCTT	ATTTTTCCTC	CCATATTTGG	60
				A111110010		- 00
CTGCCTTGAC	CCAGTGGCAA	CACTAGCTGC	ACTTATCACA	CACAACMCTC	CTTTTACCAC	120
	THE POLICE AND A STATE OF THE PARTY OF THE P	CACTAGGIGG	ACT I A LOACA	GAGAAGICIC	CITITACCAC	120
ACCAATTGGT	CCAAAACATC	AACCACATOT	TOOLLAND		TGGCGGATTC	
ACCAMITOUT	COMMANGAIG	AAGCAGAICI	IGCAAAATCA	GCTTTGGCCA	TGGCGGATTC	180
ACACCA COMO	20020000					
AGACCACCIG	ACGATCTACA	ATGCATATCT	AGGATGGAAG	AAAGCACGAC	AAGAAGGAGG	240
				1221001100110		
TTATCGTTCT	GAAATCACAT	ACTGCCGGAG	GCTACTCCAC			280
			CONCICONO			280

- (2) INFORMATION FOR SEQ ID NO:472:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 438 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

GAATTCGGCC	TTCATGGCCT	AGCAGTAAGC	CAGGATTGCA	CCACTGCACT	CCAGCCTGAG	60
TGACAGAGTG	AGACTCTGTT	TCAAAACAAA	ACAAAAAACT	TTACAGCAAT	CCTGGTCCCT	120
ACCATGGAGC	ATGTGTTACA	GGAAAACAGC	CAGTCCACTC	TGCAACCAAT	TTGGACATGG	180
CCCTGAAAAT	CCTTTTTTGCA	CAGAAAGGGG	AAAATAAGAG	TACTGGCAGA	AAGTCAGATG	240
CTGGGGATGC	CTCACCCTCT	AGTCTCATGA	CTATCACACA	TGAGACGGTG	TTCCGCTGTA	300
ACTTTTCCCC	CCCCCCCCC	CGTTTGTGGA	TCTGAATCTG	GAAAAGAGCT	TGGAGAGATT	360
TACAGGCCTC	CTCTTCTGCA	ATCAGTAAGA	GTACCATGTG	GAGGCAGAGA	GCCAGAATAG	420
GTTGTGGGGC	TTCTCGAG					438

- (2) INFORMATION FOR SEQ ID NO:473:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 455 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

GAATTCGGCC	TTCATGGCCT	AGAACAGCTC	TCCAATTCAC	ACTTATCTGT	ACAATGTACA	60
TTAATAACTA	ATTTGTTAGA	TGATTAATAC	CAATAATTAA	CTTGCTAGAG	GACCCAGGAA	120
ACAGAATATC	TGCAAGGCCC	AGAGTAGATC	ATAAATAAAT	AGGAATGCAG	ACATAAGATG	180
TTCAGTTTTG	GAACAGTAAA	GCTATAATGA	GTTTTCTTTA	AAATCAAACA	ATTGTACAAT	240
GCATTATAGT	CTACAACTTA	TTCTGTAGTT	CAAATAAATA	AAACTTTCCC	CTGTTACAGA	300
AAGACAGCCC	TCCTCCCAGC	AACATTTCAG	ACTGGATGGA	TTGATTCCTC	ACCTGACATA	360
ACTCTAAAAT	CCTCACTGAA	GAAGCCAGGA	AGTCAAACTG	AGGCTGAAGA	CCTGAAAGTA	420
CAGGGGACTA	AACCCAGAAA	GCAGTAGGCC	ATGAG			455

- (2) INFORMATION FOR SEQ ID NO: 474:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 292 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

GAATTCGGCC TTCATGGCCT ACATGGACCT CCTGCACAAG AACATGAAAC ACCTGTGGTT

GGCACAGGA CTGCCAGATG GGTCCTGTCC CAGGTGCAGC TACATCAGTG GGGCACAGGA CTGTTGAAGC CTTCGGAGAC CCTGTCCCTC ACCTGCGCTG TGAATGGTGA GCCCTTCAGT GGTTATTTCT GGACCTGGAT CCGCCAGNCC CCCGGGAAGG GCCTGGAGTG GATTGGGCAA ATCAATTATG ATGGAACCAC CAAGCACAAC CCCTCCCTCG AG	120 180 240 292
(2) INFORMATION FOR SEQ ID NO:475:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 304 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:	
GAATTCGGCC TTCATGGCCT AAGGGTGGGC TTTAATGGCA GCTGGGGTAA AAGGAAACAA AAACAGTAAT TCTGAAGAGC ACAGGGAACA GGCAGCCAGG ACCAGCCTGG CCCATTCCAG GCCAGCTGAG CTGAAATGCT GATTCTGTCC AGGGGGCTGC TGTATGTGTA GACTGGTGGC AGTCTTGGGG ACTGAGGCCT CTTGGAGAGA AGGGAAGACT GTCGGCTCAG AAGTCCATGG AGCTGTGGGC CAGGTAGTCC TTGCGACCGA TGTTGCTGAC CTGCTTGGTC TGCATAGCCT CGAG  (2) INFORMATION FOR SEQ ID NO:476:	60 120 180 240 300 304
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 325 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:	
GAATTCGGCC TTCATGGCCT ACCAGCTCTC TTCTAAAAGA GAAGTGGGTG GGCACACTGA ACTGTTTGGT GGCCCCAACC ACAGGAAGCT GCAATTCTCT GGCTTAGGGT GATACTTTTG CCCTCCTTGT GCCCCTCTCT GGACGCTCTG CACCAACCCC AGGCTACTGA GCCACCTTCC CTCCCCAACAC CCTCCCCTGAG CTTTGGTGCA TCTCATCTGG ACTATGGGTT GTACTGTGAC CATCCCAACAC CCTCACCCTC TGTCTACAAG GAAATGGGAG GTGGAGCCTC CTGGCTGAGA AATTGTTTTG CAAATGGATC TCGAG	60 120 180 240 300 325
(2) INFORMATION FOR SEQ ID NO:477:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 303 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:	
GAATTCGGCC TTCATGGCCT AAGCTCATCA ACGAGAAGCT CATCAGAACC AAGGGGCTGT GGGGCCCCGT CCATGAGCTG GGCCGCAACC AGCAGCGGCA GGAGTGGGAG TTCCCACCAC	60 120

ACACCACCGA GGCCACCTGC AACCTGTGGT GTGTGTATGT GCATGAGACG GTCTTGGGCA TTCCTCGAAG CCGTGCCAAT ATTGCTCTGT GGCCCCCAGT TCGGGAGAAG AGAGTCAGAA TCTACCTGAG CAAGGGTCCC AATGTGAAAA ACTGGAATGC ATGGACCGCA CTGGAAACTC GAG	180 240 300 303
(2) INFORMATION FOR SEQ ID NO:478:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 341 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:	
GAATTCGGCC TTCATGGCCT AGTTGTTCAG AATCCACACA GCTCTGAATT ACCAACGCTG AATTTCCAAG ATACTGTAAA CACCCTGACC AACAGTCCAG CCATCCCATT GGAAACATCT GCATGTCAGG ACATACCCAC TTCTGCCAAT GTACAAAATG CAGAGGGTAC CAAATGGGGA GAGGAGGCAT TGAAAATGGA TCTTGACAAT AACTTTTATT CAACTGAGGT GTCAGTTTCT TCCACTGAAA ATGCTGTCAG TTCTGACCTC CGGGCAGGGG ATGTACCTGT TTTATCTTTG AGTAATAGCA GTGAGAATGC CGCCTCTGTG ATCAGCTCGA G	60 120 180 240 300 341
(2) INFORMATION FOR SEQ ID NO:479:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 296 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:	
GAATTCGGCC TTCATGGCCT AAGTTTTGAA AAAAAAAATC TTTAAGTGGA TTGTGAGTAG ATTTTTTTAA GGAGCATTTT TATAATATTT TTCCTGAATC CTTGCATATT TGACAGTGTC TTTCTATTGT GTTTATGTGT GGCAGCAATT TACTTTATAT CAAAGTTTTT TGTTTTTGTT TTTGTTTTTGT GAGACACAGT CTCACCCTAT CACCCAGGCT GGAGTGCACT GGCACTATCT CGGCTTACTG CAGCCTTGC CTCGAG	60 120 180 240 296
(2) INFORMATION FOR SEQ ID NO:480:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 380 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:	
GAATTCGGCC TTCATGGCCT ACAGAGATGG ATTATCCTAC TTTACTTTTG GCTCTTCTTC ATGTATACAG AGCTCTATGT GAAGAGGTGC TTTGGCATAC ATCAGTTCCC TTTGCCGAGA ACATGTCTCT AGAATGTGTG TATCCATCAA TGGGCATCTT AACACAGGTG GAGTGGTTCA AGATCGGGAC CCAGCAGGAT TCCATAGCCA TTTTCAGCCC TACTCATGGC ATGGTCATAA GGAAGCCCTA TGCTGAGAGG GTTTACTTTT TGAATTCAAC GATGGCTTCC AATAACATGA	60 120 180 240 300

CTCTTTTCTT TCGGAATGCC TCTGAAGATG ATGTTGGCTA CTATTCCTGC TCTCTTTACA CTTACCCATG GGAACTCGAG	360 380
(2) INFORMATION FOR SEQ ID NO:481:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 296 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:	
GAATTCGGCC TTCATGGCCT AAGTTTTGAA AAAAAAAATC TTTAAGTGGA TTGTGAGTAG ATTTTTTTAA GGAGCATTTT TATAATATTT TTCCTGAATC CTTGCATATT TGACAGTGTC TTTCTATTGT GTTTATGTGT GGCAGCAATT TACTTTATAT CAAAGTTTTT TGTTTTGTT TTTGTTTTGT	60 120 180 240 296
(2) INFORMATION FOR SEQ ID NO:482:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 380 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:	
GAATTCGGCC TTCATGGCCT ACAGAGATGG ATTATCCTAC TTTACTTTTG GCTCTTCTC ATGTATACAG AGCTCTATGT GAAGAGGTGC TTTGGCATAC ATCAGTTCCC TTTGCCGAGA ACATGTCTCT AGAATGTGTG TATCCATCAA TGGGCATCTT AACACAGGTG GAGTGGTTCA AGATCGGGAC CCAGCAGGAT TCCATAGCCA TTTTCAGCCC TACTCATGGC ATGGTCATAA GGAAGCCCTA TGCTGAGAGG GTTTACTTTT TGAATTCAAC GATGGCTTCC AATAACATGA CTCTTTTCTT TCGGAATGCC TCTGAAGATG ATGTTGGCTA CTATTCCTGC TCTCTTTACA CTTACCCATG GGAACTCGAG	60 120 180 240 300 360 380
(2) INFORMATION FOR SEQ ID NO:483:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 252 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:	
GARTTCGGCC TTCATGGCCT AGGCTGGACA GACTTTCTAA TGAACCCAAT GGTTATGATG ATGGTTCTTC CTTTATTGAT ATTTGTGCTT CTGCCTAAAG TGGTCAACAC AAGTGATCCT GACATGAGAC GGGAAATGGA GCAGTCAATG AATATGCTGA ATTCCAACCA TGAGTTGCCT GATGTTTCTG AGTTCATGAC AAGACTCTTC TCTTCAAAAT CATCTGGCAA ATCTAGCAAC GGACAGCTCG AG	60 120 180 240 252

## (2) INFORMATION FOR SEQ ID NO:484:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 304 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

GAATTCGGCC	TTCATGGCCT	ACTACATCAA	GCACCAGAAC	CGCCAGCTGC	GCGCCCTGTT	60
GCTCAGCCAC	CAGTTCAAGC	GCCGGGAGGC	CGACCAGACC	CACGCACAGA	ACTTCTCCTC	120
CGCCGTGAAG	TCCCCGGTCC	AGGTCATCCT	GCTCCGTGCC	CTCGCCTTCC	TGGCCTGCGC	180
CTTCCTACTG	ACCACCGCGC	TGTATGGGGC	CAGCGGACAC	TTCGCCCCAG	GCACCACTGT	240
GCCCCTGGCC	CTGCCACCTG	GTGGCAATGG	CTCAGCCACA	CCTGACAATG	GCACCAGGCT	300
CGAG					•	304

- (2) INFORMATION FOR SEQ ID NO:485:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 380 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

GAATTCGGCC	TTCATGGCCT	ACAGAGATGG	ATTATCCTAC	TTTACTTTTG	GCTCTTCTTC	60
ATGTATACAG	AGCTCTATGT	GAAGAGGTGC	TTTGGCATAC	ATCAGTTCCC	TTTGCCGAGA	120
ACATGTCTCT	AGAATGTGTG	TATCCATCAA	TGGGCATCTT	AACACAGGTG	GAGTGGTTCA	180
AGATCGGGAC	CCAGCAGGAT	TCCATAGCCA	TTTTCAGCCC	TACTCATGGC	ATGGTCATAA	240
GGAAGCCCTA	TGCTGAGAGG	GTTTACTTTT	TGAATTCAAC	GATGGCTTCC	AATAACATGA	300
CTCTTTTCTT	TCGGAATGCC	TCTGAAGATG	ATGTTGGCTA	CTATTCCTGC	TCTCTTTACA	360
CTTACCCATG	GGAACTCGAG					380

- (2) INFORMATION FOR SEQ ID NO:486:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 380 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

GAATTCGGCC	TTCATGGCCT	ACAGAGATGG	ATTATCCTAC	TTTACTTTTG	GCTCTTCTTC	60
ATGTATACAG	AGCTCTATGT	GAAGAGGTGC	TTTGGCATAC	ATCAGTTCCC	TTTGCCGAGA	120
ACATGTCTCT	AGAATGTGTG	TATCCATCAA	TGGGCATCTT	AACACAGGTG	GAGTGGTTCA	180
AGATCGGGAC	CCAGCAGGAT	TCCATAGCCA	TTTTCAGCCC	TACTCATGGC	ATGGTCATAA	240
GGAAGCCCTA	TGCTGAGAGG	GTTTACTTTT	TGAATTCAAC	GATGGCTTCC	AATAACATGA	300
CTCTTTTCTT	TCGGAATGCC	TCTGAAGATG	ATGTTGGCTA	CTATTCCTGC	TCTCTTTACA	360
CTTACCCATG	GGAACTCGAG					380

- (2) INFORMATION FOR SEQ ID NO:487:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 380 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

GAATTCGGCC	TTCATGGCCT	ACAGAGATGG	ATTATCCTAC	TTTACTTTTG	GCTCTTCTTC	60
	AGCTCTATGT					120
ACATGTCTCT	AGAATGTGTG	TATCCATCAA	TGGGCATCTT	AACACAGGTG	GAGTGGTTCA	180
	CCAGCAGGAT					240
GGAAGCCCTA	TGCTGAGAGG	GTTTACTTTT	TGAATTCAAC	GATGGCTTCC	AATAACATGA	300
CTCTTTTCTT	TCGGAATGCC	TCTGAAGATG	ATGTTGGCTA	CTATTCCTGC	TCTCTTTACA	360
CTTACCCATG	GGAACTCGAG					380

- (2) INFORMATION FOR SEQ ID NO:488:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 380 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

GAATTCGGCC	TTCATGGCCT	ACAGAGATGG	ATTATCCTAC	TTTACTTTTG	GCTCTTCTTC	60
ATGTATACAG	AGCTCTATGT	GAAGAGGTGC	TTTGGCATAC	ATCAGTTCCC	TTTGCCGAGA	120
ACATGTCTCT	AGAATGTGTG	TATCCATCAA	TGGGCATCTT	AACACAGGTG	GAGTGGTTCA	180
AGATCGGGAC	CCAGCAGGAT	TCCATAGCCA	TTTTCAGCCC	TACTCATGGC	ATGGTCATAA	240
GGAAGCCCTA	TGCTGAGAGG	GTTTACTTTT	TGAATTCAAC	GATGGCTTCC	AATAACATGA	300
CTCTTTTCTT	TCGGAATGCC	TCTGAAGATG	ATGTTGGCTA	CTATTCCTGC	TCTCTTTACA	360
CTTACCCATG	GGAACTCGAG					380

- (2) INFORMATION FOR SEQ ID NO:489:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 290 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

GAATTCGGCC	TTCATGGCCT	AGGTTTACAG	GCATACCTCA	TTTTATTGCA	CTTCACTTTA	60
TTGTGCTTTG	CAGATAATTG	TGCTTTTTAC	AAATTGAAGG	TTAGTGGCAA	CCCTGTGTTG	120
AGCAAGTTCA	TTGGCAACAT	TTTTCCAACA	GCATGTACTC	ACTTGTCTCT	ATGTCACATC	180
TTGATAATTT	TCATATTTCC	AACTTTTTCA	TTATCATGAT	GATGATTAGT	GATCTTTGTT	240
ACTGTNGTAG	TTGTTTTGTG	GGCACCACAC	TGTATGCAGN	AAAGCTCGAG		290

(2) INFORMATION FOR SEQ ID NO:490:

WO 98/45435

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PCT/US98/06954
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 369 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEO ID NO:490:
GCTACCTTAA AAAATAGATA CTCCACTAGA GGCTGTGCTT AATTCAAATC CATGTGTGTG
                                                                       60
CCTGCATTAC ATGTGTGAAC ACGTGTTTCT GTCGTGTGTG TCATGCACAT CTGTGTGTTG
                                                                      120
CATAGCATAA GCCAAATGAA AATCATTTGT TCATGGGATT CATATGAGGA ACAAAATTAA
                                                                      180
ATTTGAATAC AGTCAGATAA CTGCCACGCA GGGCATTTGG GGAACCATCC CCGAATGCCC
                                                                      240
TGATGTGATT TCCCTCAGAA AATCCTTGTT ATTAGAGGAG AAGGTCTGGG CAGGGGCAGC
                                                                      300
AGCATCTCAG ACATCAAGTC AACTTTATCA TCTACTACAT CAGCACTGAA GTCCAACGGC
                                                                      360
ATCCTCGAG
                                                                      369
(2) INFORMATION FOR SEQ ID NO:491:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 307 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEO ID NO:491:
GAATTCGGCC TTCATGGCCT ATGCTTTTTT CTTTATTCTT TGTAGTTGTT TAGGAGTGGG
                                                                       60
GGGCCTCGCA GAACACCTAG TCCAGCCCAC TGCCCAGAGC AGGTGTGTCC CTTTCATACT
                                                                      120
TCAGTCCACT TTAAAACAGC CTTCCCCCAC CCCCTTCTAT GGTAGCAGTT CTCCTCGGGG
                                                                      180
TCTCCATGGA CACCCTGTGC CCCAAGCCGA TGGCCCCACC CAGCAGCATC AGCACAGCTG
                                                                       240
CCCCCCTTCT CCGCAGAGCA GGCTCTCCTT TACGGGACTC TCCTCTTCCC TCCCACCCCC
                                                                       300
                                                                       307
CCTCGAG
(2) INFORMATION FOR SEQ ID NO:492:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 275 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: cDNA
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

GGAATAAGAA GAGAAAGCCA	AGGAAGACAA	GGGCAAACAA	AAGTTGAGGC	NGCTTCACAC	60
ACACAGATAC GGAGAANCCA	GAAGTGCCAG	AGTCAGCATT	CTGGAAGAAA	ATCATAGCAT	120
ATCAACAGAA ACTTCTAAAC	TATTTTGCTC	GCAACTTTTA	CAACATGAGA	ATGTTAGCCT	180
TATTTGTCGC ATTTGCTATC	AATTTCATCT	TGCTCTTTTA	TAAGGTCTCC	ACTTCTTCTG	240
TGGTTGAAGG AAAGGAGCTC	CCCACGAGGC	TCGAG			275

- (2) INFORMATION FOR SEQ ID NO:493:
  - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 301 base pairs

(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

GCCTTGGGCC	CTCGCAAAGT	CTTGGAGAAG	CAGTTTTACT	TCCCTTCCTT	CACTTAGACC	60
CCALICITIA	GCATTICTIC	IGNAGCICCC	ACAAGACCCA	AGAATGGCTG	CTGCAGTGTC	120
TCCTCTTCAG	TCAGGGACCC	TGGTTGAGGT	TTGTGTATTG	TTCATTATTG	CTCTGTTTTG	180
CAGTTGTTCA	AAGTTGGAAG	ACTTGCCTGC	GGAGCAGTGG	AACCATGCCA	CAGTCCGCAA	240
				TTAGCCAAAG		
	GNACIGCICA	MADIADA	CCAGAGCACA	TTAGCCAAAG	AAACCCTCGA	300
G					•	301

- (2) INFORMATION FOR SEQ ID NO:494:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 389 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

GGAAGATGTC T	ACAGAAAAG	GTAGACCAAA	AGGAGGAAGC	TGGGGAAAAA	AGAGTGTGCG	60
GAGACCAGAT C	AAGGGACCG	GACAAAGAGG	AGGAACCACC	AGCTGCTGCA	TCCCATGGCC	120
AGGGGTGGCG TO	CCAGGTGGC	AGAGCAGCTA	GGAACGCAAG	GCCTGAACCT	GGGGCCAGAC	180
ACCCTGCTCT C	CCGGCCATG	GTCAACGACC	CTCCAGTACC	TGCCTTACTG	TGGGCCCAGG	240
AGGTGGGCCA AG	GTCTTGGCA	GGCCGTGCCC	GCAGGCTGCT	GCTGCAGTTT	GGGGTGCTCT	300
TCTGCACCAT C	CTCCTTTTG	CTCTGGGTGT	CTGTCTTCCT	CTATGGCTCC	TTCTACTATT	360
CCTATATGCC G	ACAGTCAGC	GCACTCGAG				389

- (2) INFORMATION FOR SEQ ID NO:495:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 438 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

GTGGCGATTG	GTCCTGTCAT	GGTTTATTCA	GCCATGTGGT	GGATGGCTAC	TTGTCTTCTA	60
AGCCACTTGC	CTTCTGATCG	CTGGACTGAC	TCTCTCGCCC	TCTCTTGGTG	CAGTCCTCAG	120
GAGGCTCGGT	CACACTCTCC	AAGAGCACAG	CCATCATCTC	CCACGGTACC	ACAGGCCTGG	180
TCACATGGGA	TGCCGCCCTC	TACCTTGCAG	AATGGGCCAT	CGAGAACCCG	GCAGCCTTCA	240
TTAACAGGTG	ACCTCGGGGC	ACAGGGCAGG	GCACCGAGGC	AGGCTTACCC	TGGTGCAGTC	300
GAAAACACGG	TCCCCTTTCC	TCCCGCCAGG	ACTGTCCTAG	AGCTTGGCAG	TGGTGCCGGC	360
CTCACAGGCC	TTGCCATCTG	CAAGANGTGC	CGCCCCCGGG	CATACATCTT	CAGCGACCCT	420
CACAGCCNGG	TCCTCGAG					438

- (2) INFORMATION FOR SEQ ID NO:496:
  - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

GAATTCGGCC TTCATGG	CCT AGGTAAAATT	TGTATAACAA	AAAATTAACC	GTTTTAAACT	60
GAATAATTCA GTGAGAT	TTA GTGAATTCAC	AATATTGTGC	AACTGCCACC	TCTTTCTACT	120
TCTAAACCAT TTTCCTC	ATA CCAAAAGTAA	GCCCCGTACC	TATGATGCAG	TCCCTTCCCG	180
TTTCCTTCTC TCCTCAG	TCC CTGGCAACCA	TCACTCTGCT	TTCTGTCTCT	GTGGATTTAC	240
TTATTCTAAT ATTTAAT					281

- (2) INFORMATION FOR SEQ ID NO:497:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 570 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

GAATTCGGCC T	TTCATGGCCT	ACACTTAGAG	AGGCAGTCGG	GATGGAGGGT	CGAGTTGAAG	60
ACAGGGAGGG (	GTGAGGAACG	AGCAGAGGCC	AGTTGTTTGG	CCACTTGAGG	GAGTTTGGAC	120
TTGTCCCGAG (	GGCACTAGGG	AGCCGTGAAG	GGCTTCAAGC	CGGGGAGGAT	CATGAACATT	180
TCCCCAGAGG A	AGCTCAAAAT	GGAGTTGCCG	GAGAGACAGC	CCAGGTTCGT	GGTTTACAGC	240
TACAAGTACG	TGCATGACGA	TGGCCGAGTG	TCCTACCCTT	TGTGTTTCAT	CTTCTCCAGC	300
CCTGTGGGCT (	GCAAGCCGGA	ACAACAGATG	ATGTATGCAG	GGAGTAAAAA	CAGGCTGGTG	360
CAGACAGCAG	AGCTCACAAA	GGTGTTCGAA	ATCCGCACCA	CTGATGACCT	CACTGAGGCC	420
TGGCTCCAAG	AAAAGTTGTC	TTTCTTTCGT	TGATCTCTGG	GCTGGGGACT	GAATTCCTGA	480
TGTCTGAGTC	CTCAAGGTGA	CTGGGGACTT	GGAACCCCTA	GGACCTGAAC	AACCAAGACT	540
TTAAATAAAT	TTTAAAATGC	AAAACTCGAG				570

- (2) INFORMATION FOR SEQ ID NO:498:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 487 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

GAATTCGGCC	TTCATGGCCT	AGGTGCATGC	CATCAAATAC	TCTAACGAGA	CATTTTTAAT	60
GAAAGACTTA	AACCAGATAG	GCCACAATGA	ACCAAATTAG	AAATCTGAAC	ATGTCACCAC	120
TTGCAGCATA	AAGGAATATA	AAAGGGCAGA	GCAAAGTCTT	TTTTCCTAAG	GTGAATATTT	180
CTAAGGTAAG	TATTCATTTG	TAAAAGTTTT	TTTTTTCCAN	CANGTCTGAA	NNCTTTTTAC	240
CANNINGGINGA	GNATTACAAC	AAAACATCCC	TNGGTTAAAA	AAAAAAATA	CCATCTTGCA	300
ATTCAGCACA	CACCNGCAGC	TGGTGTGCTC	ATCCAAACCN	ATCAGTAGGC	TAAGAGNATT	360
TNAAATTCCA	TACATATGAG	TTTAGGTATT	AATGCCGATT	ACACAGTACA	CAGTACAGAG	420
GGAGGTCCCT	ATATCCACAC	ACACACACAC	CCCATCCAGC	ATTTACACCN	AAAGCCTTAC	480
CCTCGAG						487

(2) INFORMATION FOR SEQ ID NO:499:

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 271 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:	
GAATTCGGCC TTCATGGCCT AACAATTCAA AGAAACTTTT TTCTGAACCA TTTGAAATTT GCCAGCCTGA TGTCCCATCA CCCCCCAAGT ATTTTAGCAT CTATGCAACA AAACATTTTC TCTGACAAAA CCACATCAGA ACTCTCAAAT CAGGAAACAA ACATTGATAC ATGTCTATCA ACTAATCCTG TCTTCAATGA CATTTTACCG ATTGTTCCAA TGATGTCAGC ATCACGGGTC ACATTTAATA GTTGCGTCCT TCAGTCTCGA G	60 120 180 240 271
(2) INFORMATION FOR SEQ ID NO:500:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 316 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:	
GCACTTCTGG ATGTTGGTTC TCTTTGTCAT TTTCAACAGT CTGCAGGGAC TTTATGTTTT CATGGTTTAT TTCATTTTAC ACAACCAAAT GTGTTGCCCT ATGAAGGCCA GTTACACTGT GGAAATGAAT GGGCATCCTG GACCCAGCAC AGCCTTTTTC ACGCCCGGGA GTGGAATGCC TCCTGCTGGA GGGGAAATCA GCAAGTCCAC CCAGAATCTC ATCGGTGCTA TGGAGGAGGT GCCACCTGAC TGGGAGAGAG CATCCTTCCA ACAGGGCAGT CAGGCCAGCC CTGATTTAAA GCCACGTCCA CTCGAG	60 120 180 240 300 316
(2) INFORMATION FOR SEQ ID NO:501:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 269 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:	
GACAAAGACC AGCAATGGAT CACTTGGAGT CCTTTATTGC TGAATGTGAT CGGAGAACTG AGCTCGCCAA GAAGCGGCTG GCAGAAACAC AGGAGGAAAT CAGTGCGGAA GTTTCTGCAA AGGCAGGAAA AGTACATGAG TTAAATGAAG AAATAGGNAA ACTCCTTGCT AAAGCCGAAC AGCTAGGGGC TGAAGGTAAT GTGGATGAAT CCCAGNAGAT TCTTATGGAA GTGGNAAAAG TTCGTGCGGA GGAAAAAGGA GNACTCGAG	60 120 180 249 269
(2) INFORMATION FOR SEQ ID NO:502:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 403 base pairs	

(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:	
GAATTCGGCC TTCATGGCCT ACTTGTCTCA CTCTGCATCA TCCCTTAGTC TACAACAGGC CTTTTCTGAA CTTAGACGTG CCCAAATGAC AGAAGGACCC AACACAGCAC CTCCAAACTT TAGTCATACA GGACCAACAT TTCCAGTAGT ACCTCCTTTC TTAAGTAGCA TTGCTGGAGT CCCAACCACA GCAGCAGCA CAGCACCAGT CCCTGCAACA AGCAGCCCTC CTAATGACAT TTCCACATCA GTAATTCAGT CTGAGGTTAC AGTGCCCACT GAAGAGGGGA TTGCTGGAGT TGCCACCAGC ACAGGTGTGG TAACTTCAGG TGGTCTCCCC ATACCACCTG TGTCTGAATC ACCAGTACTT TCCAGCGTAG TTTCAAGTAT CACAATACTC GAG	60 120 180 240 300 360 403
(2) INFORMATION FOR SEQ ID NO:503:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 282 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:	
GTTTGGATGA TTGGTGGCGT GTACGCAGCT GCTATGGCCT GGGCCATCAT CCCCCACTAT GGGTGGAGTT TTCAGATGGG TTCTGCCTAC CAGTTCCACA GCTGGAGGGT CTTCGTCCTC GTCTGGCCCT TTCCTTCTGT GTTTGCCATT GGGGCTCTGA CCACGCAGCC TGAGAGCCCC CGTTTCTTCC TAGAGAATGG AAAGCATGAT GAGGCCTGGA TGGTGCTGAA GCAGGTCCAT GATACCAACA TGCGAGCCAA AGGACATCCT GAGCGACTCG AG	60 120 180 240 282
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 222 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:	
GAATTCGGCC TTCATGGCCT ACTGAGAAAA AAAATCAAAT CTAATTTTAA AATGAAGGTA TTTAAAACCA TGGCACAAGG GAGCCTTATT TATGGAGCTG GTGGGAAGCC AGGATGTTTC CAATCCGCTG CTCTTACAGG AGCCTGTGCC TCGCCAGTTC TGTGCTGCAG TGGGCAGCCA ACTGAAGTGC ATGAGTCAAA TGCACGAAGC AGCAGACTCG AG	60 120 180 222
(2) INFORMATION FOR SEQ ID NO:505:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 192 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

GAATTCGGCC TTCATGCCCT	AGTGGTGCAG	TTTTTCAGGA	TTGTAGAGAT	GCTAACAAAT	60
TACAGGTTCT CTCATGCAAA	CACTTTGCTA	GGAATTATAT	ATATCAAGTT	TATATTTGGC	120
AATCAGGCTT TAGAAGCAGA	AGGTCTAGCT	ATCTCAAACT	ACCACCTACC	TCCCTCACCA	180
AAGCCGCTCG AG					192

- (2) INFORMATION FOR SEQ ID NO:506:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 364 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

GAATTCGGCC	TTCNTGGCNT	AGTAAAATTG	TTAAAGTTGA	CAGGATCAGT	TTTGGAAGAT	60
GCTTGGAAGG	AAAAAGGAAA	GATGGATATG	GAAGAAATTA	TTCAGAGAAT	TGAANACGTT	120
GTCCTAGATG	CAAACTGCAG	TAGAGATGTA	AGACAGATGC	TCTTGAAGCT	TGTAGAACTC	180
CGGTCAAGTA	ACTGGGNCAG	AGTCCANGCA	ACTTCAACAT	ATAGAGGNGC	NACACCAGAA	240
AATGATCCTA	ACTACTTTAT	GNATGNACCC	ACATTTCATA	CATCTGATGG	TGTTCCTTTC	300
ACTGCAGCTG	ATCCAGATTA	CCANGAGAAA	NTCCAAGAAN	NACTTGAAAG	AGANGATCCT	360
CGAG						364

- (2) INFORMATION FOR SEQ ID NO:507:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 327 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

GAATTCGGCC	TTCGATTGAA	TTCTAGGACT	TGACAGAATT	CGAGTTATCC	TTCTCAGAAC	60
ATGTGCAGAG	TCTCTTTTTG	CCTCACCATG	TGGTCCTGTG	CTCTTTCAGG	TGGGAGTTTT	120
GGGGCCTCCA	GGGCAGCAGG	CACCACCTCC	ATATCCCGGC	CCACATCCAG	CTGGACCCCC	180
TGTCATACAG	CAGCCAACAA	CACCCATGTT	TGTAGCTCCC	CCCCAAAGAC	CCAGCGGCTT	240
CTTCACTCAG	AGGCCTACCT	GAAATACATT	GAAGGACTCA	GTGCGGAGTC	CAACAGCATT	300
AGCAAGTGGG	<b>ATCAGAGCAA</b>	TCTCGAG				327

- (2) INFORMATION FOR SEQ ID NO:508:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 373 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

GAATTCAGTG AGTGGGCATG GCTGATCTTG TGCAAATTAA AAGTTATGGG GCATAAGAAT 60

AGCAAAAGTT GAACTTCTTT TAAAAAGGAA AGTACCCTGA GAGCCAGTAT TGGTTGAGGC	120
TCTTCAGTAT GCCCAGGTTG GCAGCACTGA GAACCGCAGG AACGGCCTGT TGTTACAAAA	180
AGGAGATTGA CTCAGCTGCC CTTGGTGCAT CTGACTGACT ATGACTGCTG AGAGATTCCA	240
AGGACCCTTA ATGCCAGGGC TAACCTCTCC ATGTGCAGTG AGACCTCTGG AGGAAGTGTC	300
ATCCTCTGGC TTTGTGTGGT ACTCATTATG GTGCAGTGCG GGCATGAAAT GAAGACACAC	360
AAATAGGCTC GAG	373
(2) INFORMATION FOR SEQ ID NO:509:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 313 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(x1) SEQUENCE DESCRIPTION: SEQ ID NO:509:	
GAATTCGGCC TTCATGGCCT ACTCTTCCTG GCTCCTTCTC AGCCTTGTTG CTGTAACTGC	60
TGCTCAGTCC ACCATTGAGG AACAGGCCAA GACATTTTTG GACAAGTTTA ACCACGAAGC	120
CGAAGACCTG TTCTATCAAA GTTCACTTGC TTCTTGGAAT TATAACACCA ATATTACTGA	180
AGAGAATGTC CAAAACATGA ATAATGCTGG GGACAAATGG TCTGCCTTTT TAAAGGAACA	240
GTCCACACTT GCCCAAATGT ATCCACTACA AGAAATTCAG AATCTCACAG TCAAGCTTCA	300
GTGCAGGCTC GAG	313
(2) INFORMATION FOR SEQ ID NO:510:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 203 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(44) MOLECULE WAREDNA	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:	
GAATTCGGCC TTCATGGCCT ACTTGAACAA TTTAAATATA GGAGAAGACT ATTTTTTAGA	60
AATGTTTTCC GTCGCCAACT TGTTAAAGCT TTATAGCACT TTGCATATTT TGGAGAATGT	120
CAACTATATT TTTATCAGAG CTGATTTGTT CCAGTGGAAC AACAGTGGCG TAGACATCGC	180
CCACAAGGTT CTGCATACTC GAG	203
·	203
(2) INFORMATION FOR SEQ ID NO:511:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 334 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:	
GAATTCGGCC TTCATGGCCT ACGTGGTATT AAGGAGACAA TCTGAGGCAT TCCCACCAGT	60
CAATTTGACA TGCGGTTGGC AAGGTTCCTC TTCCCTTCCC	120

CCAGGTCAGA CCCGAAAGAT TCATAGGCAC ACTTACAGCC TTCATAGTCT CAGCCATAGT CATCCTAGCA ACTGCTAGTG TGGCTGTAGC ATCTATTACT GAATCAGTAC AAACAGCTGC TTTTGTAGAT AATTTGGCCA GAAATGTTTC TAATGAACTT CTCTTACAGC AAGGTATAGA TCAAAAGATT CTTGCACATC TGCAAGCCCT CGAG	180 240 300 334
(2) INFORMATION FOR SEQ ID NO:512:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 537 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	•
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:	
GAATTCGGNC TTCATGGCCN AAAGCTCTNG AAGGAGTATT AGAGTACAGA GTCTGAGNCT NTGANAAATG GTGGTCAGAA GCCNTCTTCA TCAGATANAT TTCTCAGATG TGCCCCTTCC GCGGCAGAGG NGGATATTCA TCTCCTAGTT CATGTTCAGA AACATGTCAG TANGCAGATN ANTCACTACC AGTATCTGCT TCTACTTTTC CTGCATGAGT CACTTATCCC TGCTTTCAGA GAACNTAAGG AAAGATGTAG AAGCTGTAAC TGGCAGTCCT GCTAGTCAGA CATCCATTTG TATTGGAATT TTACTTAGAA GTGCAGAACT GGCTCTTTTG CTCCATCCAG TGGATCAAGC AAATACTCTT AAGTCTCCTG TTTCTGAAAG TGTGAGCCCA GTGGTACCTG ANTATTTGCC TACAGAAAAT GGGGATTTTT TGNCCTCAAA AAGAAAACAA ATTAGTAGGG ATATAAATAG AATTAGAAGT GTAACTGTTA ATCATATGTC AGACAACAGA TCTATGAGTA TCTCGAG	60 120 180 240 300 360 420 480 537
(2) INFORMATION FOR SEQ ID NO:513:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 243 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:	
GAATTCGGCC TTCATGGCCA AGGTGCTTAA TATTAAAAAA AAAAAAAGTA TATCCAACCA CAGATATACA GTTCTGCCTT TTTTTCCTTT TTACCTAAAT ATACTCCATA AACAGTTTCC ATGTTGTGTA ATACTCTCAT GTTTCTACTT TTCAGTGATT GCTTAAATGT CCATTGGGCT GATAGGTCAC AGTTCGCTAA CCCATCTCAT TGTTGTTCAT TGGGATCTCC ACTTTCCCTC GAG	60 120 180 240 243
(2) INFORMATION FOR SEQ ID NO:514:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 344 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:	
GAATTCGGCC TTCATGGCCT AGTCTCAAAA AAAAAAAAAA	60 120

TCTAAAAGAC GCTCTGAAAG CAGACCAGGC TGTTTTCTTG GAGCTTTTCA GGTTAGATTC TCATGTGTGT ATCTTCCATC TACCACGATT ATTTGGCTAC CAGATGCCTT AGCAAGCTGA 3	80° 840 800 844
(2) INFORMATION FOR SEQ ID NO:515:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 302 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:	
ACTGATTTAT GCAGCTTTGG TITCATTTGG GCTAAACTCT GAAGAACTGG ATGTAAAGCT TATAATTGCC CCAGGAGTAG AAGCAACTGC CTTGATAATT CGACAAATTG CTGACCACAG TTTAATGACC TCAAAGAGAG ATCCTCATGA ATGGTTGGAT AAATCCTGGC TTAAAGTTTC ACCATCTGAG GAAGAAATGT ACTTACTTGA TTTTCCATGT ATTAACCCAA TCGTGGCTCG 3	60 20 80 40 90 902
(2) INFORMATION FOR SEQ ID NO:516:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 324 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:	
AGGCTTTCGA GATGTCTCTG CTGAAAATAA ATGGAGCTCT AGTAAATGTT AGAGTTTTTG CTAGTAGAGT TTTGATGCTT TTTGTCTTTG TTCTACTACT GAGCTTGCAC CTAGGATGCC TTCTTATAGT GCCATTCAAC ATGCAAGTTT CTTTTTCTGG GGCTGTGTT CCAGGTGACT TTATGAGTTA GGCTTTGGCA AATGCCAGAC TTGTTCATCC TAACACTAGA ATGTAGGGAT	60 120 180 240 300 324
(2) INFORMATION FOR SEQ ID NO:517:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 435 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:	
TCTGCAGTCA AACTAAGTTT TGCAGTGTCT TTTTAAGAGC CAGGCAATTC TACCACAAAA	60 120 180 240

ATCATTCAGA AATGTGTAGC TGCTTCCAGA GTGTGTCTAA TACTGTTGGA ACAGGCGTTT CAGAAAGAAA TGAGAGGCCC AGTCTCAGTA ACTCCATGAA GGGTGCCGAG CTCCTCTGTT

GAGGATTIGG CITGIGAGAG GCAATGITCC TATCATTIGC CAATITGGCC TITGITATIC CCACATTGGC TCGAG	420 435
(2) INFORMATION FOR SEQ ID NO:518:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 373 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:	
GAATTCGGCC TTCATGGCCT ACCAGGTTGG CCAGGCTGGT CTCGAACTCC TGACCTCAGG TGATCTGCTC ACCTCGGCCT CTCAAAGTGT TGGGATTACA GGAGTGAGCC ACCGCACCGG GCCAAAAAAT CCAATTCTT AGAGATTAAA TAACCCTTCA GGATTATCAA AGGAAATAAT TAGGGAAAGG TAGATGTTCT GTCCCAGTAA GAGAAGAAAG TGGTCCAGAA ATTTTATCTC CCATCAAATGA ATCCATTTTA CTTAAGTATT AAACCAAGTG ACATTCTTCA GTTTAACTCT GATAAATGAA TCATATTCCT CTTCGAAAAT AACTTTTGTA TTTCGTGCTC TAAAAAGAGA ACCACCCCTC GAG	60 120 180 240 300 360 373
(2) INFORMATION FOR SEQ ID NO:519:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 397 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:	
GAATTCGGCC TTCATGGCCT AAACAATTAA TTGTGGGTGT CTGAGGGGGA AGGTCGCAGC TTTGGGCAGC TTTGAGAAGC GGTACAAGAG TTCTGTGCCT GTGTGTCCAG CCCTGGAGCC AGCCAGTGCA TTTATTTTAA GCTCTTAGAA GCAACTCCTT GGCCCAGGAA TGCGTGACCC CTGAGATGGG TCCACGCATC TCTCTACACT TCCTTCTCTC CGTGGGATAC TGGACTCGTG CCTCTGCGCC CATTCTCTC TCACGCATAT CCATGAGCTT TAATTTCACT TTCTGATCAC GGTACGTCCA TAAAGCCAGT ATTACACTTA AATGAAGTAT TCTTTTTTGT AATCGTTTTT TTTAGAAGGT AAACAAATTT AATAAAGCTA TCTCGAG	60 120 180 240 300 360 397
(2) INFORMATION FOR SEQ ID NO:520:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 472 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:	
GAATTCGGCC TTCATGGCCC ACATGAATCT NGTAATTTGT GTCCTACTTT TGTCCATTTG GAAAAATAAT TGCATGACTA CAAACCAAAC CAATGGATCT TCTACTACAG GAGATAAACC	60 120
267	

TGTGGAATCA ATGCAGACAA AATTGAACTA CCTTAGAAGA AATCTACTCA TTTTAGTTGG TATTATCATC ATGGTTTTTG TCTTTATCTG TTTTTGTTAT CTCCATTATA ATGTCTGAG CGATGATGCG TCCAAAGCAG GAATGGTCAA GAAAAAAGGC ATAGCAGCCA AGCCATGCT AACATCATCC AGTGAAGCCA AGACAGCCTC TCAATGCAGT CCAGAAACAC AACCCATGCT ATCTACTGCA GACAAGTCAT CTGATTCATC GAGTCCAGAA AGGGCATCCG CACAATCCAG CACAGAAAAA TTAATCAGAC CCTCAAGTCT ACAAAAGGCCA TCCAACCTCG AG	180 240 300 360 420 472
(2) INFORMATION FOR SEQ ID NO:521:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 328 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:	
GAATTCGGCC TTCATGGCCT ACACCTCTTC TTAGGGCTGT TTTTTTAAAC ACAATGATAT	60
TCTAAGGAAC AAGAGGTTGG CTATGGACTT TTGTATACCC ATGCCTATCA TATTTCGCTA	120
AATGTTTGAT TATATAGAGA CATTTCTTTG GAACTTTGAG CTGTGTGAAG ACAACACAAA	180
CCTGGCCATT CATGGCTGAC AGAAGGTTGG CCCTAACCCT GCTCAGGCCC ACACAGATTG	240
TGTAATATTC TTTGGATCTG GCTCTAGTCA GCAAAGTCTT GGTGTTGTAG GATACAGGTG	300
TCTTCATGCA TTCCATTTTA TACTCGAG	328
(2) INFORMATION FOR SEQ ID NO:522:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 313 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:	
GAATTCGGCC TTCATGGCCT AGAAAAAGAA AAAGTAGCTG ATGAAGATGA TGTGGACAAT	60
GAGGAGGCTG CACTGCTGCA TGAAGAGGCT ACCATGACTA TTGAAGAGCT GCTGACACGC	120
TACGGGCAGA ACTGTCACAA GGGCCCTCCC CACAGCAAAT CTGGAGGTGG GACAGGCGAG	180
GAACCAGGGT CCCAGGGCCT CAATGGGGAG GCAGGACCTG AGGACTCAAC TAGGGAAACT	240
CCTTCACAAG AAAATGGCCC CACAGCCAAG GCCTACACAG GCTTTTCCTC CAACTCGGAA	300
	313
(2) INFORMATION FOR SEQ ID NO:523:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 400 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:	
GAATTCGGCT TCATGGCCTA GCGTTGTGTG CATGCGAGCG CTCCTGCAGG CGTGTGCATG GGGCCAGGTG TGCACGTGGA TGCCCGGGTG AGTGTGTGTG CATGCACGTG TGTGCACGCA	60 120

TGTGCACATG	CCTCCAGCCC	CACCTTCCAA	CCCCTCAGTG	CCCCCAGGAC	AGGGGCCCCT	180
CTTAGCTATC	AGGGTATGGC	CGGACCGGCC	CTTCCTGCCC	AGCANGTTGC	AAGCACTTGG	240
CCAGGCCGGC	CCTCCAGGNT	GCTGCTGCGT	GGGGGCCCGG	GTGCCCCCAG	GTCCATGCAG	300
ACTGGGGATT	CGGTGGGGAG	GGGCGCTTCT	AAGGAACCAA	ACTGACGCTC	ACTCTGGGCT	360
TCCCAAGCAC	CCTTAGCACG	GAGCCCACCC	CTAGCTCGAG			400

- (2) INFORMATION FOR SEQ ID NO:524:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 388 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

GAATTCGGCC	TTCATGGCCT	ACCCACCGTG	TAGTCAACCC	CACTCGTACT	GTAGCGAGAC	50
AAAAACATGC	CATTGTGAAG	AAGGGTACAC	TGAAGTCATG	TCTTCTAACA	GCACCCTTGA	120
GCAATGCACA	CTTATCCCCG	TGGTGGTATT	ACCCACCATG	GAGGACAAAA	GAGGAGATGT	180
GAAAACCAGT	CGGGCTGTAC	ATCCAACCCA	ACCCTCCAGT	AACCCAGCAG	GACGGGGAAG	240
GACCTGGTTT	CTACAGCCAT	TTGGGCCAGA	TGGGAGACTA	AAGACCTGGG	TTTACGGTGT	300
AGCAGCTGGG	GCATTTGTGT	TACTCATCTT	TATTGTCTCC	ATGATTTATC	TAGCTTGCAA	360
AAAGCCAAAG	AAACCCCCCT	GCCTCGAG				388

- (2) INFORMATION FOR SEQ ID NO:525:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 459 base pairs

    - (B) TYPE: nucleic acid (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

GAATTCGGCC	AAAGAGGCCT	AATTGAATTC	TAGACCTGCG	TCGACCGAAC	CGAGTTGTAC	60
ATTTTTTTTG	TGATGGGTTA	TTTTTTTATTT	TAATTATTAT	TGTTGTTTTG	GTTTTTTTT	120
GGTTGGTTTT	NGATTTATGA	CAATNCCACT	CTTGGCCCCA	GTTGTCGTCC	TGTCACTCCC	180
TCCCCTGTCC	ATCACCCTGG	CTCCCAGACC	AGGCTCAGCA	ACACATTGAG	TCTTGGGTTC	240
CAGGAACCTT	GCCAACCTCA	ACCCTCCAGC	CCGTGCTCCA	CTGGCTATGG	CTCAGACCAA	300
GGGCTCCTCC	TCTCCCNTCT	TGCCCTATGG	AACAGCCCGG	GTGCTCCAAG	GGGGCCAGGA	360
GGGCATGGCT	TGGCTCCCAA	GATAAGGGGT	CCGGGGCCAG	GACACCCAGG	CAAGGTGGCC	420
CCTCCCTGCC	TAGCCCCCTT	CCCCCCACCC	AAAGTCGAG			459

- (2) INFORMATION FOR SEQ ID NO:526:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 307 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

GAATTCGGCC TTCATGGCCT ACAACCTGGA AAATTCTCTG ACTTAGAAAT TTAAACAAAA CCCTCCCCTT TCATTGAATC TCCATTGTCT GGAGTTTGCT TGTTTTAATC TAGCCTGTTC CTCCACTATG GGCTCCCTTT CAAACTATGC CCTGCTTCAA CTAACCCTTA CTGCTTTTTT GACAATTCTA GTACAACCTC AGCACCTGCT TGCTCCAGTT TTCCGGACAC TATCTATCTT GACTAATCAG TCTAATTGCT GGTTATGTGA ACATCTAGAT AATGCAGAAC AACCCGAACA CCTCGAG	60 120 180 240 300 307
(2) INFORMATION FOR SEQ ID NO:527:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 317 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:	
GAATTCGGCC TTCATGGCCT ACCAATACTA AGCTTATTT ATTGTAATAC AGTTATTTGT ACCACCTTAG AGCAATCTTT TGAAGAACAA GAAACACATA TTGAGCCACC ACGCCCAGCC TTTTTTCAGT TTATTTTTAA TCTTTTGCTG TTCATTGGCT CATTCTGTT ATAAGCATGT TAAATTTACC CAAATAGAA AATAGCCTCC CCTTGGCCCT GAACTCCTCT ACAAGCAACT ACCTCATGAT TTTATCTCTT TATCCTCAAA TTCTTTGGAA TATAATTTAT ACTTGTTTCA TCCCTACCAC CCTCGAG	60 120 180 240 300 317
(2) INFORMATION FOR SEQ ID NO:528:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 405 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:	
GAATTCGGCC TTCATGGCCT ACAGCAGTGT GCTTTCATCC AGTTTGCCAC ACGGCAGGCT GCAGAAGTGG CTGTGAGAAG TCCTTTAATA AGTNGATTGT AAATGGCCGC AGACTGTATG TGAAATGGGG AAGATCCCAG GCAGCCAGAG GAAAAGAAAA	60 120 180 240 300 360 405
(2) INFORMATION FOR SEQ ID NO:529:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 283 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:	

GGCAATACTT ATAGTGTATT AAGAAACTTG CTAGACCCCA TCCAAATTAC TCAGTCTACT

GTTGGTTGAT AGAATTACTT TAGGAAGAGT ACGTTTTTGC CTTGGAAATA CACTGGAAGT

GGTACCAAAC AAATCTAATA AAATGATGTT AAAGAGATTT GCAGTAATTT TTATCAACTT

TCAGTTTGCA AACTTTTATA AAGATATGAA CGGGACACTC GAG

(2) INFORMATION FOR SEQ ID NO:530:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 320 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

120

180

240

(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:	
GAATTCGGCC TTCATGGCCT TTCTATAAAT GAGTTCTTTA TAAGAAGCTT GTATCATTCT CACAAATTAA AAATAATAAT ATTTTAGCAA GCTATTTTTT AAATAAAT TAAGCCCACA CTTCCACATT TGGGGTAAGT GATAATTTTT TCCTCTGAAA GACAACAAAT ACTAACACAG GCCCAGACTT GGCTTTTGTG AGTCAATTAG TGATCCGAAG GTGAGTGGTA TTTAAACGTA TGATGAGGGT AAGATTTGAT TTATTTTACA TATATATCTT CTGGTATCTG TGTGTGTGTG TGTGTGGTGT GAAGCTCGAG	50 120 180 240 300 320
(2) INFORMATION FOR SEQ ID NO:531:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 435 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:	
GAATTCGGCT TCATGGCTTG GGGGTGACAG TTAATATATN CGGTCATTTT AGATTGCTTC CACTAATATT GGTTTATCCA TATTATAAAA TATTTTAGTG AGTATAAAAAT TGTCTGCATT CATAAAGATG CATAAAAATTA ACTACAGAAC CAGCTTGAGT AATGCTTTTC TCTTCTTTTC TCTTTGTCAAA TCAGAAATTA TCTTTATACA TTGTTTTAGA GTATACATCT ATCAAAATGC AACATTCTT AAAGTATTGT AATTTATACA GCAAACGTGT AATGGATAAA AATGTGCAAA AACAATCCTT AAAGTATTGT ATTTGAACNA AAACAATCTT AAACCACATA ATCTGAAAAA AAGGGGTACA TATTTTACCA AATATACTAA TCCATACAAG ACTGCTTGAG AAAAAGAATA TGCCACCTAC TCGAG	60 120 180 240 300 360 420 435
(2) INFORMATION FOR SEQ ID NO:532:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 339 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:	
GAATTCGGCC TTCATGGCCT AAGCCATCAG ATTGAAATTA ATTTAGACAG GAAGAATCTA TATAAATTTG ATGCATAGCA AACTCTGACA TAATTTGGTT TATTTTGAAG TCTGGCATAT	60 120
271	

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TTTTCATCAC	TTTTTATTTT	ACGGGTAAAT	CATAATATAT	CATATTTTCA	ATAAAAGTAT	180
TTTCTTAAAA	ATCTGCCATT	TGCTTCACAG	ATTTTAAATC	TTCTAACAGA	AAAAGAAGTA	240
AATATTGTTT	TGCCAACACA	GTCCATTGTT	CCAAGAACTT	TTGTGCTTAA	ACCAGGAATG	300
GTTCTGTTTT						339

- (2) INFORMATION FOR SEQ ID NO:533:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 480 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

GAATTCGGCC	TTCATGGCCT	AATGTGCTCC	AGGAGGCGCT	GGGGGATGGT	GACCTCCCAA	60
GGCGGGCAGA	NGACTTCTGC	CGTCAGGGTC	GCCTGCTGCT	GAGCCTGGGG	GATGAGGCGG	120
CGGCCGCAGG	GTCTGGATCC	CCTGTGCCGT	CGCCTCTTCC	TTTTTCGACG	CCTCCGCCGC	180
CGCCTGAGGA	GGCGAGCTAG	CCGGGAGTTA	CACCGCCACC	GCCAGGATGG	ATAGAATGAC	240
AGAAGATGCT	CTTCGCTTGA	ATCTGTTGAA	GCGGAGCTTG	GACCCAGCAG	ATGAGCGAGA	300
TGATGTCCTG	GCAAAGCGAC	TCAAAATGGA	GGGGCATGAG	GCCATGGAAC	GTCTGAAAAT	360
GTTGGCATTG	CTCNAAAGGA	AGGANTTGGC	AAATCTTGAG	GTGCCACATG	ANTTACCCAC	420
CNAACAGGAT	GGCAGTGGTG	TCAAGGGCCA	TGAAGAAAAA	CTTAACGGGA	ACAACTCGAG	480

- (2) INFORMATION FOR SEQ ID NO:534:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 424 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

GAATTCGGCC	TTCATGGCCT	ATATGTATTT	TTAATCTATG	ATGGTTTATG	TGAATAGGAT	60
TTTCTCAGTT	GTCAGCCTGG	GCGACAGAGC	GATACTCCAT	СТААААААА	GNAAAAAAAA	120
GAGGTGACTA	GGCCATGAAG	GCTCTGTCCT	CACAGATGGA	TTAATGCCAT	TGTTGTGGGA	180
GTGGTTTTCT	CATTGAAGGA	TGAGCTTGAG	CTTGGCCCCC	TTCCTTCTCC	CGCCTCATTC	240
CCCTCTATGT	NGCCCCTATG	ATGCCTAANG	CCATGTTATG	ATGTGGCAAA	AAGGCCCTCG	300
CCAGATGCCA	GCCCCTTGAC	CNTGGAATTC	CCAGCATCNA	GAACTGTGGA	CCNAATGNAT	360
GTTTTTTCCT	TATAAANTAA	CCNGCCACNG	GTATTTTGTT	AAAGCNGCAC	CNAGCAGACT	420
CGAG				•		424

- (2) INFORMATION FOR SEQ ID NO:535:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 340 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

GAATTCGGCC	TTCATGGCCT	ACGTTGACTT	AATCAGAGGG	TCAACATTTG	CCAAAGCAAA	60
ACCTGAAATT	CCATGGACAT	CTCTGACTCG	GAAGGGGCTT	GTTCGAGTTG	TATTTTTTCC	120
ATTGTTCAGC	AATTGGTGGA	TTCAGGTTAC	CTCTTTAAGA	ATCTTTGTTT	GGCTGTTACT	180
ACTITATITC	ATGCAAGTTA	TAGCAATTGT	CTTATATTTG	ATGATGCCTA	TTGTGAACAT	240
	CTTGGACCCT					300
	CAGATAACAA					340

- (2) INFORMATION FOR SEQ ID NO:536:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 446 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

GAATTCGGCC	TTCATGGCCT	AGGCGCTCGC	TGAGGCAAAA	GGAGGCGCTC	GGCCCGCGGC	60
CTGACAGGGA	CTTAGCCCGC	AGAGATCGAC	CCCGCGCGCG	TGACCCCACA	CCCACCCACT	120
CATCCATCTA	TCCACTCCCT	GCGCCGCCTC	CTCCCACCCT	GAGCAGAGCC	GCCGAGGATG	180
ATAAACACCC	AGGACAGTAT	TTTGCCTTTG	AGTAACTGTC	CCCAGCTCCA	GTGCTGCAGG	240
CACATTGTTC	CAGGGCCTCT	GTGGTGCTCC	TGATGCCCCT	CACCCACTGT	CGAAGATCCC	300
CGGTGGGCGA	GGGGGCGCA	GGGATCCTTC	TCTCTCAGCT	CTAATATATA	AGGACGAGAA	360
GCTCACTGTG	ACCCAGGACC	TCCCTGTGAA	TGATGGAAAA	CCTCACATCG	TCCACTTCCA	420
GTATGAGGTC	ACCGAGGGTA	CTCGAG				446

- (2) INFORMATION FOR SEQ ID NO:537:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 353 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

GGCAAATTAC	ATCACCAAAT	CAGCATATTC	TCCACTGGAA	AGGAGAGGCC	CACATAGCCA	60
AATTATAATC	TGCAGGTTTC	TGAGCCAGTG	TTAAATCTGA	ACAGAGAAAA	GATTTTTTT	120
TCAATTGGCA	AATTTTAATG	ACATCACTCA	TTGATACCCC	AAAATCTCCA	GTTCTTACCA	180
AGCTTGGCCT	TGCCCAGTGG	TTCCTCTGTT	CCCTCAACAA	TGTTTCATGG	NATCTAACAA	240
CTTCCCTACC	CACTAACCTT	CTCAGCTTTC	ATGGTGAACC	AAGCCTCCTC	TGTCGCACTA	300
ACCTTCCCAG	CTTTCATGGT	GAACCAAGCC	TCCTCTGTCC	CGCTATTCTC	GAG	353

- (2) INFORMATION FOR SEQ ID NO:538:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 230 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

GAATTCGGCC TTCATGGCCT AAGAAGGAGN AGCAAGCGGA TTTCAGAGAG GTTGTTCTTC AGAAAAAAAT GGTTATTTCT TTGAACTCAT GCCTGAGCTT TATTTGTTTA TTGTTATGCC ACTGGATTGG GACAGCATCA CCTCTGAATC TTGAAGACCC TAATGTGTGT AGCCACTGGG AAAGCTACTC AGTGACTGTG CAAGAGTCAT ACCCACATCC CTTACTCGAG	60 120 130 230
(2) INFORMATION FOR SEQ ID NO:539:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 330 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:	
GNGAACCAGA GATCCCCATA GATGGAACAG AATTATCCCA CTACCGTCAG CGTGCCCTCC TGCAATCACA GCCAGTTCGC CGGACGCCTC TCCTCCACAA TTTCCTGCAC ATGCTGTCCT CCCGCTCTTC TGGCATCCAG GTGGGAGAGC AAAGCACAGT GCAAGATTCT GNTACCCCCT CACCCCCACC GCCTCCCCCT CAGCCCTCCA CGGAGCGCCC CAGGACTTCC GCTTACATCA GGCTCCGACA GCGGGTCAGT TACCCCACAG CTGAGTGCTG CCAGCACCTT GGGATCCTGT GCCTTTGCAG CCGCTGCTCT GGCACTCGAG	60 120 180 240 300 330
(2) INFORMATION FOR SEQ ID NO:540:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 420 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:	
GAATTCGGCC TTCATGGCCT ACTCCGACTT TCGTTCTTGA TTAATGAAAA CATTCTTGGC AAATGCTTTC GCTCTGGTCC GTCTTGCGCC GGTCCAAGAA TTTCACCTAG TTACCCTCTA GAATTATTGC ATTGGGGCCA GGTGGTGTCT AGTACAGTTT TTTACTTTGG AGAATTTATT GAAATTTTCT TTGGCTGAGA ATGCCTTCAG TGTTTGTGGT TATTCCTTGG ATACTTGCAA ATCGATTGTA TTTCTCTGG GACACGGGGT TTCAGATAGA TCAGTTAAAT GAAGCTTGAT TATATCGTAT TTCACGTCGC ATGCCATGTG TCTTGTCTGT TGGACTGTCA GGTCTCAAGA GACGGGCTTG GGTTTCCCTG TGTGGCTGCT GCCTTGCCCC TTCCCCGATC CACACTCGAG	60 120 180 240 300 360 420
(2) INFORMATION FOR SEQ ID NO:541:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 462 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:	
GTGGGCAAAG AAATGAAGTA CATTAAGGAG GCCTTTTTTT TCCTCCAATG GCTGTTAGAT TGTGTATTGC AACCAGGAGT TGTCAAGCTC CTGATCCTAA TCCAAGCTGG GGACTGTGGT ACAGTGTGGC CAGCTGCCTT GCCAGCTGCC TTACCAGGCA GGTCTCGCAT CTGCCATTGT	60 120 180

AGTTACAGCT TAAAAGCCTT TGCTGCCCTT TTTCAGATCC TGTTCCTGGG AGAGTCTCCC ACACTAAGTT CAGTGTGGGT ACCAGCTGTG GTGAGGGTGT GCTGCCACTG CAGCTGCTGT CTGGGCATCT GTGTTAGGGC CAATACTTCA AGAAGTGTGA GTCATTGTGA AGTGACTGTA GGCAGCTGGG AAATAACAGC TGTGAACAGA GAACAACTCG AG	240 300 360 420 462
(2) INFORMATION FOR SEQ ID NO:542:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 347 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:	
GAATTCGGCC TTCATGGCCT ATGGGAGATA GGGGACTTAA TTATTTTGTG GGTTTTTCT TTTTTAGGTC TTAGGAAGGT CTTTGTTCCA TAGGTATCTG TATAATACAA TTTTATTAGG TGTAATACAG ACAGTTTTGT GGAAACAGAA TGCTGACACT GATTAAAATT AAGGTGTATA TATGTTTAGT CTTTGAGATG ATCTGTATGC TACATGTAGG TGTACATTGT AATTTTCTGG CTTGTAATTT TTTGTATCAT ACTCTGTTTC GGGAATTTGC AAATGCCTAT GACCAGCCTA TGACATCTGA ACCATACCAA CTGACCTTAG AAACAACGAC ACTCGAG  (2) INFORMATION FOR SEQ ID NO:543:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 346 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	60 120 180 240 300 347
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:	
GAATTCGGCC GCCTAGCAAA AGTGAAAAAA TAAATAAAAC AAGCCACAGA TTGGGACAAA ATATTTGTGA AGGATATATC TGATTAAGAA GTTATATCCA GAATATATGA AGAACTTTCA AAACTAAAGA AAACAATTCA TTTTTTTAAT TGGGCAAAAG ATTTAAACAA ATATTTTACT AAAGAAGATA TCCAGATAGC AAATAAACAC ATGATATTCA CCGAAATTAT TAATTAGGAA AATGCAAATT AAGATGAATA TCATTATATA CCTACTAGAA TGGCTATATT TTAAAAGTTT GACACTGCCA ATTACTGGTA AAGATGCAAA TCAGCGGAAG CTCGAG	60 120 180 240 300 346
(2) INFORMATION FOR SEQ ID NO:544:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 399 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:	
GAATTCGGCC TTCATGGCCT ACTITCTTCC TACATTAGTG GCATACTCTG AATGACCTAG TGAACAGACT GAGAAGAGGC CTCTGAATTG CAGAGTCTCG TCTGTAGGAG AAGGTTCAGG AGAGTATTGA ATTTTAGGGA CTAGAATCCA TCTTACCTAT GCTGTTGCAA TCGCATGCTG	60 120 180

ACTGGAAGTG T	GGGAAAGAG	ACTTACAAGT	AAGGACATGG	GTTTGTTTTG	TTTTTTTTTT	240
TTTGTGACAG A	GTGAGACCC	TGTCTCGNAA	AAGGAAAAA	AGTAATAGAA	CATTAAATAC	300
AGTATCACAC C	ATTTATGGT	TAAAAAAGNA	AAAAGACAAG	ACACTATATG	AAGTGAGTGT	360
CTTTTAAAGT T	TTAAAAAATT	AAATGAAAAC	AAACTCGAG			399

- (2) INFORMATION FOR SEQ ID NO:545:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 367 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

GAATTCCGCC GCCTC	CATCT CCCTGGCCAT	GTTCTTCTTG	AAGACCCTGA	CAGTGGCTTC	60
TTCTTTGTGG CAGCT	GGCCA ACAGCCAGAC	CCTGACAGCC	AGCCCCCAAG	CACCTGGGTC	120
CCCAGAGGAT TCTGA	GGGTG TCCCCCTCAT	CAGCCTGCCC	CGCGTGCCAC	AGGGAGGAG	180
TCAGCCTGGG CCCAG	CCGGG GATTAAGTCT	CATGTCCAGT	CAGGGCAGTG	TGGACTCAGA	240
CCACCTAGGT TATGA	TGGTG GCAGCAGTGG	CTCAGACAGT	GAGGGTCCCA	ATGACACCCT	300
TGGTGAGAAG GCCCC	CTTCA CATTGCGGAC	TCCACCTGGG	CCAGCACCTC	CACAGACTTC	360
ACTCGAG					367

- (2) INFORMATION FOR SEQ ID NO:546:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 455 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

GAATTCGGCC	AAAGAGGCCT	AACCGCGGNC	GCTCTACAAC	TAGTGGATCC	CCCGGGCTGC	60
	TATCAAGCTT					120
CCCGCTCCGT	GCCCTACCAC	TACTTTGAGA	AGGGCCGGCT	AGATGAGTGT	CAGATGTACC	180
GTTTGCATGA	GCAGGCTCCA	AGGAGCGCCC	ATCGCTTCAT	TACCGAGAAC	CCTGTGTTCT	240
CCCGCTGGGC	CAAGAAGCGA	CCCATCGTGT	TCGCCCACCC	GTCCTGGAGG	GCCAAGTAGT	300
TCCTGTTGCC	AGTGACTGCC	AGGCCTCAGC	CAGGCCTGTG	ACCCATTCCA	GGCCAACACG	.360
GCTCTAATGT	GAGCATTTAT	GACTCACCTT	CTACCTGACA	CCAGGTAGAA	CATGAAGTCT	420
CTATTACCCA	ACACTGGGTA	CACTCGGAGG	TCGAG			455

- (2) INFORMATION FOR SEQ ID NO:547:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 401 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

GAATTCGGCC TTCATGGCCT AGTCATTTTG TCAGCTTTCA CACAAGAATC TTTGATCCTA

TTGTAATAGT TAATAAGGAA GTTCTTCTCT TGCTCAAAGA AGTCATCTAC CTCCTTAACT CCAGTAAAAA GGACTTCATC AGCACTTTTC ACCACACTTT TGAAGAAGCC ACCAAACATT TCTTTAGTAT TTTTCCGCCT AACACTTAGA TCCTGATCAT ATTCCAGGAA AACATGAAAG TTGCGATCTT TACTGAGAAC AGGGTGAGAA GAAAGCCGCT GAAGAAAGAC TTCATGGGAG GACACAGTCT TCTTAAACAC AGCGAGATAC TCAGCTTCCA GTTCTTGTTT CATCTGGGCT TATTATTCCA CCTTCTCCA GTTCTTCTGA G	120 180 240 300 360 401
(2) INFORMATION FOR SEQ ID NO:548:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 364 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:	
GAATTCGGCC TTCATGGCCT ACAAGCCCCT CTTACCTCTC TGGATGCTTT CTTTAACACT AACTCACCAC TGTGCTTCCC TGCAGACACC CAGAGCTCAG GACTGGGCAA GGCCCAGGGA TTCTCACCCC TTCCCCAGCT GGGAGGAGCT TGCCTGCCTG GCCACAGACA GTGTATCTTC TAATTGGCTA AGTGGGCCTT GCCCAGAGTC CAGCTGTGTG GCTTTTATCA TGCATGACAA ACCCCTGGCT TTCCTGCCAG ATGGTAGGAC ATGGACCTTG ACCTGGGAAA GCCATTACTC TTGTGTCTGC TACTGCCCTC CCACAGTCAC CCCAATATTA CAAGCACTGC CCCATTGGCT CGAG	60 120 180 240 300 360 364
(2) INFORMATION FOR SEQ ID NO:549:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 195 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:	
(XI) SEQUENCE DESCRIPTION: SEQ ID NO:549:	
GAATTCGGCC AAAGAGGCCT ATGCTTTTCT TTGCAGCACT TAGCACAAAT AGTAATTTTT ATTTTACTTT TATAGATGTA TTTTATGTCC CTCCACCAGA CTGTATACTC CATGAGGACA AGGATATTGA TGTTTATGTT AACTCTTGTA CACTCAGTGC CTGGCACCAT GCCTGACCCA GAAGAGGGAC TCGAG	60 120 180 195
(2) INFORMATION FOR SEQ ID NO:550:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 335 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:	
GAATTCGGCC AAAGAGGCCT AACATAATGC GCTAGCAGAC TTGGGAATTA GGGGCAGAAT GCTGCTCTAA ATTCAGGAAA TCATGGCACG GTTTCATATT GAACATGGTC TATTCCTACC ACTAGCGCTT TCCTGGCTGA TTTCTTCTCC AGCTGGAGAC TTCTTTCTGG TTTTCCAATT	60 120 180

TATGCTCCAC CCTCACCCCA ACCCACCCAT AAACCAGTGG CTGCCGGAAG CAGTATCTTT CATAGTGGTG AGTTCTGGAT TTTCAGCAGT AATGGCCGAG AGTCAGGGAC CAGATGAGTG TGTGTGAGCT GGTGAGAAAA GGTAGATTCC CTCGA	240 300 335
(2) INFORMATION FOR SEQ ID NO:551:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 662 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:	
GCCAAACATG TCTCACCNAA NNCCAAATGT CCCCNGGGGG AGCAAAATCT CCCCTGGACA ACTGTGGAAT CACTGTNNGG AAGTGTTTAC TTGAGTGGTT TNCTGGCCTG GGCCTCATAC	60 120
TCTGAATTTT TGAAGTAAAT GGTCTGGGGG TGCTGGGGGT GGAGAGCAGA GCACTGGTAT	180
TTTTAGGAGA TCCCCCTGTC ATTCTAAAGC ATATCCAGGG TTAAGCACCA TTAATCTGAN GATCTNCNGT CTGATCTGCG GGCCCCCTTT CATCTANGTG CAGTATTTTT CTCTATGCTT	240 300
TTTAAAATAA TGAAAGTTTC TNGAACTCCA TCTGGACTTG AAATATAGCC TGCCACACAG	360
TTAGCAAATA TAGCAAGAAT AACAAGTGTT CTAAATGGAT TTTTAATTTA TTATGGCAAT	420
AGTACATTCC AANAGGGTGG CATTTTTTAA AATGAGATTT TTCTTTTGGG CCTAAGATTA CAGTCACATG GTTCCAAATT CAGAGGGTTC AAAAGGACAC AGAAAAGCCT GCTTCCCACT	480 540
TGNGCCCACT GGCCTCCCCT TTTTTCGCAT AAATGGCAGT ATATAGCTTT GTCTGTTCCT	600
TGTTTNNNGA GCTTAATACC TTAGAGACAG ATTTTNGTAT ATCTGTACCT ACAGAACTCG	660
AG	662
(2) INFORMATION FOR SEQ ID NO:552:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 306 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:	
GCTGTTTTAA AAGAGTTGGG GGAAGAGGTA GAAATGAATC TTTTGGTTTA GTTTTTTAAT TCTCTAAGGA CAACATTGGG GAAGTGAGCT TTAGAGTTAT ATTTGCAGTA TTTATTTTTA TCATGAAATA TTCAAGTCTA GGCCCTTGGT GAATTGAGGC CTGGTGAGTA TTTCTGCTTT CCCCCTGGAG AGATTGAGAT GGTTTCTGAT TGGGAGCTTT AATTCTGTGG GCATTTGTGG GACTTACCAA AGAGGTATCT AGAGTTCCTT TAAAACCCCC GCCCTGTCCC TGCCACAAAA CTCGAG	60 120 180 240 300 306
(2) INFORMATION FOR SEQ ID NO:553:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 290 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:	

GTCAAAAGAG GAGCTAGGAC CAGATCTCTA AGTCTTACNG TCCAGGTCAA AAAACAAGTA

CTTTCCTATC TGGTTATACA GAAATCTGGA AACAGTCACT CCCAGCCTCA CAATTAAAAA

60

AACTTGGACA TACAGAAAGT TCATAGTTTT CCTTGAACTC ATGATAGTGC TGAGATTTCA CGGCAACCAA CTGGCCCAGA TACTCCAGAG TCAAAGACAC TGTAAGGAGA GTTGACATNT GAGCATTAGA CAAGACACAG ATGGTANGAG TTAAGCTAGG GTTACTCGAG	180 240 290
(2) INFORMATION FOR SEQ ID NO:554:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 370 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:	•
GAATTCGGCC TTCATGGCCT ACTCTATGGG GATGAGGTAG AGGAGAGCAA GATATTTCGG CAGCAGGGAA AAGGGTAGAA CACAATAGGG TGACACAATT TACACTTGAT ACTGCATTAA CATCTGGTAG AGTGTCTAGG GCAAAGGTTA GCCAAAATAT AGCTGGATGG TTGAGGGATT TAGAAGGAGT TGGGATGAT CCATAGTCTC AATGAATGGA GAAAAAGTAA CTCAGGAAAG TAAATGCTGG TGACTTATCA GCGGGTGGCT GGTGATGTTT GGTTTGGATT GTGAAAGCTG CTTAGACCAA GATGGCTGA GGGAAGGGGA GGAGAGTGAG CATGTAGAGG TTGAGGCACT TGGTCTCGAG	60 120 180 240 300 360 370
(2) INFORMATION FOR SEQ ID NO:555:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 304 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:	
GAATTCGGCC AAAGAGGCCT AATTGCCAAT CAACAACTTT TCCTAATCCA CCTTGATCCT CAATCATAAT ACTCAAAAAC TGCCAAAAAC AAAATCTTCC TGACAAAAAT ACAGGCCAAA CTTCCTCATC TGCTTTCCAG GTCTTCTGTA ATCTTATCCC AGCTTATTTA CAGTCCTCCA TTTACTAAGA AAACCCAAAA TAATCTTTC CTGCCCCAAA TTCATGTTCT TCCCTTTCCT TTTGTTCATA CTACCATACA TATCTAGAAA TGATACTCAA ATATTCATCC TCAGCACCCT CGAG	60 120 180 240 300 304
(2) INFORMATION FOR SEQ ID NO:556:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 285 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:	
GAATTCGGCC TTCATGGCCT AGAGGGGAAA GCATATCACT AGGACTGTGA CCCCTGTGCC TACCCATCTT ACTCTCTACC TCTTAGGAAA GTTTCACTGT GTTTACTTGG GACTTCTGGA	60 120
279	

CTAGCTGCCG TTTGCAACAG TGGACTTACC AGTTTGCCAC TACTCTGCTA CCTTTCTACT GGTGCACACA CCTTAGTAAG GCAGTTTGAT TACTAAATGC AGCTGTCTCC AGAAATGGAA TGATGCTATA GGCCACTTAC TAAATGAATG ATCAGGAGTC TCGAG	180 240 285
(2) INFORMATION FOR SEQ ID NO:557:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 409 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:	
GAATTOGGCC TTCATGGCCT AGCTGGATCT GCCCACTGTG CACTCCATCA TCAGCAAAAT GATCATTAAT GAGGAGCTGA TGGCCTCCCT GGACCAGCCA ACACAGACAG TGGTGATGCA CCGCACTGAG CCCACTGCCC AGCAGAACCT GGCTCTGCAG CTGGCCGAGA AGCTGGGCAG CCTGGTGGAG AACAACGAAC GGGTGTTTGA CCACAAGCAG GGCACCTACG GGGGCTACTT CCGAGACCAG AAGGACGGCT ACCGCAAAAA CGAGGGCTAC ATGCGCCGCG GTGGCTACCG CCAGCAGCAG TCTCAGACGG CCTACTGAGC TCTCCACTCT GTTTCCCGCC TGGGCCATCC AACCTTGAAG TCCTAAACCA CACCTCAGTC ACTAAAGGGTC TGTCTCGAG	60 120 180 240 300 360 409
(2) INFORMATION FOR SEQ ID NO:558:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 287 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:	
GAATTCGGCC TTCATGGCCT AGGAAAAAGA GATATAAAAA AAAGAAAAAG AGGNGGTACC AGCCAACAGG AAGACCACGG GGAAGACCAG AAGGAAGG	60 120 180 240 287
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 380 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:	
GAATTCGGCC TTCATGGCCT ACTTCTCAAA AATAGATGTA CTTGACTACT CTTTTCTTGA TTCTTCTGGG AGTAACCATC TCTTTGGAGA TGGTTGTTAG TAAGGTTATA AAAATAACCT TACTGAGGAA CTCCCATGCA ATCCTCTGAA AATAATAAAA ATTTCCTTAT TTAAGAACT CTTATTAAC AAAGTAATTG TTAGGGTTGA ATACTCTAGG GGCAAATGAT TTAATTGTGCC TTTTTGTAAAA GTCAACACTT GGCAGGTTGT TCTTTGACAC TGGCTGATGC	60 120 180 240

TCTCTAAGAG TATGGTAATT CTAGTAAAGT AAAGAAAATT GTTTATCAGA TATTAGGAAC 360 TGTACATAGG CCCCCTCGAG 380 (2) INFORMATION FOR SEQ ID NO:560: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 208 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:560: GAATTCGGCC TTCATGGCCT AAAATTGTTC ACGAGGGATT ACGTGGTTTA CTTGTCTGTT 60. GTCCAGATAG CTTTATATTC TTTAAGATTC AGCTCGGATT CTTATCCTAT TTTTGCCATT 120 AACTTTCATT ATGATTTTGG CAAAGCCATT TTGTTTGCTT ACATTTTTCA CTTTTAATGT 180 GGTGTCTGGC CTCCCCCCA CACTCGAG 208 (2) INFORMATION FOR SEQ ID NO:561: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 505 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:561: GAATTCGGCC TTCATGGCCT ACAAACANTT TTTACTGNGT TATAAATAAA AACAGCGACA CATCCTAAAT GTGCACCTGT GCCGTGGCTG AGCCGCTGCA GTGAGGGCTA GTGTGCAACA 120 CCGATGCTGT GCTGGACGCG TGCCCAGCCG GGTCCCCTGA CAGGAGGCAN CCGGGGCCGG 180 TGCGTGTGTT TGCATGTTGC AGTCATGGGG CGGGGNCGGC AGANGCCTGT GTGATNGTNG 240 CGTCCCTGGA AAAAGAAGNN GGGNAGGCCC CTCNCACNTG TANCCCAGCC TGCAGANGGG GNGTTNTGTG GGTCCTTCCC CGTGCATATG CGTGTGATNT CACCCATCCC GTGTGGGTGC 360 GCAGGAGGGG CCGAGGGAGG AGGGTGCTGG AGGGCGGAAG TTACCTCTGA CTGGAGGAGA 420 NACCCGGCCC GTGTNACCAG CANAGGTGTG NTCGTTCTAA AACTGGGAAA AATTTGTTCT 480 TAATTTAAC CACAGTCCCC TCGAG 505 (2) INFORMATION FOR SEQ ID NO:562: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 351 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:562: GAATTCGGCC TTCATTTAAA AGATAAGTTA GAAAAGTCAA AGCGAGAACG GCATAACGAG 60 ATGGAGGAGG CAGTAGGTAC AATAAAAGAT AAATACGAAC GAGAAAGAGC GATGCTGTTT 120 GATGAAAACA AGAAGCTAAC TGCTGAAAAT GAAAAGCTCT GTTCCTTTGT GGATAAACTC 180 ACAGCTCAAA ATAGACAGCT GGAGGATGAG CTGCAGGATC TGGCAGCCAA GAAGGAGTCA 240 GTGGCCCACT GGGAAGCTCA GATTGCGGAA ATCATTCAGT GGGTCAGTGA CGAGAAAGAT 300

GCCCGGGGTT ACCTTCAAGC TCTTGCTTCC NAGATGACCG AAGAGCTCGA G

(2) INFORMATION FOR SEQ ID NO:563: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 353 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:563: GAATTCGGCC TTCATGGCCT ACAAAACTGT CCATGGCATG AAAGACTTGG ACCGCCATCT 60 CAGAATCCAC ACGGGAGACA AACCGCACAA GTGTGAGTTC TGTGACAAGT GCTTCAGCCG GAAGGACAAC CTGACCATGC ACATGCGGTG CCACACCAGT GTGAAGCCAC ACAAGTGTCA 180 CCTGTGTGAC TACGCTGCCG TGGACAGCAG TAGCCTCAAG AAGCACCTGC GGATCCACTC 240 TGATGAGCGG CCGTACAAAT GCCAGCTCTG CCCCTATGCC AGCCGCAACT CCAGCCAGCT 300 CACCGTCCAC CTGCGATCTC ACACGGGTGA GTCCCTGACC AGGGGTCCTC GAG 353 (2) INFORMATION FOR SEQ ID NO:564: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 416 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:564: GAATTCGGCC TTCATGGCCT ATAGAATTCC TAGACTTTAC AGACTAATAG TTTGACATCT ATCTCTGGCA AAATTCGAAA CTTAAACATT AAACAAGGGA AAATGAGGGG TGGAGGNAAA 120 GACTGCGGAT TTCTAGGAAC TAACAATTTG CTAAGNATCA TTCATTTTTA AACTAATGTT ATTTACTTTT GTGGTAGATC AGGGNATATG CAAGATCTTT ACTTTTCAGC AAGACATTTT 240 TCTCATAATG TCCTTATGGA GAAGACTGCT CTATGGACTA GNATAGTTTG ATAAGAAAGG 300 GCTGAGTCCA GCGNATTCAT TAGTTCAAGC AAAATCTACT GGAGGCCAAC TAGATTTCCA 360 GCCATTATCG TACTTGGCAC TTTCNATACT TTGAATTTTA ACCACCACAC CTCGAG 416 (2) INFORMATION FOR SEQ ID NO:565: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 465 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:565: GAATTCGCCC TTCATGGCCT AAGACGGGT TTCACCATGT TAGCCAGGAT GGTCTCGATC 60 TCCTGACCTC GTGATCCTCC CGCCTCAGCC TTCCGAAGTG CTGGGATTAC AGGCGTGAAC 120 CACCACGCCC AGCCATATAT CAGGAACTTG AGCATCCATG GAGTTTGGTG TCCAAGGGAG GTCCTGGAAC CAATCCGCCA TGGATACTGA GGGATGACTA TAATATGAAC CTTGTATGTA 240 TGTAATTTAC CATTTTCTAG TTAGCCACAT TAAAAAAGGA AAAAGAAACA GGTGAAAAAT ATTTAAAAAA TACGTTAACA CAATATATCC AGAACATGAT TTCACATTGA AATCAATATA

AAAATTACTG AAATAGTTTA CAGTCTGGTG TGCATTTTAG ACTTAAAGCA TATCCCTTTG GGCATGGTGG CCCATGCCTG TAGTCCTAGC CACTGAAGGC TCGAG	420 465
(2) INFORMATION FOR SEQ ID NO:566:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 357 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:	
GAATTCGGCC TTCATGGCCT ACAGCGAGAA GGAGTGTATG AGTGTGAGTG TGTGTGCATG GAAGTTGGGC ACTGGGCGTC TGANTCCTTC CCCACCCAAG AGAGGAAGGA CCCCTCACCA CCCCCACTGG CGAGACAGTT TACTTTGCCG ACTTGCCATG TTTTTGCCAA AACCAAGATT TTGAAGGAAA TGAGTGGCCA GCGCCAGGGC CCAGGCCATG TGGCCTGCCC AGCCTCAATG TNACTTGGTG GCGGGGTGG GTGGGGGTGG GCAGCAGCAT CCCAGCCTTC AGATGCTTCA CTTTCCTTCT CTGTAACCAG ACTTTGAAAA ATTGTTCGTT TCATCAGGCA TCTCGAG  (2) INFORMATION FOR SEQ ID NO:567:	60 120 180 240 300 357
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 336 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:	
GAATTCGGCC TTCATGGCCT ATCTGCACTG AATTAGAACA AAATTTAGGA GACTTCTAAT TTGAAGCCAG AGGTGCTGAC TTTTGAGTCT TTGGAGATTG CCTGTTGGAA ATATTCCTGT TGAGGGCCAA TGTCCCAATG GGCTCTGAAG ATGAGAAGGA TCCCTGCCCT ATGTGGATGC CACTGGATCT CGGAAAAGA AGGGGGACAA TAACTAGAAA CGAACTAAGA TGTGGCCCTT GCTTTTGTAC TTTTAATTTA ATGGGAAACA CTCGAG	60 120 180 240 300 336
(2) INFORMATION FOR SEQ ID NO:568:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 481 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:	
GAATTCGGCC TTCATGGNCT ACCTGGACCT TGGGTGGCAG GCCTGGGGCC TTCAGTCCTT AATTCAGGAG GTAGCCAGTC GCTGGAACTA AGANTGAACT TCAGCTGTTG TTGCCATAGC TGGAGGGAAG AGGGAAAGGA GCGCTGCAGG GGAGCAGAGA CCTCACCCTT CCTCTGCCGA CATCAGGCTG CCGGTGCTGG ACGGGGCCCT GGCAACCGTG GCAGGAGTGG TGATGTCCGA TGATGGTAAC AAGGGCTTCC TGAGGACCCC GAGCTGTCTT AAGGGCTCTT TACCTGGAGT AAGTATCCCC TTTAATCCTC CCAACAACAC TGTGAAATTG ATTCTGTTGT TATTCCCATT	60 120 180 240 300 360

TCACCGATGA GGAACCCACA GCCCAGAGAT GTTAAGTAAC CTGCCCAAGC CTCCCTCTGA	420
GCATGGCAGA GGGAGGGTCC GAATGCGGAA AGTCTGGCTT CAGTGCCCCC ATCCTCTCGA	480
G	481
(2) INFORMATION FOR SEQ ID NO:569:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 472 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(with appropriate the second	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:	
GAATTCGGCC TTCATGGCCT ACTCATCATT TGGAAAATAC TTGATGGCAG GAGAACTTGC	<b>C</b> 0
TTAAAACTAA AGGTGGAGAA AGAGTTAACT TCCAGGACAA CCCATTATAG CTCACTTCTT	60 120
ACCAACAAAG CAGTTTTAT ACAGCACCTT AGGACTCATT TCTAATGTCA ACCCAGATGG	180
CCAGTAAAGG CAAGGGAAGA GGCTAAGTGA CTCACAAAAA TCTCTGATAT TGAGGTCTAA	240
TGTGAAGGCT ATAGATAGGA ATTCCCCACA AACTTCTAAT GAGGACTAAT ATGAACAGCA	
AATTGGAGAA GACACCAAGG ACCTAATTTT AGTTTCACTA GCCGTGGGAC CTTAGAAAAA	300
AGACCATTTG CTCTGGACTT TTGTTTCCCA AGCCATAAAA TGTGGAAGAA TCTTCACAAT	360
TTCAAGTTGG TCATGTATAT TTCCCTTTTA CAGAGAAAAGC TGAAGCCTCG AG	420
TICAMBITOS TERIGIRIRI TICCCITTIA CAGAGARAGE TGAAGECTES AG	472
(2) INFORMATION FOR SEQ ID NO:570:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 487 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:	
GAATTCGGCC TTCATGGCCT AGAAAGGATC AAGCTGATCA GAAGCGGGAG CTGCATTGAG	60
GGAAAAATAT GGCCAGAGAA GGCCTCACTG AGGAGGTGAC GTTGGTGATG CTGGAGCTCA	120
GATCTGAAGG GGAAGAAGGA AGCAGCCACA TATAGAAGTG AGGGAGGGGG CTTAGGCAAA	180
AGGAACAGCA AGCGGAGAGG CCCTGAGAAA GGAAAGGCTT GGCTCGCTCA CCTGCAAGGG	240
CCCCTGGCT TGACATAGTG AGAAAGGTGT GAAGATGAAT TTGGAGAAAG GCAGGGACAG	300
ACCACAGGAG ACCTTAGATT TGATTCTGAG GGCGATGGGA TCCCTTGAGA GGATGCTGAG	360
CAGGGGAGAG ATGTGATCTC CTTTTCATTC TAACATGATC GCTGCAGCTG CTGCTGGAGA	420
ATGGTTGCAG GAGCGAGAGT AGAGACTGGG AAGGTCTGTG CATCCTCTAA GCNACAGGCG	480
TCTCGAG	487
	30/
(2) INFORMATION FOR SEQ ID NO:571:	
(i) COMENCE CUADACTEDICTICS.	

- (i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 456 base pairs

  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

- (2) INFORMATION FOR SEQ ID NO:572:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 399 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

GAATTCTAGA	CCTGCCTCGA	GATGCCCGAC	TACTACAAAC	CTCAGTACCT	GCTGGACTTT	60
GAAGACCGCC	TTCCCAGCTC	GGTCCACGGC	TCAGACAGTC	TGTCCCTCAA	CTCTTTCAAC	120
TCCGTCACCT	CCACCAACCT	GGAGTGGGAT	GACAGTGCGA	TTGCCCCATC	TAGTGAGGAT	180
GGAGACCTCA	CAGACACGGT	CAGTGGTCCC	CGCTCCACAG	CCTCCGACCT	GACCAGCAGC	240
AAGGCCTCCA	CCAGGAGCCC	CACCCAGCGC	CAGAACCCCT	TCAACGAGGA	GCCGGCAGAG	300
			CACACCACCT			360
	ACCCGCCGGA					399
						377

- (2) INFORMATION FOR SEQ ID NO:573:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 256 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
    - (b) TOPOLOGI: Timear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

GAATTCGGCC	TTCATGGCCT	AGATTTGGGT	TAGTGGTTTT	CTTTTAGCAT	GTTGAAAATG	60
TCACCCAACT	GTTTTCTGGG	TTCCTTTGAA	AAGCCAGCTG	TCTGTCTGTC	TGGTTGTCAT	120
GTCTGAAGGT	GATGTGTCTT	TACCTCTGGC	TGCTTTAAGT	ATCTTTTGCC	TTTTTCCCCT	180
TTGTGAATGT	TTTTGCTGAA	<b>GTGTAACATA</b>	TACACAAAAG	AGTGTGCAAA	TCATCAATGC	240
TTGATGGATT	CTCGAG					256

- (2) INFORMATION FOR SEQ ID NO:574:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 199 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

GAATTCGGCT TCATGGCCTA GAATCATGCA TTTTCTTTTC	60
TTTGTCTATG CTGGTGGCAT CCAGGGCATT GCTTTGTCTC CCTGATTATG CCCAGGATTC	120
AAGGTCTTCT TATTTGTGGG GAGGCAGGCT GCCCACTGGG ACGGTTTTTA GTGTGTTTNC	180
CATTCCTGGC TCCCTCGAG	199
<u>,                                      </u>	133
(2) INFORMATION FOR SEQ ID NO:575:	
10. 11. 10. 10. 10. 10. 10. 10. 10. 10.	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 349 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

GAATTCGGCC	TTCATGJCCT	AGGATTTGAA	GAAGTTGGGA	AAGCATTATG	TAGATTAATA		60
TACTGGTTGG	TTCCCTATCT	ATGTGGAAGG	TCATATTAGC	TGCAATTATT	TAATTTGCTG	,	120
TGTTATTTTG	TGTTATATAA	CACAAATATA	TTTGTATATT	AACTTCATTT	TTACTGTCAT		180
TTTTCCTGTT	GTATACAAAA	TGAACTAATC	TTGTAATTAT	TTTCAAATAT	AGAAGTATAT		240
ACATTAGATG	GATTTCCAAG	ATTTTGTAAG	NAAATCTTAA	ATCAGTGTTT	TGAGTTATTT		300
AATTTTTAAA	TTAATCTACA	AATTATGCAC	NACAAACTAG	CAACTCGAG			349

- (2) INFORMATION FOR SEQ ID NO:576:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 494 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:

GAATTCGGCC TTCATGGCC	T ACAAATTTTG	CTCACTTTCA	TTAATCAGTT	GCTCAGATAG	60
AAGGAAATGA CATCTGGTT	C TGTCTTCTTC	TACATCTTAA	TTTTTGGAAA	ATATTTTTCT	120
CATGGGGTGG ACAGGATGT	C AAGTGCTCCC	TTGGCTATTT	CCCCTGTGGG	AACATCACAA	180
AGTGCTTGCC TCAGCTCCT	G CACTGTAACG	GTGTGGACGA	CTGCGGGAAT	CAGGCCGATG	240
AGGACAACTG TGGAGACAA	C AATGGATGGT	CTCTGCAATT	TGACAAATAT	TTTGCCAGTT	300
ACTACAAAAT GACTTCCCA	A TATCCTTTTG	AGGCAGAAAC	ACCTGAATGT	TTGGTCGGTT	360
CTGTGCCAGT GCAATGTCT	T TGCCAAGGTC	TGGAGCTTGA	CTGTGATGAA	ACCAATTTAC	420
GAGCTGTTCC ATCGGTTTC	T TCAAATGTGA	CTGCAATGTC	ACTTCAGTGG	AACTTAATAA	480
GAAAGCCCCT CGAG					494

- (2) INFORMATION FOR SEQ ID NO:577:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 229 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

GAATTCGGCC TTCATGGCCT AGGCACGTTA AATTTTAAAA GTTANAAAAA GAAAGATGCT

TTTTGCAGCA GTTCCAGGGT AAACGGCCCC ATGCAACACA AACCCTCGGG AAGGGCATTA CAGCCTTGCA GTGGGCCACG GAGTGCACCA CGCGGCGCTC AGCCCCCCAG GGAAGCGATG CCCCACATCG GGCCAGAAAC AAAAGGGGGT GAGATAAAGC ATGCTCGAG	120 180 229
(2) INFORMATION FOR SEQ ID NO:578:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 400 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:	
GAATTCGGCC TTCATGGCCT AAGGAGTTTG AGATATATTT AGGAAGCAGA GCCTATAAGA CATGCTGATC ACTTGCATAC ATAAACTGAG AGAACTAGAG GTATAGAAGA CTTCTAGAAC TTGGAGAAAT TGGATGAATG GATGTATTGT TATTGATGTA ATGAACCTTA GAGGTGGGTG GGATCAGAAA GATCTATTTG CTTTCAAAGG AAATGGGGAG TGGACAGGTA TGTTGGCAGC ATAAGAACTG GAATAACAGC ACATCTCATT CATGCCTTAA AAGAACGTGA AACTTTGAAT GTACAGCAAT GGTATTCAAT AGGTATGACT TTGCCCCTAA AGGACATAGA CACCAGGGAT GTTGCTAAAT ATCCTCCAAT GCACAACACA ACCCCTCGAG	60 120 180 240 300 360 400
(2) INFORMATION FOR SEQ ID NO:579:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 316 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:	
GAATTCGGCC TTCATGGCCT ACGAGGACGA GGACGTCAAG GATAACTGGG ATGACGATGA TGATGAAAAA AAAGAGGAAG CAGAAGTAAA ACCAGAGGTA AAAATTTCAG AAAAGAAAAA AATAGCAGAG AAGATAAAAG AGAAAGAACG GCAACAGAAG AAAAGGCAAG AAGAAATTAA AAAGAGGTTA GAAGAACCCG AAGAACCTAA AGTGCTAACA CCAGAAGAAC AATTAGCAGA TAAACTGCGG CTAAAGAAAT TACAGGAAGA GTCAGACCTC GAATTAGCAA AGGAAACTTT TGGTGTTAAT CTCGAG	60 120 180 240 300 316
(2) INFORMATION FOR SEQ ID NO:580:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 325 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:	
GAATTCGGCC TTCATGGCCT AAGCGAGGCC TGAGCCTCTG CGTCTAGGAT CAAAATGGTT TCAATCCCAG AATACTATGA AGGCAAGAAC GTCCTCCTCA CAGGAGCTAC CGGTTTTCTA GGGAAGGTGC TTCTGGAAAA GTTGCTGAGG TCTTGTCCTA AGGTGAATTC AGTATATGTT TTGGTGAGGC AGAAAGCTGG ACAGACACCA CAAGAGCGAG TGGAAGAAGT CCTTAGTGGC	60 120 180 240

AAGCTTTTTG ACAGATTGAG AGATGAAAAT CCAGATTTTA GAGAGNAAAT TATAGCAATC AACAGCGAAC TCACCCAGAC TCGAG

(2) INFORMATION FOR SEQ ID NO:581:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 353 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:	
GAATTCGNCC TTCATGNCCT ANGAGAAGNA CCCAGACCCC CCCAAGAAGG AGGAGGANCN CCNNNGAGNC NCTNCTCCAG NCGGANGAGG AGGCCAAGGC CAAGTNCGCC AAGATNGAGG CGGAGCNCGA GGCCNTGNNC CAGGGCATCC GAGACAAGTA CGGCATCAAG AAGAAGGAGG AGCGCGCAGA CGCCCCCAA GAAGGAGGAG GAGCGGCAGG AGGCGCTGCG CCAGGCGGAG GAGGAGCAGA AGGACCAGTA CGCCAAGATG GAGGCGGAGC GCGAGGCCGT GCGCCAAGGAGA AAGAACGCTC GAG  (2) INFORMATION FOR SEO ID NO:582:	60 120 180 240 300 353
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 426 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:	
GARWWYKCSS YYTTNANGGC TAGTCAGTGG CAGGGCCACC CAGAAGCCCC GCAGATGACG GAGCTGAGAA CAGGGAATTN ACCTNCACGT GTTGCCATTT CCTCANTGGA AAGTCCTTGG GAGGTGGCTG GGCTCAGCCT GAGCTCAGGG CTTTTCGGTG GGGTTGGGGC AGGGGCAGGG CGGGCNNTTG CAGGTGGCAC AGGCTTCATC AAGGCAGGAC ACGGGNTTCA TCAAGGCAGG AGCCACAGCG CCCGAGCCCT GGCAGGGGAG GTAAGGCCCA GGATGGGGCA GGGCCGTGTG CTCCTGGNAC GGACATCCTT NTCTGCCAGA GACCTGCTCC CCAAGCCCTG TCCCTCCCAA TCCCCAGGCA GCCCACTCTG CCCTCCATAG ATGAATCTAA TATTGAATTT CTAGACCTGC CTCGAG	60 120 180 240 300 360 420 426
(2) INFORMATION FOR SEQ ID NO:583:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 368 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:	
GAATTCGGCC TTCATGGCCT AAGAAAAGAA AGTAAGATTA TCTCCAGCCA AAATGTCAAC CAAGAATTCT ACAGATCTAG TTGAATATGT TGACAAGAGT CATGCTTTTC TCCCCATCAT TCCAAACACC CAGAGAGGTC AGCTAGAAGA CAGACTGAAC AACCAGGCAC GTACCATAGC TTTCCTTCTT GAACAAGCCT TCCGCATCAA GGAGGACATC TCTGCTTGCC TGCAGGGGAC	60 120 180 240

CCATGGCTTT CGAAAAGAGG AATCGCTCGC CAGGAAGTTA CTGGAAAGCC ACATCCAGAC

300

CATCACCAGC ATCGTCAAAA AACTCAGCCA AAATATTGAG ATTTTAGAAG ACCAAATAAG AGCTCGAG	360 368
(2) INFORMATION FOR SEQ ID NO:584:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 437 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:	
GGAATTCGGC CAAAGAGGCC TAAACGACTC TTTGCCCTGT TTCTTCTTGG CTTCCCTTGC GTAACAAGGA TGAAGGAGGT GGTTTAACTT TATTTTTGTC CTTTAACTTT TTAAAGTCTA AAGTAAGTGC TTGAATCGG TGGGTTTCA TTTTTTTGCT TTCTCACCCC TCAGGTTGGC CCCTAACTTG GCCTCTCACC CTCGTGTCAG CTGTTAGACA CTGACTCAGT GGCTCAGAAT ATGAAAGGCT CAGGAAGTAG CATGCTGGCC CCACCTCCCT GTCCCCATAC CTTAGCAGAG CAGCTGCCCA GCAGGGCCTC CTTCTCTTTC CTAAGAGTTT ACTCCATCCA TGGTGGGTGT CTTGGTAGGC CCGAGATACG AGAGGGAGTG CTGCTGTTAC AAGAATTTAC AGTTGTTCTC TTCGGCACAA GCTCGAG	60 120 180 240 300 360 420 437
(2) INFORMATION FOR SEQ ID NO:585:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 565 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:	
GAATTCGGCC AAAGAGGCCT AGTGCAGAGT TGCAAGCAAG TTTATCAGAG ATACGCCATG AAGTTCGTCC CCTGCCTCCT GCTGGTGACC TTGTCCTGCC TGGGGACTTT GGGTCAGGCC CCGAGGCAAA AGCAAGGAAG CACTGGGGAG GAATTCCATT TCCAGACTGG AGGGAGAGAT TCCTGCNCTA TGCGTCCCAG CAGCTTGGGG CAAGGTGCTG GAGAAGTCTG GCTTCGCGTC GACTGCCGCA ACACAGACCA GACCTACTGG TGTGAGTACA GGGGGCAGCC CAGCAATGTG CCAGGCTTTT GCTGCTGACC CCAAACCTTA CTGGAATCAA GCCCTGCAGG AGCTGAGGCG CNTTCACCAT GCGTGCCAGG GGGCCCCGGT GCTTAGGCCA TCCGTGTGCA GGGAGGCTGG ACCCCAGGCC CATATGCAGC AGGTGACTTC CAGCCTCAAG GGCAGCCCAG AGCCCAACCA GCAGCCTGAG GCTGGGACGC CATCTCTGAG GCCCAAGGCC ACAGTGAAAC TCACAGAAGC AACACAGCTG GGAAGGAATC TCGAG	60 120 180 240 300 360 420 480 540 565
(2) INFORMATION FOR SEQ ID NO:586:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 305 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA	
ILL, MODECODE TIPE: CDMM	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

GAATTCGGCC	AAAGGGCCTA	CAGAATAGCG	GTACCATGAT	AGAATACTGC	AATTGTGGTC	60
AGAATTACAG	TATGCACAAA	GAATTAATTA	GCATTATTAA	AGAGTCCTCA	CTAAACATTT	120
CATATGATCA	CACTGAAGAA	CTGTAACATT	CCATAGAGTG	AAGTGGTTCA	AATTTCTCTT	180
GGAATTTTTA	CTTTTGTTGG	CCTTATTTTA	TGATCCTTTT	CATATTTCTT	TTGACTTAGA	240
GTATTAATAC	ATGGCCAAAA	TAATTTAGTT	ACTACCTCAT	ACAAACAATA	TAATGGTTAC	300
TCGAG						305

- (2) INFORMATION FOR SEQ ID NO:587:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 348 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

GAATTCGGCC	AAAGAGGCCT	AGTTGTTTTT	AATGGCACAG	GACTCTTCCA	CTTTGTGGTC	60
CTCCTCTAGC	ACAATACTGG	ATGGCTGGGG	CAAAAGATTA	AAGGAAGTCT	TTTCCACATC	120
ATTTTTCTGC	TGTTCCTCAA	ATCTTTTTAC	TAAATTTGAT	ACAAATTCCT	CTATTTCTTG	180
ATGATATTGC	TTTGAAATAG	CATTGTTCAT	GAATAGAATC	TGTAATATAG	GTCCATCTAA	240
CTTAGTATCG	TTCACCAATA	TTCCACTCGG	TCGAGTCAGA	ATGTTCAATT	TTCGTTTAAG	300
TTCTTGATTC	TCGGCGCGGA	GCTGCTCGAT	GGTCTCCACG	CACTCGAG		348

- (2) INFORMATION FOR SEQ ID NO:588:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 486 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

GAATTCGGCC	AAAGAGGCCT	ACTCATGACA	GGATGACAGT	CACATTTGGT	AGACACCATC	60
AACCAATGAT	CTCTAATTTG	CGGCCCCCAA	CAAGCAATGG	GGTTCTGTGG	GCTACATCTG	120
GAATTTGAAA	TGTCTCATGG	AAATCATGTT	CTTACCCTGG	AGAAGGGTGG	CTGCTTAGGT	180
GCTACTTAGG	AAACCAGTCT	GGCAGACCAG	ATCTTCCCCA	ACTCAGGGGC	TATGCGGGGA	240
GAAGTATTAG	GAGCCCCTGA	GCAGGAAGGA	TGTACTTAGG	AAGGCTACCG	GGGATGGGGA	300
AGGGTAAAAG	AGCTTAGAAG	CCTGGGTGAA	GTTTGGGTAG	ACCAAAAACA	GGAGGGAGGG	360
AGGGAGGATG	TTCCCTTGGA	ATACAAACTA	GAGAAAAGCT	TAGGGGANCA	AGTCTTTTTA	420
TTTGGGGACA	GTGAAGAGTT	TCCTAAAAAT	TCCCTGGCCC	CCAGGCCTTG	GCTAAAAACC	480
CTCGAG						486

- (2) INFORMATION FOR SEQ ID NO:589:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 410 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

GAATTCGGCC AAAGAGGCCT AATTGATTGT GATTAACCAA GATGTATGGA AAACAGTTTT

AAGTGTGTAG TGCATGTATC TCATAAGGTC CATTAAGACG TTCATTATTT TTCAATTGAT

GCGTCTTAAG CCCCACTTGA TGTTTGTTGT AGTGCATTTC CACAGAAGGA TTCTGCACTG

60

120

180

TGGGATTGAG TTCATTTTGT TAATTGCATA ATACAACCCC ATCGTGTTTC ATAGAAAATA GTAAATACTC TTGCTTTTAT TCATTGGTAT TCTTTGATAT TACTGAAGAA ATACCAAAGA AGCAAAGGAG CAAAGAAATA CCAAAGAAGC AAAGGAGCAA GTGAATAGTT CTTCAAACTT TTACATATTA AGGGCACGAA TGTTTCTTGA AATGTGGACA CATACTCGAG	180 240 300 360 410
(2) INFORMATION FOR SEQ ID NO:590:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 61 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:	
GAATTCGGCC AAAGAGGCCT ACGGCCAAAG AGGCCTAATT GAATTCTAGA CCTGCCTCGA	60 61
(2) INFORMATION FOR SEQ ID NO:591:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 211 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(x1) SEQUENCE DESCRIPTION: SEQ ID NO:591:	
GAATTCGGCC TTCATGGCCT ATCTAGACCC AAATATTTTG AATATGTTAT CTTGTCTCTT TTCTTTTTGT TATATAGAGA GATTGATGCA TAAAATCTGT GTTTGTATGA CTGTAATTCC AAGTTTAGCG AAATTGTCCC TAGGACAACA CACCAACGGC CATGAGCTGT CTCGGTCCTG CAAGCTTAGT CTCCGATCCT GCCCACTCGA G	60 120 180 211
(2) INFORMATION FOR SEQ ID NO:592:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 253 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:	
GAATTCGGCC TTCATGCCTA GCCGGACCTG GTGCTCCTTT CCTTGGTGCT GGGCTTCGTG GAGCATTTTC TGGCTGTCAA CCGCGTCATC CCTACCAACG TTCCCGAGCT CACCTTCCAG CCCAGCCCCG CCCCCGACCC GCCTGGCGGC CTCACCTACT TTCCCGTGGC CGACCTGTCT ATCATCGCCG CCCTCTATGC CCGCTTCACC GCCCAGATCC GAGGCGCCGT CGACCTGTCC CTCTATCCTC GAG	60 120 180 240 253
(2) INFORMATION FOR SEQ ID NO:593:	
291	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 190 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:	
GAATTCGGCC TTCATGGCCT AAAGAAATGA AATAATATCT CTGAATTTTA GTCCATGTTC	60
TCAATGATTT CTGACTTTAT TATATTAACT CTTATTAATG ATCACAATTT ATTTTGTAAA TTTTGCAGCC AAAGGGACAA TTTATTTTGT AAATTTGGGA TTCTATTTGC AAAATAGGGA	120
TCGACTCGAG	180 190
	130
(2) INFORMATION FOR SEQ ID NO:594:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 208 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(b) Topologi: Timear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:	
GAATTCGGCN TTCATGGCCT ACGGGGAACA GAGGATGGCG GAGGAGGGAA CACACAAGCA	60
GGAGCCCATG CAGCTGGGAG CCACTGAGAT CCCAGCTGGA GGAAGAGTGC CCTGGCACTG	120
AGGTCTAATG GCTGTCCAGC TGCTGCCCCA GGATGTGAGG GCAGGTGGTA GGCCATGAAG	180
GCCGATTGAA TTCTAGACCT GCCTCGAG	208
(2) INFORMATION FOR SEQ ID NO:595:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 120 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(wi) CENTENCE DESCRIPTION, CDO VD VO. COS	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:	
CAGGOTATILA AGIGNAMAG ATTGGATAGGAT GGAGANAGA TIGATAGGATAGA	
GAGCTATAAA ACAGAAATAC ATGCATAGCT GCAGAAACCA TGATAGGTAG AGGACTTTTC TTTTGGTTTT GTTTTGTTTT GTTTTTGTTTT TTACAGAGAA GAGACTCGAG	60 120
THE THE THE THE THE TENT OF TH	120
(2) INFORMATION FOR SEQ ID NO:596:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 282 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	•
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:	

GAATTCGGCC TTCATGGCCT AAGAAACCAA ATTAGCAGAC GGATAGAATA TAAAGCANGA GGCAATACTT ATAGTGTATT AAGAAACTTG CTAGACCCCA TCCAAATTAC TCAGTCTACT GTTGGTTGAT AGAATTACTT TAGGAAGAGT ACGTTTTTCC TTGGAAATAC ACTGGAAGTG GTACCAAACA AATCTAATAA AATGATGTTA AAGAGATTTG CAGTAATTTT TATCNACTTT CAGTTTGCAA ACTTTTATAA AGATATGAAA NGGACACTCG AG	60 120 180 240 282
(2) INFORMATION FOR SEQ ID NO:597:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 184 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:	
GGCCTTCATG GCCTAGACAC ATACAAAGAT AAGGCTTTGA TAAAATTCAA GAGTTATTTG TATTTTGAGG AAAAAGACTT TGTGGATAAA GCAGAGAAGA GCCTGAAGCA GACTCCCCAT AGTGAGATAA TATTTTATAA AAATGGTGTC AATCAAGGTG TGGCTTACAA AGACATTTCT CGAG	60 120 180 184
(2) INFORMATION FOR SEQ ID NO:598:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 370 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:	
GAATTCGGCC TTCATGGCCT ACTTTGAGTT AAATAGAGAG TTGATTAAAT GCATATATTG ACAGTTACTG ACTCAGTAAG CTTCATAATT CTAGGAATCA ATCACTGCTG ATTCATATGT TTAGATATAT TCATTTCTGT CTTTCTGTTT CTTAGGCCAA AAAGAAAAAA GAAAACCAAT ATTTAAGAGA AGAGAAAAAT GAAGACGGGA CATTTTGAAA TAGTCACCAT GCTGCTGGCA ACCATGATTC TAGTGGACAT TTTCCAGGTG AAGGCTGAAG TGTTAGACAT GGCAGATAAT GCATTTGATG ATGAATACCT GAAATGTACG GACAGGATGG AAATTAAATA CGTTCCCCCA ATCCCTCGAG	50 120 180 240 300 360 370
(2) INFORMATION FOR SEQ ID NO:599:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 376 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:	
GAATTCGGCC TTCATGGCCT AAGACTCTTA GATCTAAAAG GAAACTGACT TGCCACCTTG CCAGAGGAAT TCTTGAAATG TTTCTGCAGC CACTTGGCCT TGAAAATAAA GGGTGCAACT CTCAAATCTT GTTCTAACCC GGCTGGAGGA ACCACAAGAC CCAATGAAAT AGCATTTTCT CTCCTTTTCC CAGCACTAGT ATATAACCTA TGAGGAACCC TTGTCTCTGA ATCTGCTCAG	60 120 180 240

CTTGAAATTT	TGTCTCTGAA	GGAAGAGAAT	GATCTCAGCC	CTAGTCTGAC	AGTCCTAGAT	300
TTCTGTGAAA	TAAGAGTATT	CTTCAACTTA	GTGCTCACAC	TCACATACCA	TGAGGGTTCT	360
CTGCAGAGGA	CTCGAG		•			376

- (2) INFORMATION FOR SEQ ID NO:600:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 479 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

GAATTCGGCC	TTCATGGCCT	AAGTCACTAT	TTGGTAGCTG	ACTTTGTGCC	CTGATTAGAA	60
ACGTGGCTCC	TTTTCTGGT	AGTTGTTCTT	AGAACCTATC	AACCTGCAGA	GATTTTTATT	120
TTCATGGAAG	GGAACTGAGT	GTTTCTTTCT	TTGCTTCAGA	CGGTCACATC	TTTAGATCCT	180
GAAGGGAGAG	ATGCAGCTTG	CTCTCTCCAG	AGTCCAAATG	CAGCAACAGA	TTTTGCCTCC	240
ANGCAAGCAA	GATATGCTAT	AAAAACCTGC	NACATTCCTT	CACCAGCTCC	TCTCTTTGAA	300
TTTTCGATGC	CTCGATGGTC	ATTTCGAGAT	GACAGCTTGT	AGTGAGATAG	CTGTGGCATT	360
GGAAGGGGGG	AAGCATGCAC	CATTTTCCCT	AGGGCCTTCC	TGCTTTTGCT	TGATAAGCAA	420
TTCCTTGAAT	GGCATGTTCT	CCACCTCTAG	CCACTTTGTT	TGTAGTCCCT	ACTCTCGAG	479

- (2) INFORMATION FOR SEQ ID NO:601:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 483 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

GAATTCGGCT	TCATGGCCTA	CACAGGCATA	ACAGTCAGTC	GGGAAAAGGT	CACTGAAGTT	60
GCCCTTAAAG	GTGAAGGGAC	AGAAGAAGCT	GAATGTAAAA	AGGATGATGC	TCTTGAACTG	120
CAGAGTCACG	CTAAGTCTCC	TCCATCCCCC	GTGGAGAGAG	AGATGGTAGT	TCAAGTCGAA	180
AGGGAGAAAA	CAGAAGCAGA	GCCAACCCAT	GTGAATGAAG	AGAAGCTTGA	GCACGAAACA	240
GCTGTTACCG	NATCTGAAGA	GGTCAGTAAG	CAGCTCCTCC	AGACAGTGAA	TGTGCCCATC	300
ATAGATGGGG	CAAAGGAAGT	CAGCAGTTTG	GAAGGAAGCC	CTCCTCCCTG	CCTAGGTCAA	360
GAGGAGGCAG	TATGCACCAA	AATTCAAGTT	CAGAGCTCTG	AGGCATCATT	CACTCTAACA	420
GCGGCTGCAG	AGGAGGAAAA	GGTCTTAGGA	GAAACTGCCA	ACATTTTAGA	AACAGGTCTC	480
GAG					•	483

- (2) INFORMATION FOR SEQ ID NO:602:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 296 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

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GGGCCGTGCA GGCAGTGAAT CGGAAAGTGG AGATGATGAA TGAAAAGAAC TTGGAGAAAG
GACTGGGCGT GGACAGTGTG GACAAGGATG CCATGAACGC GGCCATCCAG CAGGCCATCA
                                                                      120
AGGCCCAGCC GTCCATGTCT CCCAAGAAGG CGCCCCCAGC GCCTGCAAAG GAGGCCAGGA
                                                                       180
ATGTCGTGGC CGTGGGTACT GGTGGCCGTG GGACCCACGA CCGAGACCCG AGTGAGAAAC
                                                                       240
CACCCCGGCT CCAGTGGTTT GAACAGCAGG CGAAGAAGTT GGCAAAGCTA CTCGAG
                                                                       296
(2) INFORMATION FOR SEQ ID NO:603:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 424 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: CDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:
GAATTCGGCC TTCATGGCCT AGAACTTTTT CATCTTTCCA AACAGAAATT CTATACCCAT
TAAACAGTAA CTCTCCCTTC ACCACTCTCC CCAACCCCGG AGACCTCTAT TCTATTTTCT
GTCTCTATAA ATTTGCCTAT TTTAGGTACC TCACATAAGT GAAATCATAT ATTTGCCCTT
TTGCATCTGG CTTATTTCAC TTAGCATGAT GTCTTCAAGG TTCATCCATG TGGTAGTAGC
                                                                      240
AGAATTTACT TCCTTTTTAA GACTAGCATA CTCACACTGT TTTTTTGTTT GTTTGTTTGT
TTGTTTGTTT TTGGGATGGA GTCTCACTCT GTTGCCCAGG CTGTGGTGCG GTGGTGCCAT
                                                                      360
CTCGGCTCAC TGCGGCCTCT GCCTCCCGGG TTCAAGTGAT TCTCATACCT CAGCCATCCC
                                                                      420
                                                                      424
(2) INFORMATION FOR SEQ ID NO:604:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 308 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:
GCGATTCGAT GTCCGTGCCC ACCTGGACCA CATCCCCGAC TACACCCCCC CCTCTGCTCA
CCACCATCTC CCCAGAACAG GAGTCGGACG AACGGAAGTG TAACTACGAG CGCTACAGAG
                                                                      120
GCCTGGTGCA GAACGACTTT GCCGGCATCT CAGAGGAGCA GTGCCTGTAC CAGATCTACA
                                                                      180
TTGATGAGTT GTACGGAGGC CTCCAGAGAC CCAGCGAAGA TGAGAAGAAG AAGCTGGCAG
                                                                      240
AGAAGAAGGC TTCCATCGGT TATACCTACG AGGACAGCAC GGTGGCCGAG GTAGAGAAGG
                                                                      300
                                                                      308
(2) INFORMATION FOR SEQ ID NO:605:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 506 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

60

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TGGTTGCTCC CATAACAACG GGCTATACGG TGAAAATCAG TAATTATGGA TGGGATCAGT
                                                                      120
CAGATAAGTT TGTGAAAATC TACATTACCT TAACTGGAGT TCATCAAGTT CCCACTGAGA
                                                                      180
ATGTGCAGGT GCATTTCACA GAGAGGTCAT TTGATCTTTT GGTAAAGAAT CTAAATGGGA
                                                                      240
AGAGTTACTC CATGATTGTG AACAATCTCT TGAAACCCAT CTCTGTGGAA GGCAGTTCAA
                                                                      300
AAAAAGTCAA GACTGATACA GTTCTTATAT TGTGTAGAAA GAAAGTGGAA AACACAAGGT
                                                                      360
GGGATTACCT GACCCAGGTT GAAAAGGAGT GCAAAGAAAA AGAGAAGCCC TCCTATGACA
                                                                      420
CTGAAACAGA TCCTAGTGAG GGATTGATGA ATGTTCTAAA GAAAATTTAT GAAGATGGAG
                                                                      480
ACGATGATAT GAAGCGAACC CTCGAG
                                                                      506
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- (2) INFORMATION FOR SEQ ID NO:606:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 522 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

GGTGGAATGA	AAGATATACC	TAGAACGCCA	TCTAGAGGGA	GAAGCGAATG	TGATTCTTCC	60
CCAGAACCGA	AAGCTTTGCC	TCAGACTCCT	AGGCCGAGGA	GTCGTTCTCC	ATCATCCCCA	120
GAGCTCAACA	ACAAGTGTCT	TACCCCCCAG	AGAGAAAGAA	GCGGGTCAGA	ATCATCAGTT	180
	CTGTGGCTCG					240
	TGAAACCCAG					300
GATTCTAAAG	CCAAGACACG	AACCCCACTT	CGGCAGAGGA	GTCGGTCTGG	ATCATCTCCA	360
	GCAAATCTCG					420
GTGAAAGATA	AGCCAAGAGC	AGCACCCAGG	GCACAGAGTG	GTTCTGATTC	CTCTCCTGAA	480
CCTAAAGCTC	CAGCCCCTCG	GGCCCTTCCC	AGACAACTCG	AG		522

- (2) INFORMATION FOR SEQ ID NO:607:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 320 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

GAATTCGGCC TTCATGGCCT	AGGCGCACCA	AGAGCAGGGC	TGTGTGTGGG	AGGCTGCAGC	60
CAGGATTGCC TCAGCTCCTC	CCCCTCAGGC	TGGGAGGATA	GCACAGGCTA	GGGGCTCGGG	120
GTGGAGGGTC TCAGCTCTGC	TGCCCCCACC	CCAGTACTAG	CCTAGCTTCC	CAAGCTGTGG	180
CTTAGAGGAT AGTTGGCTTC	CTGCCTCTCT	CCTCTAAAAT	AGCAAGTCTG	GGAAATCCTG	240
GGGTGAGTGG AGTCACCCCA	CTCCCAGTTG	CTGGCAGAGA	CTGAGACTAA	AGCATCACTT	300
AATAAACCCC CCAGCTCGAG					320

- (2) INFORMATION FOR SEQ ID NO:608:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 283 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

GAATTCGGCC	TTCATGGCCT	AGTTGTGTAT	TCTTTTCTCT	GTATCATATG	TGATAGTGGG	60
GTAGTGCCAA	ACATTGTTAA	CTCTGATGAA	TAATGTCTCT	TTTGGTTAGA	TCATTCTTAC	120
					ATGGCTGTGC	180
CAGCTGCCCG	<b>AAGCTAACTT</b>	GTGAGAGGGA	AGGTTGCCAG	ACTGAGTTCT	GCTACCACTG	240
CAAGCAGATA	TGGCATCCAA	ATCAGACATG	CGATCTACTC	GAG		283

- (2) INFORMATION FOR SEQ ID NO:609:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 287 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

GAATTCGGCC TTCATGGCCT ACACATGAG	T GTGACCTCTG	CCATGGGGAA	ACACACACAG	60
AGATATCTAT ACATATATAC ATACATACA	A ACATAGGCTA	TCTTGGCACA	CTAAATGCTA	120
AGCACTGTCT TAAGAGGTAG AGCTGGTGT	G AGTGAAATTA	ATGTTACATT	TTCCAGCTGT	180
AAACAGACAT CTGCATTTCC TAGTGAGCT	G CCAGGAGCCA	GATTCGGGAA	CCGTAACTGA	240
TGTGCCAGGA ATGGTGCATT GATTCCCAG	T TCCAGGGATC	TCTCGAG		287

- (2) INFORMATION FOR SEQ ID NO:610:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 356 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

GAATGATAGG TCCTAGG	GTTT AACAGGGCCC TATT	TGACCC CCTGCTTGTG GT	GCTGCTGG 60
CTCTTCAACT TCTTGT	GGTG GCTGGTCTGG TGCG	GGCTCA GACCTGCCCT TO	TGTGTGCT 120
CCTGCAGCAA CCAGTT	CAGC AAGGTGATTT GTGT	TCGGAA AAACCTGCGT GA	GGTTCCGG 180
ATGGCATCTC CACCAA	CACA CGGCTGCTGA ACCT	CCATGA GAACCAAATC CA	GATCATCA 240
AAGTGAACAG CTTCAAG	GCAC TTGAGACACT TGGA	AATCCT ACAGTTGAGT AG	GAACCATA 300
TCAGAACCAT TGAAAT	TGGG GCTTTCAATG GTCT	GGCGAA CCTCAACACT CT	CGAG 356

- (2) INFORMATION FOR SEQ ID NO:611:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 393 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

GAATTCGCCT TCATGGCCTA ACCACATGAT CCTTCGTGTT TCTTGCCTTC CATTTCCCTT

60

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GGGTGGATGG TTGGGTAGGT GGGGTTTCCT GGTTTGGGGT TTCTCAGACA AGGGCCCTCT
                                                                     120
AGGGAGGGTG CCCTGGACCC CCCACCACTC CTGGGCTGAG GAGCGTGTCA CATGATGCCG
                                                                     180
TTGGTGAGGT ACTGGAAGCC GTCATAGAGT TTGGTGGTGA TAGACCGCAT ACTGCCATCC
                                                                     240
ACCATCTGCT CCACCAGCAG CTGCAGCTGC TCCTCAGTCA TGCTCATGTG GAACCTCTCT
                                                                     300
TTGAGGTTNC GAATGGTGCT GGAGCCATGG AAGCAAGGAA GCTGAGAACC TTGTCCATGT
                                                                     360
GTTTCCGAGC GGCAATCAGC CCTTGCAGCA TCA
                                                                     393
(2) INFORMATION FOR SEQ ID NO:612:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 645 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:
GAATTCGGCC TTCATGGCCT AGGCGGGTTA AAGTCACATT TTTAAAAAGG CTAAACTCTA
AATTGCTGTA TTTGCTCTCT CTGGAGATTA ACAAAGTGCT TGGTTTGCAG ATTTGCTGGT
                                                                    120
ACGGTGATCT CAATGATATG ACCGAGGGTG GGAGGGATGT GAGGAGGGAA ATCGGCAAAA
                                                                     180
CCCTGGCCAG CCAGCCAGCC AAGGTGACAC ACAGCCAGAG GGGGCTCCCC TCTCCTCCTG
                                                                    240
CCGTCCGGCC ACGCTCACC ACGCTGTCCA CTGGGAACGC GGCCCCGCGG CCCGCAGAGT
CAGGCGTGAG CTTCGCCCTT TTCTGAAAGG GCCTCCGCCT GGGCAGGCGC CGGGGGGCAG
                                                                    360
TCCTCGGGTC CCATGGCTTA GGAGCACAGC ACTGACGGCT GCAGTGGCTC GAAAGGCTGA
                                                                    420
AATTCCACAT TGCTCTCTAG CGATCCCGCA CTGCTGCGAC GCCCTCGCTT CCCGGCTTCC
                                                                    480
GAGAGGTCCC GCAGGGAGCT GCTGAGGGCG CTGCGCTTGA GGCCCTCACC GCTGGCATAG
                                                                    540
CTGTCGTCCA GGCAGGCCCG GCTCAGTGTT TCCGTTGCCC GACTCCTTTT TGAGGCTAGA
                                                                    600
GCACTGGGAC ATGCTGGGCC GCACGACGCC TTTCTGCTTC TCGAG
                                                                    645
(2) INFORMATION FOR SEQ ID NO:613:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 337 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:
GCGATTGAAT TCTAGACCTG CCTCGCACCA CCCCAAATCC CACATCCTGC ACCCCTGCCT
120
GAGACAGAGT CTTGCTCTGT CTGTCGCACA GGCTGGAGAG CAGTGGCGCG ATCTCAACTC
                                                                     180
ACTGCAACCT TCACCTCCCA GGTTCAAGCA ATTCTCCTGT CTCAAGTGCC TAGATACCTT
                                                                     240
GGTAATGATT CCATTGGCCC CACCATGCCC TGTCCTGCCT TCCTGGCTGT GCCCAAGCTT
                                                                    300
GGTCCCTGCC TGCCTGCCTC ACTCTCTGGG TCTCGAG
                                                                     337
(2) INFORMATION FOR SEQ ID NO:614:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 431 base pairs
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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

GAATTCGGCC	TTCATGGCCT	AGGTTTTAGA	ATTTTATATG	AAGTATCTTA	TTTGATTTTC	60
ATAATAACCA	TAGAAGATAG	ATACTATTAT	TATCCTTGGA	TTATAGATGA	AATTGAAGAT	120
TGCTTCGCAG	GTAGAGTTAA	GATCCAGAAT	GGTGACAAGA	AGTATAATGT	CTGCTTTTAT	180
GCCATAATAT	ATCAGACTAT	TCTGACTCAT	TTAGATTACT	TCAGGGCTAT	CACTGAAGCT	240
TACAGTATTA	TCACTACTGT	GATACCCCTG	CTCACACAAT	TTGGTAAGTG	TTTTTGTATC	300
TTTTAGAACT	TATACATTAG	GCAGCAGCTA	TCTGTTTGGT	CAGCTGAAAG	ACGGCCACAG	360
GATTTGCTTC	TGGGTGGCCA	TTAGCACCTT	TCACCCATGC	ACCAGAGAGA	TACTTCCAGC	420
ACGAACTCGA	G					431

- (2) INFORMATION FOR SEQ ID NO:615:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 484 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

GAATTCGGCC TTCA	TGGCCT ACCAAAATTG	TGCATACCCT	TGGGATGAAA	ATCATTGTAA	60
	CAGGAN TATTTGAACA				120
	TTGTCT TGGTCCTTCT				180
	TCATGG CTTGCAAAAC				240
GTTTGATCCT CCTC	ATTATG AACTGTTTTC	ACTAAGGGAC	AAAGAGATTT	CTGCAGACCT	300
GGCAGACTTG TCGG	AAGAAT TGGACAACTA	CCAGAAGATG	CGGCGCTCCT	CCACCGCCTC	360
CCGCTGCATC CACG	ACCACC ACTGTGGGTC	GCAGGCCTCC	AGCGTCAAAC	AAAGCAGGAC	420
CAACCTCAGT TCCA	TGGAAC TTCCTTTCCG	AAATGACTTT	GCACAACCAC	AGCCAATGCT	480
CGAG					484

- (2) INFORMATION FOR SEQ ID NO:616:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 231 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: CDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

GAATTCGGCC	TTCATGGCCT	AGCGTTCCTG	GTTCCGTCCT	TGTACATAAT	ATTGTACAGC	60
ATTCAACCAC	TTTTGTCGAT	CAGCAAAGTA	GTCTCCAATG	GCATTGTTGG	CTTGTTCCAG	120
GAGACTGTCA	TCTGCATCAC	CAGATCCAGT	TTTCAGGAGC	TGGAGTACTC	TAAACCAATC	180
CCCCAATTTC	AGCCGGAGGC	CAATAGCAAG	ATCCCTTCTG	TCCATCTCGA	G	231

- (2) INFORMATION FOR SEQ ID NO:617:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 627 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:

GAATTCGGCC	TTCATGGCCT	ANAATGCTTC	ATGAACTNGC	NGACAGGACT	GACACAGCTN	6(
AGCTTTCCTG	ACTGATTCGG	GGCCATGCAG	TCTACCAAAG	GGCTAGCTGT	TGAGACAATG	120
AGGATCAGGG	ACATTTGCCC	TCGTTCTGAA	TGTCCCCAGC	CACAGTACNT	ACATNGTTCT	180
TACATGTACC						240
TTCCCTTTCT	NNTNGNGNNG	NACACTCACA	CCCGTCTCTG	NGAGGTGAGG	CCACATATTC	300
TCTTTTCTGG						360
ATAAAGGCAA						420
					CTCAAGGCCC	480
CAGGCACTTG						540
ATCTGGTAGA			GAGGTNCAGA	GGCAAGAGAG	AATTTGGCAT	600
ATTTGGGAAG	CTGCAAAAGA	TCTCGAG				627

- (2) INFORMATION FOR SEQ ID NO:618:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 130 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:

GAATTCGGCC	TTCATGGCCT	ACGACTTCAA	AAATATGGGA	ACACAGTTAG	TTATTTTTAC	60
ACAGTTCTTT	TTGTTTTTGT	GTGTGTGTGC	TGTCGCTTGT	CGACAACAGC	TTTTTGTTTT	120
CCTCAATGAG						130

- (2) INFORMATION FOR SEQ ID NO:619:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 495 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

GAATTCGGCC	TTCATGGCCT	ACTGGGGGAG	GGGAAGGATG	TGGTTTGNAG	AGNGGAAGCA	60
GAGTTTGGAA	ACGCATGAGA	GCAGAGCTTC	GTGTGTTCCC	ACCCTCANTG	AGGANGTGTG	120
AGTGGGTGAG	CATGTGAGAG	TTGGGTGTTC	CTACCCTCAG	TGAGGAGGTG	TGAGTGGGG	180
TGCATATAGA	GGCAGTGCCT	GCTGTGGGGT	CACAACTGGT	GCATGCCAGC	GCCAAAGGGA	240
CCTGTCTTTA	GGGGTCATTT	CAGCCAGCTC	CTCCCATCAC	AGATGACAGC	TCCAAGCCTA	300
GAAGGGGCTC	AGTGACAGGG	CCAGGACAAG	CCCTCAGGAC	TGTGGCCTCC	TGGCCCTTGG	360
TTCCCCTGCC	CCACAACATG	GTCTCCACAT	GGCTGGCTGG	CTGGCTGTCC	CTGTGTGTGT	420
GTGACACACG	GTGTGAGTGC	AGGGCTGTGC	CCGGGGTGGG	AGGGTGTCTA	TGTGGCACTG	480
ACTATCGAGC	TCGAG					495

- (2) INFORMATION FOR SEQ ID NO:620:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 348 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:

GAATTCGGCC	TTCATGGCCT	AGCTGATGAT	TCCAAACATT	TNGTAAATTA	ATTTTTCTCT	60
CTTTACCTTT	CAGCTTGGAA	GGAAGACAGA	AGCCTTAACC	TCCAGGGTAA	CATGTTGCAA	120
TTTGTTCACT	TATTAATCTA	ACAAGAATGC	ACTGAGGTGC	TCATTAAATG	TCAGACCTTG	180
TGTGAGGTTG	AGGAAATCCA	AAAGCAAAGG	AGGCATGAAC	CTCCATGCCC	ATTCAGAAGG	240
GCACCAGGCC	TTTTAAGAAG	GGTGGATATG	CACAATTTGA	AAATAACTGA	TAGTCCTGAC	300
TTATCTTTGC	AATTAATAAG	GCAATTTCAT	ACACATTTTA	TACTCGAG		348

- (2) INFORMATION FOR SEQ ID NO:621:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 294 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:

GAATTCGGCC	TTCATGGCCT	AGCAGGATGG	CACCGGACCC	CTGGTTCTCC	ACATACGATT	60
CTACTTGTCA	AATTGCCCAA	GAAATTGCTG	AGAAAATTCA	ACAACGAAAT	CAATATGAAC	120
GAAAAGGTGA	AAAGGCACCA	AAGCTTACCG	TGACAATCAG	AGCTTTGTTG	CAGAACCTGA	180
AGGAAAAGAT	CGCCCTTTTG	AAGGACTTAT	TGCTAAGAGC	TGTGTCAACA	CATCAGATAA	240
CACAGCTTGA	AGGGGACCGA	AGACAGAACC	TCTTGGATGA	TCTTGTAACT	CGAG	294
	CTACTTGTCA GAAAAGGTGA AGGAAAAGAT	CTACTTGTCA AATTGCCCAA GAAAAGGTGA AAAGGCACCA AGGAAAAGAT CGCCCTTTTG	CTACTTGTCA AATTGCCCAA GAAATTGCTG GAAAAGGTGA AAAGGCACCA AAGCTTACCG AGGAAAAGAT CGCCCTTTTG AAGGACTTAT	CTACTTGTCA AATTGCCCAA GAAATTGCTG AGAAAATTCA GAAAAGGTGA AAAGGCACCA AAGCTTACCG TGACAATCAG AGGAAAAGAT CGCCCTTTTG AAGGACTTAT TGCTAAGAGC	CTACTTGTCA AATTGCCCAA GAAATTGCTG AGAAAATTCA ACAACGAAAT GAAAAGGTGA AAAGGCACCA AAGCTTACCG TGACAATCAG AGCTTTGTTG AGGAAAAGAT CGCCCTTTTG AAGGACTTAT TGCTAAGAGC TGTGTCAACA	GAATTCGGCC TTCATGGCCT AGCAGGATGG CACCGGACCC CTGGTTCTCC ACATACGATT CTACTTGTCA AATTGCCCAA GAAATTGCTG AGAAAATTCA ACAACGAAAT CAATATGAAC GAAAAGGTGA AAAGGCACCA AAGCTTACCG TGACAATCAG AGCTTTGTTG CAGAACCTGA AGGAAAAGAT CGCCCTTTTG AAGGACTTAT TGCTAAGAGC TGTGTCAACA CATCAGATAA CACAGCTTGA AGGGGACCGA AGACAGAACC TCTTGGATGA TCTTGTAACT CGAG

- (2) INFORMATION FOR SEQ ID NO:622:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 304 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:

GAATTCGGCC	TTCATGGCCT	AGGTCAAGGG	ACAATGAAAA	TGTGACCCTT	ACCAACGACA	60
GAAACTCCCA	GGAAGCCACA	ATTAACTCAA	GACCACCAGG	ATATTTGGGG	AAGTTTATCC	120
TTCTGGAAAC	CAGAATTTCT	GATTTGTGGA	AAATTCTATA	GATATTCTCT	GCCAGACTCC	180
AGCCTATTTG	TGTGAGACAT	CTGGGGAGGC	TCCCCTTTTT	TTCACCATTT	GAGGACTGAA	240
AGTAAATTTA	GCTTCCTCAG	CAGAAAGAAA	AGAAGCTGTT	TTGGAGGTTA	GGAAGAAGCT	300
CGAG						304

- (2) INFORMATION FOR SEQ ID NO:623:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 497 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

GAATTCGGCC	NTCATGGCCN	ACTCTATTGG	TGCAAAGTAA	GATTTACATC	TGTGTTCAGA	60
ATCTTTGAGA	TAATACCCCT	TTTCTACATT	TCTGCATTTT	TTTTCTGTGA	NCCCCACTAG	120
TATTNCNCCA	TTTTNACCTT	TTCATTTAAC	TTATCCTCAC	ATTATAAGAG	ATGGATGACC	180
TATACAGACT	TGGCCTTTGG	GCTTTGGCTT	CATTCAATAT	CATCTTGGGT	ACCACTGAAT	240
ACCGTTCAAT	CTAGAGCTGG	GTGGTAGGTT	GAGATGTATA	TTTCCTAGCC	CAGATCCCAG	300
AATCTAGAAG	AAGTTAAATC	TGATATGACT	TTGATAAATA	AGACAGTATG	TTCTTCTAAC	360
CCCATCTCCC	GTTCTCTGAC	ACTGAACATA	TATATGAAGT	ATATATAACA	TATACCGAGT	420
ATTTAAAATT	TTAGAATAAA	AATGTGCATT	ACTGCACATC	TTCCTGTCTT	TCATTCTCTG	480
GTTGAGTTTC						497

- (2) INFORMATION FOR SEQ ID NO:624:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 331 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

GAATTCGGCC	TTCATGGCCT	AGAGCAAGCA	GAGGTGGCCT	GCGTGTGTAT	GTGCTCATGT	60
GTATGTGTGC	ACATGCATGT	CTGTGTGTGG	ATGCCCATGC	GTGTAACATC	TGATGTGGCA	120
CATGATACAA	CATAATTTAT	TTATTATAGA	AACCTGCAAG	TAAAGATTCA	AGAGGAATCG	180
CAGATCCCAA	TCAAAGTGCC	AAGTGGTAGG	TTACCCTGAC	AGATAGTACC	TCCCTTTTTT	240
ATTTTTCAAA	TGCTGGCATA	GTTTTGTGTT	CTTTACCAAC	TCATTGATTT	ACTGGGGACA	300
TCCTCTGTAC	TTATCACAAC	AGGTTCTCGA	G			331

- (2) INFORMATION FOR SEQ ID NO:625:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 334 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

GAAGTTGCAT	TACACCTTCT	CTTCTGAAGT	AAACACTAAA	AATATCAGGT	AACTTCTGCA	60
TTAAAATTTC	TGCCATCTGA	AGTGCTCCCA	CTTACTATCT	TCAGGTCTTG	GCTTGACAGC	120
ATGGAAGCAA	TGTGACTTGA	AACAGCATGA	TTTTTCAGAA	CATCCTTCAG	AAGTTCAGCA	180
TCCGCAAAAT	AAATTATCCT	AAGAATTGCT	CTAAGGCACT	TATGTCTGAC	CGCAGGTCCT	240
GCTGAGGAAC	TATACACTTC	ATAAAGAACA	CCAAATAATG	TCTTAATAAA	AGACTTAGCC	300
AGTTCCGGAT	CCTCTTTCAT	AAGCTGTGCT	CGAG			334

- (2) INFORMATION FOR SEQ ID NO:626:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 371 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:

GAATTCGGCC TTCATGGCCT AGTCGGATTC CCAGTGGAAC TTTAGTAGTA CTCAGATCCT	60
CCTTTGTTTG GTGCGTAGTA TATTAACAAG TAAACCTGCC TGTATGCTCA CCAGAAAGGA	120
AACAGAGCAT GTCAGTGCTT TGATCCTGAG AGCCTTTTTG CTTACAATTC CAGAAAATGC	180
TGAAGGCCAC ATCATTTTAG GAAAGAGTTT AATTGTACCT TTAAAAGGTC AAAGAGTTAT	240
AGATTCCACT GTATTACCTG GGATACTCAT TGAAATGTCA GAAGTTCAAT TAATGAGGCT	300
ATTACCTATC AAAAAATCAA CTGCCCTCAA GGTGGCACTC TTTTGTACAA CTTTATCCGG	360
AGACTCTCGA G	371
(2) INFORMATION FOR SEQ ID NO:627:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 522 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
() CROUTINGS BECCRIPTION CRO TO US CO.	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:	
GAATTCGCCT TCATGGCCTA GATGTTTCAA TTTCGAAGTA CTTTTGAACT TTAGTAATGT	60
CAGAGTTGAA CATTTTCTGT AGCATGACTA TCGACTTGTC TTTTCAAGGC AGCCTGCAAA	120
GCCATTGAAC AAGCAAAGAC TCAAAACATC AATAAACTGG TTCTGTATAC AGACAGTATG	180
TTTACGATAA ATGGTAAGCT TTCACATTTG ATTTCTTCTG TTTTTCCAGT AACTGTGAAG	240
GGAAATTGGT AGGAGGTGTT GTAACAGGGC AGGACCCAAA TGGGAACGGG GGGATGACAT	300
TGGTTTGTCA GGTACCGAGC AAAGAGTGAG GATTTTGGAG TCTCCCTTCT GCTGCTCTGA	360
TGTTTTCCAC ATGCTTATTT CTTTGCCAGG CACTGGAGAT GCAGTCAGAA GTGGAAGTGG	420
CTCTTACTTC TAGTCTGTGT GTGTATAAGT CACTTAAGAT GGCGTGTTGA CTGCTTCTTT	480
GGGAAATGCC CTGAATAGGA GCATGTAGGG GATGTGCTCG AG	522
(2) INFORMATION FOR SEQ ID NO:628:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 212 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
To the second se	

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:

GAATTCGGCC TTCATGGCCT	ACAAAATATC	TGTGGGAAGG	TGAGCTACTT	AGCATTCAAC	60
11TCC111CT TTC111CC1T					
AATGCAAAGT TTCAAAGCAT	TTTGCAAATT	TTAAATATAC	GCTATAATTC	TICTGTAATT	120
GGTGTCTTTG GTACTTTTTG	GGTAAATTGG	ACTTATTCCA	<b>אמדדממדממ</b>	ATTTTATACC	180
			MATTERITAL	VIIIIVIVOC	100
ACTITIGACA CCATAACACT	TAGCATCTCG	AG			212

- (2) INFORMATION FOR SEQ ID NO:629:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 358 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:

GAATTCGGCC TTCATGGCCT ACTCCTTCCG CGCGAGTCTC TGGAGAAGCC GCAGCGCGAG TTGCCGCCGC TGCTGCCGG GGCCGGCTTG CCTTGCGCCA TGGACTGGCA GCCAGACGAG CAGGGCCTGC AGCAGGTCCT GCAGCTGCTC AAAGACTCAC AGTCGCCCAA CACAGCCACT CAGCGCATCG TGCAGGATTA ACTCAAACAA CTCAATCAGT TTCCTGACTT CAACAACTAC CTGATTTTCG TCCTGACCAG ACTCAAGTCA GAAGATGAGC CAACGCGCTC TCTCAGTGGC CTCATCCTCA AGAACAACT GAAGGCACAC TATCAGAGCT TCCCACCCC CGCTCGAG	60 120 180 240 300 358
(2) INFORMATION FOR SEQ ID NO:630:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 168 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:	
AAGAGAACAA TAAAATAGGC AGTCTCCTAC CTCTTGTCTT ACTCTAATAT AAACTCCATG AAGATAAGTA TTGTATCCAT ACTGTTCATG CTGCACAGCA GTTGCCCTTA TCTGCAGGGC	60 120
GACGCATCCC AAGACCCCCA GTGGATGCTT GAAACTGCAG AACTCGAG	168
(2) INFORMATION FOR SEQ ID NO:631:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 477 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:	
GAATTCGGCC TTCATGGCCT ACATAACTGC ATTCTGACCT CCTTCTTGCA GTGCCAAGAG	
AAATGATGGT GAACTAAGTG CGGGGTGTGG GGTCGTTCTC AAAATGCGGT CATTGCTACA	60 120
GAACTAGGGT TTTTGGTTAG TTACATNCTT TGTGGAAGGA CAGGGTGGTG GGTACAGGTC	180
CCTGAGAAGC AGACATGTGG AATTGTTTGA GACAATCCTA CTCCCTGTGG TACTCTCTCT ATGTATATAT TCCAATGAAG GTAATTTACC TCATGCTTTC CTAAATACAT AAATCTTTAC	240
ATISTATATAT TUU AATISAAG GUAATTUACU TUATGUTTUU UU TUAAATAUAU AAATUTTUUU	300 360
ATTTCAAATG CCTTGTTAGA CTGTACTCAA GATTCCAGAG ACATTTTAAA ATAATTCATT	
	420 477
ATTTCAAATG CCTTGTTAGA CTGTACTCAA GATTCCAGAG ACATTTTAAA ATAATTCATT TTCAAATCAT AAATTTGGGA AANGGGGCCC TGGGATAAGC AAGTTGACTG GGCCACTGCT	420
ATTTCAAATG CCTTGTTAGA CTGTACTCAA GATTCCAGAG ACATTTTAAA ATAATTCATT TTCAAATCAT AAATTTGGGA AANGGGGCCC TGGGATAAGC AAGTTGACTG GGCCACTGCT TATGCCATTC CCTGCACAAT TCTGGGCATG GAGCAGCTCT CCCAGAGCCC ACTCGAG	420
ATTTCAAATG CCTTGTTAGA CTGTACTCAA GATTCCAGAG ACATTTTAAA ATAATTCATT TTCAAATCAT AAATTTGGGA AANGGGGCCC TGGGATAAGC AAGTTGACTG GGCCACTGCT TATGCCATTC CCTGCACAAT TCTGGGCATG GAGCAGCTCT CCCAGAGCCC ACTCGAG  (2) INFORMATION FOR SEQ ID NO:632:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 330 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	420
ATTTCAAATG CCTTGTTAGA CTGTACTCAA GATTCCAGAG ACATTTTAAA ATAATTCATT TTCAAATCAT AAATTTGGGA AANGGGGCCC TGGGATAAGC AAGTTGACTG GGCCACTGCT TATGCCATTC CCTGCACAAT TCTGGGCATG GAGCAGCTCT CCCAGAGCCC ACTCGAG  (2) INFORMATION FOR SEQ ID NO:632:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 330 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	420
ATTTCAAATG CCTTGTTAGA CTGTACTCAA GATTCCAGAG ACATTTTAAA ATAATTCATT TTCAAATCAT AAATTTGGGA AANGGGGCCC TGGGATAAGC AAGTTGACTG GGCCACTGCT TATGCCATTC CCTGCACAAT TCTGGGCATG GAGCAGCTCT CCCAGAGCCC ACTCGAG  (2) INFORMATION FOR SEQ ID NO:632:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 330 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:	420 477
ATTTCAAATG CCTTGTTAGA CTGTACTCAA GATTCCAGAG ACATTTTAAA ATAATTCATT TTCAAATCAT AAATTTGGGA AANGGGGCCC TGGGATAAGC AAGTTGACTG GGCCACTGCT TATGCCATTC CCTGCACAAT TCTGGGCATG GAGCAGCTCT CCCAGAGCCC ACTCGAG  (2) INFORMATION FOR SEQ ID NO:632:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 330 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA	420

TTCAACAGTA ACAGCAACAA CAGTCAACAA CAACTTTGAT GATGACTACT GCTTCGATGT CTTCGATGGC TCCTACCCGT TTCTCCCACT GGTGGAACAT TCCCAGCCTC NGTCTCCTGC TCTAGGATCC CCGACCCATT AAGACTCGAG	240 300 330
(2) INFORMATION FOR SEQ ID NO:633:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 391 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:	
GAATTCGGCC TTCATGGCCT AGGAGAAGGC CCTGCAGGCC GCATATGGCG CCAGCGCCCC CAGTGTGACC TCGGCTGCCC TCCGGTGGAT GTACCACCAC TCACAGCTGC AGGTAACCAG CGACCCTGGG TGCTCAGCTT CTTCCCTTCC	60 120 180 240 300 360 391
(2) INFORMATION FOR SEQ ID NO:634:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 505 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(D) TOPOLOGY: linear	
(D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA	60 120 180 240 300 360 420 480 505
(ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:  GAATTCGGCC TTCATGGCCT AAGTACAAAT ACCTATTATG TTGGTTGGGA ATAAGAAAGA CCTGCATATG GAAAGGTGA TCAGTTATGA AGAAGGGAAA GCTTTGGCAG AATCTTGGAA TGCAGCTTTT TNGGAATCTT CTGCTAAAGA AAATCAGACT GCTGTGGATG TTTTTCGAAG GATAATTTTG GAGGCAGAAA AAATGGACGG GGCAGCTTCA CAAGGCAAGT CTTCATGCTC GGTGATGTGA TTCTGCTGCA AAGCCTGAGG ACACTGGGAA TATATTCWAC CTGAAGAAGC AAACTGCCCG TTCTCCTTGA AGATAAACTA TGCTTCTTTT TTCTTCTGTT AACCTGAAAG ATATCATTTG GGTCAGAGCT CCCCTCCCTT CAGATTATGT TAACTCTGAG TCTGTCCAAA TGAGTTCACT TCCATTTTCA AATTTTAAGC AATCATATTT TCAATTTATA TATTGTATTT	120 180 240 300 360 420 480
(ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:  GAATTCGGCC TTCATGGCCT AAGTACAAAT ACCTATTATG TTGGTTGGGA ATAAGAAAGA CCTGCATATG GAAAGGTGA TCAGTTATGA AGAAGGGAAA GCTTTGGCAG AATCTTGGAA TGCAGCTTTT TNGGAATCTT CTGCTAAAGA AAATCAGACT GCTGTGGATG TTTTTCGAAG GATAATTTTG GAGGCAGAAA AAATGGACGG GGCAGCTTCA CAAGGCAAGT CTTCATGCTC GGTGATGTAT TCTCTGCTGCA AAGCCTGAGG ACACTGGGAA TATATTCWAC CTGAAGAAGC AAACTGCCCG TTCTCCTTGA AGATAAACTA TGCTTCTTTT TTCTTCTGTT AACCTGAAAG ATATCATTTG GGTCAGAGCT CCCCTCCCTT CAGATTATGT TAACTCTGAG TCTGTCCAAA TGAGTTCACT TCCATTTTCA AATTTTAAGC AATCATATTT TCAATTTATA TATTGTATTT CTTAATATTA TGACCAAGAC TCGAG	120 180 240 300 360 420 480
(D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:  GAATTCGGCC TTCATGGCCT AAGTACAAAT ACCTATTATG TTGGTTGGGA ATAAGAAAGA CCTGCATATG GAAAGGGTGA TCAGTTATGA AGAAGGGAAA GCTTTGGCAG AATCTTGGAA TGCAGCTTTT TNGGAATCTT CTGCTAAAGA AAATCAGACT GCTGTGGATG TTTTTCGAAG GATAATTTTG GAGGCAGAAA AAATGGACGG GGCAGCTTCA CAAGGCAAGT CTTCATGCTC GGTGATGTGA TTCTGCTGCA AAGCCTGAGG ACACTGGGAA TATATTCWAC CTGAAGAAGC AAACTGCCCG TTCTCCTTGA AGATAAACTA TGCTTCTTTT TTCTTCTGTT AACCTGAAAG ATATCATTTG GGTCAGAGCT CCCCTCCCTT CAGATTATGT TAACTCTGAG TCTGTCCAAA TGAGTTCACT TCCATTTTCA AATTTTAAGC AATCATATTT TCAATTTATA TATTGTATTT CTTAATATTA TGACCAAGAC TCGAG  (2) INFORMATION FOR SEQ ID NO:635:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 325 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	120 180 240 300 360 420 480

60

CACAGCCCCT GAGCTCCAGA TTTCCACCTC CACAGACCAA CCTGTCACCC CTAAGCCCAC ATCTCGGACC ACTAGGAGCA GGACAAATAT GTCCTCTGTG AAGAACCCTG AATCAACTGT CCCTATAGCC CCTGAGCTC CACCTTCCAC CTCCACAGAG CAGCCTGTCA CCCCTGAGCC CACATCTCGG GCTACTAGGG GAAGAAAAAA TAGATCCTCT GGCAAGACCC CTGAAACACT TGTCCCCCACA GCCCCTAAGC TCGAG	120 180 240 300 325
(2) INFORMATION FOR SEQ ID NO:636:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 201 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:	
GAATTGGCCT TCATGGCCTA GCTTCCTCTT CAAAAATGTG TCTACCTAAG ATACTATTAT TTAAGCCTCT GTGTACTTTT AACCGTAGAA CTGATTTTAT AGGAAGACGA AACTTGTCGG CTTTCAAGAC ATGGAGTGT TGCCTTGTGG AGACCCTCCT CCTCCTTACG AACCGCACTC TCATCCACAA AGAACCTCGA G	60 120 180 201
(2) INFORMATION FOR SEQ ID NO:637:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 417 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(x1) SEQUENCE DESCRIPTION: SEQ ID NO:637:	
GAATTCGGCC TTCATGGCCT AGGCAAAGCC TGAAAGTCCT TGGACTTCTC TGACCAGAAA GGGAATTGTT CGAGTTGTAT TTTTCCCCTT TTTCTTCCGG TGGTGGTTAC AAGTAACATC AAAGGTCATC TTTTTCTGGC TCCTTGTCCT TTATCTTCTT CAAGTTGCTG CAATAGTATT ATTCTGCTCC ACTTCTAGCC CACACAGCAT ACCTCTGACA GAGGTGATTG GGCCGATATG GCTGATGCTG CTCCTGGGAA CTGTGCATTG CCAGATTGTT TCCACAAGAA CACCCAAACC TCCTCTAAGT ACAGGGGGTA AAAGAAGAAG GAAATTAAGA AAAGCAGCCC ATTTGGAAGT ACATAGGGAA GGAGATGGTT CTAGTACCAC AGATAACCAC CAAGAGGAAT GCTCGAG	60 120 180 240 300 360 417
(2) INFORMATION FOR SEQ ID NO:638:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 351 base pairs  (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(C) STRANDEDNESS: double	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	

GCCTTCCCGC TCTTCTCTGC CTTTGGCCGG GCGCTCAGGT ACCACACAGG CTCCCTGGCC 300 TTTGGCGCGC TCATCCTGGC CATTGTGCAG ATCATCCGTG TGATACTCGA G (2) INFORMATION FOR SEQ ID NO:639: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 567 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:639: GAATTCGGCC TTCATGGCCT AATTTTTTTG AGACAGAGTC TTACTCTGTT GCCCAGGCTG 60 GAGTGTGGTG GTGCGATCTC GGCTCACTGC AACCTCTGCC GCCTGGGTTC AAGCTATTCC 120 CTGCCTCGGC CTCCCAAAAT ACTGGGATTA CAGGCGTGTG CCGCTGTGCC CAGCCGCTGT 180 CTAGTCTTTT AAAACTTGGT GTTTGAGCAT GCACATTCTC CTTCTGGAAT ACCTGATCAC 240 CCAGCACAAC TCACGTTNTC TTTCTGCTGG CTACCCTTGC CTTGCTGTGA CTGTGTCATG GTTCTCAGCT AGACTCGGTG GCGTGTTTGA TGGCCCAGGC ATCGTCTGCC CAGTGGGTGT 360 CCTGTTACCC ATGTATGACA GACTGTACCC AAGATATCAG TCTTACGAAT AAGGCCACGA 420 TGAACACTTT GAGCTTTTTC TGTATCTAGC ATATCCCCAG GGTAGATGCT CAGGCAGGAA 480 ACTGGTGGGA GATGAGGGAT ACACAGATGG CTCCCNACAG GTGCTGTGAG GTGCTCAGGA 540 GTTTATCATC ACTTAACTGA GCTCGAG 567 (2) INFORMATION FOR SEQ ID NO:640: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 474 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:640: GAATTCGGCC TTCATGGCCT AGCTCCGCAN AGGTAGGGAG GGAAGGGCCC CTCAAATANA TGGAGGGAGC AACATCCCTC CAAGGGAAAG GGCTTCCAAN ACNAAATCCT GGACAGAAGC 120 GGAGCANGGG ATGGGCCTCC TTACAGAGCA GGAGGAAGAC AGCGCTCTTC NAANANGAAA GGAGAGGGGC ATCAAGGTCC CTCACAATGG TGGAGGGGGC GGGGCTTCTC ACCGAAGGCA 240 GAGGAGGGG CCTTAACTGA GGGGCAGGGC GCCTCCCAGG GATGAAAGGA GGAGGCCTGC 300 CGCAGAGCAG GGAAAAAGTT CAGTCCTTTC CTGCATTTCT TGGCTGAAGG GGTCTTAAGA 360 TGAAGGGTTC AGTGTCCAGA AGGAAAAAAC CCTGAGATGG GCCTAGACCA ACATGAACTC 420 AGCTAGCAAG TTCATACATG ACATGGGACT GATAGACTTG TGTGGCATCT CGAG 474 (2) INFORMATION FOR SEQ ID NO:641: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 278 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:

GAATTCGGCC	TTCATCCTTG	AGAATATCAG	AATTAGAAAG	CCAGGTTGTT	GAAATGCATA	60
CTAGTTTGAT	TTTAGAAAAA	GAACNAGTAG	AAATTGCAGA	AAAAAATGTT	TTAGAAAAAG	120
AAAAGAAGCT	GCTAGAACTA	CAGAAGCTAT	TGGAGGGCNA	TGAGAAAAA	CAGAGAGAGA	180
aagaaaagaa	AAGAAGCCCT	CAAGATGTTG	AAGTTCTCNA	GACAACTACT	GAGCTATTTC	240
ATAGCAATGA	AGAAAGTGGA	TTTTTTAATG	AACTCGAG			278

- (2) INFORMATION FOR SEQ ID NO:642:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 413 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:

AGGGAGAGGA	GGCTGGGAAC	AACGTGACCC	ACTAAGGATT	CTGCTCCAAG	GACAGTGGGT	60
TTCCCGCTGG	GCACCCACTC	TTAAGTGCAG	ATCGGGAGAC	TAAGACAGGA	ACACCCGCCG	120
TGGGCAGGCC	AGGCTGGAAG	GATAGAGGAC	TGTGGTCGAA	CCAAGAGGAG	GTTCAACTGT	180
GACTTATGCC	AGTGTGGTCA	CGAAGGCAGA	TGGGTTGAAC	TGAAAAGGGG	GCACCGGTTC	240
CTGGCATGGA	GGCACCCAAG	GTCTTAGGAG	GTGGATGGAC	TGTCACATGG	GCAAAGAAAT	300
GTCCCAGGGC	AGGACTGCAA	AGGCCACAGA	AGAATAATTT	GGGAGAGA	CAACCCATGA	360
GAAGTCACTC	AGACCAGGGT	CAGAAACAGA	ACAGGAACAA	CAATGGACTC	GAG	413

- (2) INFORMATION FOR SEQ ID NO:643:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 658 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:

TTTCNTCCCT	TNGAATGTTT	GTCCCTTTTT	CCTGTTTTTT	TTTCGCACAA	AATTNCAAGT	60
TNTACCAAGC	AAACATTAAA	TCCAAGTTGG	AATTTTAATT	AAGGAATTCG	GCCTTCATGG	120
CCTACTGGTG	CCTTCCCGGA	AGGGCTCAGA	GGCGGGCTCG	GGCAAGCACT	TTAACCTTTT	180
AAGCCCAACC	AGATGAGTTG	CCTGCAGTTT	TGGAGGCCTT	CAGAGCATTT	CACTAGACCT	240
CTGTCTGTGT	CGGTCCAATG	TCTTTAGCCA	AGCTTTGATT	AAAGATGACT	TCCTTGTTTG	300
CTCAAGAAAT	TCGCCTTTCT	AAAAGACATG	AAGAAATAGT	ATCACAAAGA	TTAATGTTAC	360
TTCAACAAAT	GGAGAATAAA	TTGGGTGATC	AACACACAGA	AAAGGCATCT	CAACTCCAAA	420
CTGTTGAGAC	TGCTTTTAAA	AGGAACCTTA	GTCTTTTAAA	GGATATAGAA	GCAGCAGAAA	480
AGTCACTACA	GACCAGGATT	CACCCACTTC	CACGGCCTGA	GGTGGTTTCT	CTTGAGACTC	540
GTTACTGGGC	ATCAGTAGAA	GAATATATTC	CCAAATGGGA	ACAGTTTCTT	TTAGGAAGAG	600
CACCATATCC	TTTTGCTGTT	GAAAATCAAA	ATGAAGCAGA	AAATACCATT	CCCTCGAG	658

- (2) INFORMATION FOR SEQ ID NO:644:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 282 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:

GAATTCGGCC TCATGGCCTA CCAAAGAGTG TTATACATGC TCAGCAAACA ATATCTACAG GAACTAGCCC TCAGGAAAGT AAAAAAAAAA	60 120 180
ACTCCATGAC AAAAAATACA AAGGAGAGAA TGGGAGCTCG AG	240
ACTECATORE AMAMATACA AMOGRAGARA TOGGAGETEG AG	282
(2) INFORMATION FOR SEQ ID NO:645:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 172 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
·	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:	
GAATTCGGCC TTCATGGCCT ACCTTTCTCT GACCTGTGCC CTCGGCCTCT TGGCCTCCAT	60
CGCCATGACC TTTGCCACCC AGGGCAAGGC ACTGCTGGCT GCCTGCACTT TTGGGAGCTC	120
TGAACTACTG GCCCTCGCAC CTGACTGTCC CTTCGACCCC ACACCACTCG AG	172
(2) INFORMATION FOR SEQ ID NO:646:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 293 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:	
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GAATTCGGCC TTCATGGCCT ACCAGAAACC GGCCAGGCAA GGAAAGAGGC CGGTCACCAG	60
AAGCCAGCAG GCGTGGGGTG TGATACTCTC TATAGCCACT ACAGGGCGCG CGCAGGTCGC	120
GGATCTCCCC AGTTGCTAAT CCCGGCTCTG CCACTCAATC CTATCCCTAG TTCCCGAGCG	180
CGGGTCCCCC GCCTTGCAGT CTCCAGCCGT GCGGGGCCGG GAGCAGGCCT CCGGCCTCCC	240
AGACTTCTAG AGCCCGCCGG GCCCATCTTT GTACTCATCC ACCCCGGCTC GAG	293

- (2) INFORMATION FOR SEQ ID NO:647:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 272 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:

GAATTCGGCC	TTCANGGCCT	ACAGAAACAG	AAATGCTAAC	TGAAATGTAT	TCTTCTAACA	60
AAGCATTTCT	<b>AACTTTCTAG</b>	AATGTAGTCT	TTCATTTTTC	TTTATCTTTT	TTCAGCTTAT	120
TCCCAAATAT	ATACTTTGGC	CATTTAAATA	AATGGCCAAA	GAAATGGCCA	AAAAATGCTT	180
TATTTAGTTT	TTGTTTTATT	ATGAAGGATG	ATTACTCTTT	AATGCTGCTA	AATTCTTTTC	240

TAGCTCTGTA TTTCACTTCA AGAAAACTCG AG

272

(2) INFORMATION FOR SEQ ID NO:648:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 256 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:	
GCGAGCTGTT GGGATTACAA AGTTGCGCGT TTCATCGGTA CAAACTGGTC TTTGAACCTC	60
CTTTGTGAGA GCAATTGTAG TGTCCAAATT GTTAGGGAAA ACAAAAAAA AAAATCCCAA	120
GGAGGAGGGT TTTTCCCCCT TCCCTGTTTG GTTTATCACA GCATTTTGCT TTTTTTTTGG CACAGCTTTT TACGTTTCTT TCCATTCAGC CATCACAGAG CCTGTTCCGG GTGGAAACCA	180 240
ATCCACACGC CTCGAG	256
(2) INFORMATION FOR SEQ ID NO:649:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 266 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:	
GAATTCGGCC TTCATGGCCT ACCCACCTTG GCCTCCCACA GTGCTGGGAT TCCAGGCGAG	60
AGTCCCTGCG CCCAGCCCCA CTTGTCTATT CTTGTTTTTG CTGCCTGTTT TTGGTGTCTTT	120
ATCTGCACAT GAATATTTAT AGCAGCTTTA TTCATAATTG CCAAAACTTG GAAGAAACCA	180
CAATGACAAT GTCCTTCTAT AGGTACACCC ATACAATGGA ACATTCAGTG ATAAAATGAG CCATCAAGCC ACCCAAAAGG CTCGAG	240 266
CONTINUOU ACCUMANDO CICOMO	200
(2) INFORMATION FOR SEQ ID NO:650:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 490 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(x1) SEQUENCE DESCRIPTION: SEQ ID NO:650:	
GATTTCTCAG CTTTTGAACA GAGTGGACTT GTCAATATCA GAGCAGAGCA	60
GATGTCTCAC AGAGACAGTA ACCACCAGCT TCAGCTTTTG GACACTAAAT TTAAAGGTAC	120
AGTTGAGGAA CTCAGTAACC AGATATTATC TGCACGGAGT TGGTTGCAAC AGGAACAAGA ACGGATAGAA AAAGAGCTTT TACAGAAAAT TGATCAGCTT TCCTTGATTG TTAAGGAAAA	180 240
CAGTGGAGCC AGTGAAAGGG ATATGGAGAA GAAGCTCAGC CAGATGTCAG CCAGGCTTGA	300
CAAAATAGAA GAGGGTCAAA AGAAGACTTT TGATGGTCAG AGAACAAGGC AAGAAGAGGA	360
GAAGATGCAC GGGCGAATCA CCAAGCTGGA GTTACAGATG AACCAGAACA TCAAGGAAAT	420
GAAAGCAGAA GTTAATGCTG GGTTTACAGC CGTCTATGAA AGCATAGGAT CCCTCAGGCA AGTTCTCGAG	480 490
	200

98/45 <b>43</b> 5	PCT/US98/06954
(2) INFORMATION FOR SEQ ID NO:651:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 498 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:	
GAGATAGAGG GGACCCTGGC TATGGACATT TTGAATTATG TCGGGAGAGC AGAGGCTCCN GGAGACTGG TTAAACTGAA GCCNGGAATG AGATGAAATG TCTTGAATGA TTATGAATAT CGTCAGAAAC AAATCNTAAT GGAAAATGCA AGGTTCTCA ACAAATGAAA AAGGAAATGA TTTNTCTTCT TTCTCCCCAA CTCGAGAAAG AGTAGATGAT AGTACAGGAA CTGTTAATTC CGATGTTGAA GGGAACTAAG CAGAGAGAGT ATGTGGGACC TTTCCTTGGA AACTGTGAGA AACTGTAAAA GGTACACCTG GAAGGTTTTA ATGATGAAGA TGTAAATCCA ATGAACAAGA AACTGAAA	TATAAAATTC         120           GAACTTAAGA         180           AAGAAGAAAC         240           GAAGATGCCN         300           GAGCAGCTTA         360           CTTGATAACC         420
(2) INFORMATION FOR SEQ ID NO:652:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 203 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:	
GAATTCTTCT TTCTCTATAA ATTTGCCTAC TATTGAAGAT TCTTCAGAGG GAGAGAGAA GAAGAATTAT TAAAGGAGCA AGAAAAGCAG AGGGAAATAG AAGAAAGAGT TCTAGTAAAA AATCAAAGAA AGACAAAGAT GAACTTCGAG AAGGGAAAGG CCAAAGACTC GAG	AACAGCAACA 120
(2) INFORMATION FOR SEQ ID NO:653:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 242 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:	

GGAAAGAAAN	GGACAAACCT	ATAAATTAAC	TCAACCTATA	TCTCCCTTGA	AAATACTTTC	60
AGGCTCCACC	AAAACGTAGA	ACTGAAAGCA	TGTATTTTGG	AAGAAAGAGA	TACATTTTGT	120
	TTCCTTTTGT					180
GTCACCAGCC	CTGGGACCTG	AGACCAAGGG	GGTGTCTTGT	GGGCAGTGAT	GGGGNCCTCG	240
AG						242

(2) INFORMATION FOR SEQ ID NO:654:

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 241 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	•
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:	
GATTCGGCCT TCATGGCCTA GGGAGGAGAA GAAGGGGGAG AAATCACAAA GAGATTGGGG AGGAGATGAA GTAGCAGGGC TCAGCGATTC TTTCAATTCC AGTGCACACC CAATAGTGTG TTGGAAGAAT GCACACTGTT CGGGATTTGT GGGAGAATTG TCCCATGACA AAGGAGGCAG GGTTATGCTT GTTATAGTCC AATAAGCCGT GCCAGTCAAA CAAGAACCCA CACTCCTCGA G	60 120 180 240 241
(2) INFORMATION FOR SEQ ID NO:655:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 278 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:	
GAATTCGCCC TTCATGGCCT AGTGGTGAGA CTGAGCAGAT TTAATTAATG TCTGTTATGT TCAGGGCACA AGGGTGAGCT CTTCGCAGGG GCTGATGCAC TGGGTGTGGA GCTGAGCAGA GAGGCCTAAC CAGGATCAGG CAGGAGGGCA GGGATGGTG CAGCCATAGG AGGGCAGGGT AGGGTAGGGC CTCTGAGGAG GAGGGAAAAA GTGAAGGAGA GGCTTTGGAC CTGGTGACAG AGTGATCAGA TGACAGAGGG GTTTTTGGGA GACTCGAG  (2) INFORMATION FOR SEQ ID NO:656:	60 120 180 240 278
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 224 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:	
GGAAGGAGAA GTGGAGAAGA AATCAGTCAG CCGCAGTGAA GAGCTCAGAA AAGAAGCAAG ACAATTAAAA CGGGAACTCT TAGCAGCAAA ACAAAAAAAA GTAGAAAATG CAGCAAAACA AGCAGAAAAA AAGAAGTGAA GAGGAAGAAG CCCCTCCAGA TGGTGCTGTT GCCGAATACA GAAGAGAAAA GCAAAAGTAT GAAGCTTTGA GGAAGCAACT CGAG	60 120 180 224
(2) INFORMATION FOR SEQ ID NO:657:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 253 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:	
ATACAGTAAT CAAAGTAAGT AATATTTCAA TCCAATATTT TTAAAAATCA GAATTAATGC AAAAAAAAACC ATGATGAACA AAATATTAAA ATTTAAAAATA AAGACAGGAT TAGTATTACT GAGTTTTCCT TTTGTCCCAG GCTCTAATAT GGCTTGGCAT GGGGCAGAAC ATTACAACAT ACCAGTCGTG TCATGGTGCC CAAGGCTCCA CAGACCTCAG TGGCTCCCTG CTGCCTGCCA CAGCAATCTC GAG	50 120 180 240 253
(2) INFORMATION FOR SEQ ID NO:658:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 244 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:	
GAATTCGGCC TTCATGCACT TTTGAGCATC AGTTTCTTTT CACTCCTTCT TCATGTGCTA TTCCTTCCAA ATCTTTCCCA CCTTCTTCCT TCTCTCCTT GTCTTTTCCT CTCCCTTCT TGTTGTTCTC TGGTTTCCAT CTGTTTCTCC TTCTCCTTCC CCATTCTCA CTATCCTCTC TTCTGTCTCC TCACTTACTT CTCCATCCCT CCTCTCCCA GCCCTCTCTC CCCCCTGTCT CGAG	60 120 180 240 244
(2) INFORMATION FOR SEQ ID NO:659:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 75 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:	
GAATTCGGCC TTCAGCCTAG TCTCAAACTT CAAGCAAACC TCCTGCAATC CCAGCGCTTT AGGAGGCCGC TCGAG	60 75
(2) INFORMATION FOR SEQ ID NO:660:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 450 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:	
GCNTTCATGG CCTAAGTTCA CCTTTAANTC TTTCATGACC ATTTCCAGAN GCCCTTACCG TGGGCTATCT TAGCTTGATG TGCTAATCAA GTTCCCCCTA ATTTGACATA CTAGAATCTA ATACTAGAGG CAGCATGACA TTATTAAGGG GGAGGAGGTT GAGAAGCACT AACCTCGAAG	60 120 180

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TTAGAATTTC TGGTTTGTCA TCCCAGTCTG CTAATTAGCT TTCTGATTTA AGACAAAATA
CTTTTTCTGT GCCTTCTGGG GGTCAAATTC GATTTTTAAG ATTCTCTCAG TTGGAAGAAA
                                                                      300
TCTAACTAAA AATATACTTA AAATAATTCT TTGGTAGTAT ATTATTTTGA AATTTGGTCC
                                                                      360
AGAATCCTAT TTGTTTATTC CTGTAGTATA CATACATCTG TAGTTACCCA GCAAGCGCGC
                                                                       420
TCCCTATAGT GAGTCGTATT AATTTCAGAG
                                                                       450
(2) INFORMATION FOR SEQ ID NO:661:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 495 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:
GAATTCGGCC TTCATGGCCT AGAGAAAAA AATTAGAGTG ATTTCAGGAC TCAAAGGAAG
AGCCTTGCAA AGAGTTGGGA GGATTAAACT CTATGGATTT AAGCTCTGCC TGCAAAATAA
                                                                      120
CATCGCTGGG AATTTAGACA CAAATTAGGA ATATTCTGGA ATTCATTTAG CAGCAAATCT
                                                                      180
CCTGACTAGT TGTCAAATGG AGCTGTTCTA ATTGGCCTGT TCTAAATGGG CCTGTCCTAA
                                                                      240
TTGCAGAAAT ATTGCAGAAT ATGTTTTTAG TAAGCTCTCT ATAGAAAGTC ACCTCTGAGT
TGCTCAGCAT TTAGATTCAA ATATTCAAAT GTTTTTTAAA AATGCCAGCA TATCAATTAT
                                                                      360
ATTTGAAGAA CAGTATAGAG GCTTGAAACA TGCCAAACAG CAGGGAACAG GAATAACCTT
                                                                      420
TAATGAGTGC CTACTCTGGT GCAGGGTCCT TTACACACAT TACATTATGT GATCTTCACA
                                                                      480
ACAAACCGAC TCGAG
                                                                      495
(2) INFORMATION FOR SEQ ID NO:662:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 474 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:
GAATTCGGCC TTCATGGCCT ATAGGCCATG AAGGCCGGCC TTCATGGCCT ACGAGGAAAG
                                                                       60
GTCAGAGAGA TGCGAAGTTT CTGGCTTTGA AGATGGGGAA AGGTCTCCAG CCAAGTGTGA
GCAGCCTCTA AGAGTCAGAG AAGCCAAGGA ACAGCTTCTA CTCTAGAGCC TCCAGAAGGA
                                                                      180
TGGCAGCTCT GCTGATGTCT GGCCTTATCT CAGGGAGCCC TGTTGGATTT TGAGCTGGTG
GAACTGTGAG ATAATGACTG TGGTGTTTAA GCCAGTAAGT TGGTGTAATT TGTTAATGTG
                                                                      300
ACTGCAGAAA CCCAATAGAC CGAGTGCGTG TTGGGCTCTC CCTGTACAAA GGCAGAGGGA
                                                                      360
CAGCAAGTGT GAGCAGGCCC TGCTGTGAGG TAGAGGGCAT CCTCTGAAGT GTGTGGGGAA
                                                                      420
GGGGGAGCCT CACATGAGCC CAGGGCTGCC ACATGTTCAG TCTGAGCGCT CGAG
                                                                      474
(2) INFORMATION FOR SEQ ID NO:663:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 360 base pairs
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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

GAATTCGGCC TTCATGGCCT ACTCTACTCG TGCGGTGCTT CTTCTCCTTG GCATACAGCT CACAGCTCTT TGGCCTATAG CAGCTGTGGA AATTTATACC TCCCGGGTGC TGGAGGCTGT TAATGGGACA GATGCTCGGT TAAAATGCAC TTTCTCCAGC TTTGCCCCTG TGGGTGATGC TCTAACAGTG ACCTGGAATT TTCGTCCTCT AGACGGGGA CCTGAGCAGT TTGTATTCTA CTACCACATA GATCCCTTCC AACCCATGAG TGGGCGGTTT AAGGACCGGG TGTCTTGGGA TGGGAATCCT GAGCGGTACG ATGCCTCCAT CCTTCTCTGG AAACTGCAGT CAACCTCGAG	120 186 240 300 360
(2) INFORMATION FOR SEQ ID NO:664:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 379 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:	
GAATTCGGCC TTCATGGCCT ACCCTGTGAA AGTGGTGCCT GACTGTCTGA GGAGGGACGT GGGCTAGAGA GTTCTCCCTG GGCTCAGGAA GGATAGCTTG GTTGGTAAGG GAATGCAGTG TGGATGACAC TGAGGCTGCC AGAGGTCTTG GGTTGGCTGC TCCTAGGTGG CTTGATGAAA ATGGGAGGAC CAGAAGAATT GGAAGTTGCA GCCAACTGAT GGCTGCTACT GAAGATTCCT GACAGGAAAT AGAAAATAGG ATGTAAGACC CTCCTCTCCT	60 120 180 240 300 360 379
(2) INFORMATION FOR SEQ ID NO:665:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 206 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:	
GAATTCGGCC TTCATGGCCT AATCACACAC CAACAAAACA CATTTATTT GTAATTTATT TTCTCCTGAT ATTTATGCTA GAAAAGTCCA TTTGTATTTC TTTTACTATG GCATGTTTTT ATAGGTTCTG TCTTATTTTT ATTAAGTTCA TGTTTTTACT CTTCATTATC AGGAGTTCCT ACCATATTTT ATTNGCAAGC CTCGAG	60 120 180 206
(2) INFORMATION FOR SEQ ID NO:666:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 469 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:666:	
GCCGATGAGG ACCAAGATNA AAACAGTGCT CAAAAGTCGT GGCCGCCCAC CTACAGANCC GCTGCCCGAC GGGTGGATCA TGACATTCCA TAACTCTGGA GTCCCGGTGT ACCTACACAG	6( 12(

AGAGTCTCGG GTGGTCACCT	GGTCCAGGCC	ATACTTCTTG	GGAACGGGAA	GCATACGGAA	180
ACACGACCCT CCTCTGAGTA	GCATCCCTTG	TCTGCATTAT	AAGAAAATGA	AGGACAACGA	240
GGAACGGGAG CAAAGCAGTG	ACCTCACCCC	TAGTGGGGAT	GTGTCCCCCG	TCAAGCCCCT	300
GAGCCGATCT GCAGAGCTGG	AGTTTCCCCT	GGATGAGCCT	GACTCTATGG	GTGCTCACCC	360
GGGGCCCCCG GACGAGAAAG	ACCCACTAGG	GGCTGAGGCA	GCCCCTGGGG	CCCTCCCCCX	420
GGTGAAGGCC AAAGTCGAGG	TGTGCAAAGA	TGAATCCGTT	GATCTCGAG	CCCIGGGGCA	469

- (2) INFORMATION FOR SEQ ID NO:667:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 331 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:

	TTCATGGCCT					60
ACTTCTCCAG	CAATTTAAAC	GGGAGGAGGT	GTCCCCAACA	GGGAGTTTCA	GTGCCCACTA	120
CTTGTCGATG	TTTCTCTTAA	CTGCTGCCTG	CTTATTTTTC	CTAATACTGG	GACTGACTTA	180
CCTAGGAATG	AGAGGGACAG	GAGTATCTGA	GGATGGAGAA	CTCAGCATAG	AAAACCCCTT	240
TGGTGAAACA	TTTGGAAAAA	TACAAGAAAG	TGAAAAAACT	CTTATGATGA	ACACATTATA	300
TAAGCTTCAT	GATCGATTAA	CACAGCTCGA	G			331

- (2) INFORMATION FOR SEQ ID NO:668:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 471 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:668:

GAATTCGGCC	TTCATGGCCT	AGGACCCAAA	GTCCGCGTGG	AACCGCGATA	GGGATCTGTC	60
AGGGCCCGCG	GCCGGGTCCA	GCTTGGTGGT	TGCGGTAGTG	AGAGGCCTCC	GCTGGTTGCC	120
AGGCTTGGTC	TAGAGGTGGA	GCACAGTGAA	AGAATTCAAG	ATGCCACCTA	ATATAAACTG	180
GAAAGAAATA	ATGAAAGTTG	ACCCAGATGA	CCTGCCCCGT	CAAGAAGAAC	TGGCAGATAA	240
TTTATTGATT	TCCTTATCCA	AGGTGGAAGT	<b>AAATGAGCTA</b>	AAAAGTGAAA	AGCAAGAAAA	300
TGTGATACAC	CTTTTCAGAA	TTACTCAGTC	ACTAATGAAG	ATGAAAGCTC	AAGAAGTGGA	360
GCTGGCTTTG	GAAGAAGTAG	AAAAAGCTGG	AGAAGAACAA	GCAAAATTTG	AAAATCAATT	420
AAAAACTAAA	GTAATGAAAC	TGGAAAATGA	ACTGGAGATG	GCGCACTCGA	G	471

- (2) INFORMATION FOR SEQ ID NO:669:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 389 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:669:

GAATTCGGCC TTCATGGCCT AGAGAGGTTG CTCATTCGTC AGAGCGTGCT GCCCACCCTC CACCCCTGCA TGGCAGAAAC TGTGCAGGGG ACGAGGGCCAA GGAATCAGGA GACCCAGAGG CAGGGGTGGC CCGGAGACGG TGAAGAAACC AAGACGCAGA GAGGCCAAGC CCCTTGCCTT GGGTCACACA GCCAAAGGAG GCAAGACCCAG AACTCACAAC CAGATCCAGA GGCAACAGGG ACATGGCCAC CTGGGACGAA AAGGCAGTCA CCCGCAGGGC CAAGGTGGCT CCCGCTGAGA GGATGAGCAA GTTCTTAAGG CACTTCACGG TCGTGGGAGA CGACTACCAT GCCTGGAACA TCAACTACAA GAAACGGAGG TATCTCGAG	60 120 180 240 300 360 389
(2) INFORMATION FOR SEQ ID NO:670:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 209 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:	
GAATTCGGCC TTCATGGCCT AGTGTCACAA AATATAGAAA GAAAAGAACA AACAAAAAAA GAGACAAAGGCT TTTTGAAATA AAAGAGAGCT AGCAATGCAG TACATGGTCC TTGCCCTATT ACTATCCATC CTCATCCTAG CAATAATCCC CATCCTCCAT ATATCCATAC AACAAAGCAT AATATTCGC CCACTCGAG	60 120 180 209
(2) INFORMATION FOR SEQ ID NO:671:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 271 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:	
GAGTTCATTC AAGATATTTT TCACTTGCTG TTCAGGAGCT TTGATGTGCG TCACCATTCC TGGCATGTTC ACGCTGTTCC TGTGCAGGTA TTTCAGGAAG ACGTCTGCAT TCCTCCGAGC AAGGGTGCAA GCCTTCAGGA ATGCCTCCTT CTGCTCCAGG TGCTTGCTGA TCATGGGCGT CACGTGGTCC GTCTCAGAGT TTGGGCCCAG CTTATCCGCC CCGCCACACC AGTCTTCTTC TCTCTTGTAC TCCCTGTTCC AGGCTCTCGA G	60 120 180 240 271
(2) INFORMATION FOR SEQ ID NO:672:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 382 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:672:	
GAATTCGGCC TTCATGGCCT AAGATAAATT TGACAAAGTT AACTGAAATT TATCTGGTCC ATTTTATTCA TGCTACTAAG ATGGGAATCT TTAAACACAA GGGTCAGCAA GCTTTGGCCC ATGGATTGGC CACCTGTTAC GTAAATAAAG TTTCTTTGAA ACAAGCCTAC ACTCATTCAT TTATGTTTTTG TCTGTGGTTG CTTTCCACAA CTGCAGAGTT GTATGGCTTG CAAGTCTAAA	180

AACATTTACT ATTTGGCCCT CTAAGAAAAA GTTAAGACAC CTAGTCTAAT GGCCTTTTGG GAAAAAACAA ATCACTAACT CATAATCATT TATATCCATT ATTTTCTGCA TAAATGTAAT GCTATTGTAC AGGGTACTCG AG	300 360 382
(2) INFORMATION FOR SEQ ID NO:673:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 526 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:673:	
GAATTCGGCC TTCATGCCTA CCAAATTTGT CTAAGCACTG GCCAGTCTGT TGTGGGCATT	60
GTTTTCTACA ACC.AATCTG GGTTTTTTTC TTCTTTCTTT AAACATAGAG GTACCACCAC	120
AAGGGATGCC CTACTCTCTC GCAGCTCTTG AAAGCATCTG TTTGAGGGAA AGGTCTCTGG GCAAGCAAGT GGTTATTTGG ATTGCTTGCT TCCCTTTTTC CACCTGGGAC ATTGCAATCA	180
TARAMANA CONTAINING AND CONTAINING CONTAININ	240
TAAAATAACA GTAAATTCCA AACCTCAAAA ACTATTATGG CCTGAGCACA GCTGAAATCT	300
AGCAGAGTTT AACTCTTCTG CCTCCATGTC TGTCACTTAT AATTCAGGTT CTGCTGTTGG	360
CTTCAGAACA TGAGCAGAAG AATCGTTTTA TGCTAGTTAT TGCATTCATG GTTGAAACTC	420
AACTTAGGGA AAGGGTTCCA ATGTATTAAG CAATGGGCTG CTTCTCCCCA ATCCTCCCTA	480
ACAATTTGTT GTGTGGACTT CTCATCTAAA AGGTTAGTGA CTCGAG	526
(2) INFORMATION FOR SEQ ID NO:674:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 131 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(b) TOPOLOGI: Timear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:674:	
GAATTGCTTC TCAATTTACC CGAGATTTCA TTCGAGATTC AGGTGTTGTC TCACTTATTG	60
AAACCTTGCT TAATTATCCA TCCTCTAGAG TTAGGACAAG TTTTTTGGAA AATATGATTC	120
ACTGGCTCGA G	131
(2) INFORMATION FOR SEQ ID NO:675:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 352 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(x1) SEQUENCE DESCRIPTION: SEQ ID NO:675:	
GAATTCGGCC TTCATGGCCT ACCTAATCTT CCTTTTCTTT TTAGCATTTT TGGGCTTTTC	60
AAAGCAATCT CCCCAAAAAA AGAATCATTT GGTTTTGGAA AAGAAAACAG AATCAGCAAC	120
TTTTCGGGTG TGTGGTGAAA ATGTCACGTG TGTGGAATAC GCTATCTCCT GGCTACAAGA	180
CCTGATTGAA AAAGAACAGT GTCCTTACAC CAGTGAAGAT GAGTGCATCA AAGACTTTGA	240
TGAAAAGGAG TATCAGGAGT TGAATGAGCT GCAGAAGAAG TTAAATATTA ACATTTCCCT	300

GGACCATAAG AGACCTTTGA TTAAGGTTTT GGGAATTAAC AGAGGACTCG AG

352

(2) INFORMATION FOR SEQ ID NO:676:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 251 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:676:	
GAATTCGGCC TTCATGGCCT AAACCCATAA AACAGGAATT CCTTATAATC CTAGAGGACA AGGCATTATA GAATGGGCAC ATCAAACATT ACAACGAATG TTGAAAAGAC AAAAAGGGGG TATAGGAGGC CAACTACCAC CTCAATCAAA ACTACATTTA GCCTTATTTA CTTTAAAATT TTTGACTCCT GGTACGGATG GTAAGACTCC AGCAGAAAGA CATTGGCAAG TGTTAGAGGA AAAGACTCGA G	60 120 180 240 251
(2) INFORMATION FOR SEQ ID NO:677:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 331 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:	
GGGCATTTGC AGTTTTCTTC CCTGCTGCAT GTAATGTCTC AGAATCAACA TTCTTTTAAA ATCTAGACTA TATTTTGAGG CAATGAATTA CTTATATTCA ACTTAGGCTT GTTTTGACAT TCAGTAGAAC TTTAAGTTCA ATCTAAAGGC TTCAGTCCAC ATTTTTTTAT ACGTTGTATT TTAAAAACGT TTGAAAGGAG TCTTACACCT GTATCATGAA AACTGAATCC TTTTGAAATA CCACTATATG AAGAGAGAGA TGAAATTTAG TGAACAGAAT TGAAAAGGTG CTCATAATTT CACTATGCAA ACTTACCCCA GTCAACTCGA G  (2) INFORMATION FOR SEQ ID NO:678:	60 120 180 240 300 331
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 262 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:	
GAATTGAACA ATGCTGACAG GCTGGTANTC CTGCCCTGAA GCAACTCACA GACTCATAGT TATAGAACAT CTTTATCTTT AGTTAATCCA TNGCACAGCA TTGGCCAAGG GTCAATACCT TGTAATAAGC ATGTGTGTAT TGGTCAGGGT TCTACAGAGA GACAGATCAA TAGGAGCTAT CGATAGATAT AGACATATGA GAGGGGGTTT GTTAGGGGAA TTAGCTCACT TGATTACAGA GGTTGAGAAG TCGCTCCTCG AG	60 120 180 240 262
(2) INFORMATION FOR SEQ ID NO:679:	

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(i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 336 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: double
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:
GAATTCGGCC TTCATGGCCT AGCAGCCCGA GGCCTTGAGG CCACTGCCTC CCCAGGGCTC
                                                                        60
CTGAAGCCAA AGAATGGAAG TGGTGAGCTG AGCTACGGAG AAGTGATGGG TCCCTTGGAG
                                                                       120
AAGCCTGGTG GAAGGCACAA ATGCCGCTTC TGTGCCAAAG TATTTGGCAG TGACAGTGCC
                                                                       180
CTGCAGATCC ACCTTCGTTC CCACACGGGT GAGAGGCCCT ATAAGTGCAA TGTCTGTGGA
                                                                       240
AACCGTTTTA CCACCCGTGG CAACCTCAAA GTGCATTTCC ACCGGCATCG TGAGAAGTAC
                                                                       300
CCACATGTGC AGATGAACCC ACACCCAGTA CTCGAG
                                                                       336
(2) INFORMATION FOR SEQ ID NO:680:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 389 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:680:
GAATTCGGCC TTCATGGCCT AAATTAAAGA TGATTTTTTT AATGTGAATA AAGTTATGTT
                                                                        60
CTGATAGTTT GTACAGAAAA AATAAAATGG ATGCCCATGT TTTATTGCTA TTACTAAATG
TCAAGATTGT ATGCTATTAT GTCTTGTAAA TTTCTTTTGT TGGTGTAAAT ATGGAAATGC
                                                                       180
CACATTGGTT AAGTGCCATC ATTTGTAATG CAATGTGTCA CTTGAAAAGA GATTTGAAGA
                                                                       240
AACTGACAAC TTCAAAAACA AATGAGAAGC CCAAGGAACT GTGAGCAATT AAAAGCAAAC
                                                                       300
CGCGACACCC TTTGTCTCCA CCACACATAG TGTACTTTGG AAGCACAACG TCCAGGCTGG
                                                                       360
TACCGCAGCG CCATGCCCAT TCCTCGCCG
                                                                       389
(2) INFORMATION FOR SEQ ID NO:681:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 400 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:
GATTTCTCTG TTGACTTCTG CAGTGAACCA CCTCAAAGCC AATGTTAAGT CAGCTGCAGA
CTTGATTAGC CTGCCTACCA CTGTAGAGGG ACTTCAGAAG AGTGTAGCTT CCATTGGCAA
                                                                       120
TACTTTAAAC AGCGTCCATC TTGCTGTGGA AGCACTACAG AAAACTGTGG ATGAACACAA
                                                                       180
GAAAACGATG GAATTACTGC AGAGTGATAT GAATCAGCAC TTCTTGAAGG AGACTCCTGG
                                                                       240
AAGCAACCAG ATCATTCCGT CACCTTCAGC CACATCAGAA CTTGACAATA AAACCCACAG
                                                                       300
TGAGAATTTG AAACAGGATA TCCTGTACCT TCACAACTCT TTAGAGGAGG TAAACAGTGC
                                                                       360
CCTAGTGGGG TACCAGAGAC AGAATGATCT TAAACTCGAG
                                                                       400
(2) INFORMATION FOR SEQ ID NO:682:
```

(i) SEQUENCE CHARACTERISTICS:

```
(A) LENGTH: 311 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA.
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:
GGAGATCGAA AATTGAAACT CTCAAAGAGA CAACAAATAG CATGGTAGAA TCAATTAAAC
                                                                       60
ACTGCATTGT GTTGCTGCAG ATTGCCAAAA GTACTATTAA TCCCGTAGAT GCAATATATC
                                                                      120
AACCTAGTCC TTTGGAACCT GTGATCAGCA CAATGCCTTC CCAGACTGTG TTACCTCCAG
                                                                      180
AACCTGTTCA GTTGTGTAAG TCAGAGCAGC GTCCATCTTC CCTACCAGTT GGACCTGTGT
TGGCTACCTT GGGACATCAT CAGACTCCTA CACCAAATAG TACAGGCAGT GGCCATTCAC
                                                                      300
CACAACTCGA G
                                                                      311
(2) INFORMATION FOR SEQ ID NO:683:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 308 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEO ID NO:683:
GTGAGGGGTT CCGTGACTGA GGTTCTGAGC TGCTGTTGAT GTGCTATACC TCCTTCAATT
CTCAGCTCTC AAAGGGGAAA ACAACTGCAG AGGATGGGAA ATGCTATACT GCCATGCCTG
                                                                      120
GAAACACCCA CAGGAAAATT ACCAGTTTTG AGCTTGCTCA ACTGCAAGAA AAACTGAAGG
                                                                      180
AGACAGAAGC AGCCATGGAA AAATTAATCA ACAGAGTGGG ACCTAATGGT GAGAGAGCAC
                                                                      240
AGACTGTGAC TTCTGACCAA GAGAAACGGT TGCTACATCA GCTCCGAGAA ATCACCAGAG
GTCTCGAG
                                                                      308
(2) INFORMATION FOR SEQ ID NO:684:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 448 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:684:
GCTCCGGACA ATGAAACATA ACCAATACTA CCAATCAATA CTCATCATTA ATAATCATAA
                                                                       60
TGGCTATAGC AATAAAACTA GGAATGGCCC CCTTTCACTT CTGAGTCCCA GAGGTTACCC
                                                                      120
AAGGCACCCC TCTGACATCC GGCCTGCTTC TTCTCACATG ACAAAAACTA GCCCCCATCT
CAATCATATA CCAAATCTCT CCCTCACTAA ACGTAAGCCT TCTCCTCACT CTCTCAATCT
                                                                       240
TATCCATCAT AGCAGGCAGT TGAGGTGGAT TAAACCAAAC CCAGCTACGC AAAATCTTAG
                                                                       300
CATACTCCTC AATTACCCAC ATAGGATGAA TAATAGCAGT TCTACCGTAC AACCCTGACA
                                                                       360
TAACCATTCT TAATTTAACT ATTTATATTA TCCTAACTAC TACCGCATTC CTACTACTCA
                                                                       420
ACTTAAACTC CAGCACCACG GGCTCGAG
                                                                       448
(2) INFORMATION FOR SEQ ID NO:685:
```

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 312 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685:	
GTTGACAAAC AAGCTCAAGC TGCGGATAAA ATGAAGGAGC AGGAAGACCT GGCCAAGGTG GTATCTAAAG AAGAATCAAT TGTTTCATCA TTACGATTAG CCTATAAGGA TCTTGAAATT CAAATGAAGA AAGACGAAAA GATGAACATT AGTGGCAAAA AAAATGTTGA CTCAGACAGA CTCGGCATGG GATTTGGAAA TTGCAGAAGT GTTATTTCAC ATTCAGTGAC TTCAGATATG CAGACCATAG AGCAGGAATC ACCCATTATG GCAAAACCAA GAAAAAAGTA TAATGATGAC AGTGAACTCG AG	60 120 180 240 300 312
(2) INFORMATION FOR SEQ ID NO:686:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 264 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686:	
GTAATGGCAC AATGGATTCA AATGGGACAT TTGTTAATGT AACAATGAGC ACATTTAACT GGAAGGATTA CATTGGAGAT GACAGTCACT TTTATGTTTT GGATGGGCAA AAAGACCCTT TACTCTGTGG AAATGGCTCA GATGCAGGCC AGTGTCCAGA AGGATACATC TGTGTGAAGG CTGGTCGAAA CCCCAACTAT GGCTACACAA GCTTTGACAC CTTTAGCTGG GCTTTCCTGT CTCTATTTCG ACTCATTCCT CGAG	60 120 180 240 264
(2) INFORMATION FOR SEQ ID NO:687:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 277 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:687:	
GGGAACAGCA GTTCCTATGG CTTTTTTTT TTTTTTCTG TGTATGAGCA ATTCGACTCA GTGGGATGAT ATTTTCTTT ATAACTCATT AATGTTTGCG ATACCGTGTA CTCAAATATT CAATGTCAGC TGTCAGCTAC CATTGGGATC CATCCCACAG ACCATCAAAA TGTACTTTTG GGCTGAATTA GTCCTATGCC AAGACTTGTG GGTGGATCCA GCAGCAGTTG GGAACCACGT GCCAGGCCTG GTGTATGTGC TCACGAACAC ACTCGAG	60 120 180 240 277
(2) INFORMATION FOR SEQ ID NO:688:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 393 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:

GAATTCGGCC	TTCATGGCCT	AAATAGTTTA	GTTCTCTGGT	GCAATTTGAA	GTATATCTTA	60
TAGTCACTTT	TAGTAATGTG	TGTTACTTCC	CTGTAAGGAA	TAGCAATGTT	ATACTTCTCC	120
TTTTGCAGTG	AAGAAATTGA	GATGTAGAAA	GGAAGAGACC	TGCCCAAGGT	CAAAGAGCAA	180
GGCAGTGGAA	AGCCTGAGAT	TAGACTTGTG	GTCTTTTAGA	TTTTTCATCT	GTTGTTCACC	240
ACTGAGGAGC	CAGCTTTCTG	TTTGCTGGAG	ACAGTTCAGC	CTAATGGAAT	TTTCTCTGCC	300
				CTAATACCCA	TTCTCCTCCA	360
AAGTGGCCCT	TTAGTTCCCC	ACCAGAACTC	GAG			393

- (2) INFORMATION FOR SEQ ID NO:689:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 477 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:

GAATTCGGCC	TTCATCCCCT	D CALCALLCACC	TOOTOOONON	CACACCCOMM	GGGMG3 GGGG	
						60
AGGGGGTCAG	GGGGTGAGGG	AAAGGCTCTG	TCTGGGAGGA	GCAGAACAGC	AGAAGAGAGG	120
AGGAGGCAGG	GAGTTACAGG	AACCTGGGGT	ACCAGGCTGC	TGGGAAGATG	CAGATTATGA	180
CAGAGCTTGC	ACGATGCTGG	CACCCCATGC	CAACCACTCT	ACGTGGCTTT	CCTCTTCGGA	240
GAGGTGGTGG	GCTCCCTTCT	TCACTGTGCC	CTCCCTCCTC	TGGCCACTAG	GGGTGGGAAA	300
TACGAGTGAG	AATCCTTCCA	GATTTACTTC	CGCCAATCCA	GAGGTACAGG	CTTTTAGGCA	360
AGGGGCAGAG	AACTGCCCAA	TTTGCTGCTT	CATGGCCTAG	GGGTGGGGTT	CCTTAGGAGC	420
TGAAAAGTTG	AACAAGGTGT	GTGAGCAGGT	GGCTTGTTCC	TTGGTTTCAA	GCTCGAG	477

- (2) INFORMATION FOR SEQ ID NO:690:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 598 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:

GAATTCGGCC	ATCATGGGCT	AAGACGTGGT	ANTGACATGC	CTGTAGACCC	AAGTATTTGG	60
GAGGCTGAGG	TGAGAGGTTC	GCTTGAGCCC	TGGAAGTCGA	GGCTTCAGTG	AGGCAAGATC	120
ACACCACTGC	ACTCCAGCCT	GGGAGAGCAA	GACCCTGTCT	CCAAAACCAA	AAAAAAAGGG	180
AAAAAAGTAA	ATGTTATAGA	TACTTGCTAA	GGGCTTTGTA	TATACTTATT	ATTGTTATTT	240
CTCAGCACGT	ATGTAGCAGA	TGAGGAAATG	AAGGCTAAAG	GTCATATATN	TACAAAGTGG	300
GGAGGTCAGA	CTTTGAACCC	ACAACCTGAC	TGTGGAGCCA	CTTCAGTATA	CTCTCTCCCC	360
ATAAGAAAGT	TCCAATAGAA	AAAAAATGCT	ACTTAAGTAG	GGAAATCACA	AAATAAGTGC	420
CAATGAACAA	TAAATGTTCA	ACCTCACTAC	AGTTAAAATG	TATATTAAAG	CAAGAGTTGA	480
GATGACACTT	TTCCTTATAA	AACAGACAGG	GATTCAGGGA	CATTGGGACT	CTAATGCTGC	540
TGGTAAGACA	TGAATAAATA	CATACCATCT	CTGGCAATCA	ATACCAGAAG	ATCTCGAG	598

(2) INFORMATION FOR SEQ ID NO:691:

(i) SEQUENCE CHARACTERISTICS:

```
(A) LENGTH: 406 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:691:
GAATTCGGCC TTCATGGCCT AGTTCTCCCT TCCATTCTGC CCTTGTATCT TTGCAGTCAT
                                                                       60
TGTATACAGC AGATTCTAGA AAGTGTTAAT CATTGTCACC TAAATGGCAT AGTTCACAGG
                                                                       120
GACCTGAAGG TCAGTATATG GAGTCCATAA ATCTGAATCA AAGCAGTTTT ATTTTTTTT
                                                                       130
CTGGGGAAAG GGCAGAGGGT GGGTATTTAA AATGGTTCCC TTGCCTTTCC CAACTTGTTT
CTAAAATGAG TAAATGATGA AATGATAATG CATGATGCCT CTTCCAGTTT GCTCATCTAC
                                                                       300
AGGCTAAATA TACATCATAG CAAAAAGGGA AGAATACTAA AGAATACAAC CTGCTAAGTT
                                                                       360
TCCAAGCAGT AAACTACCTA CCAAAAGGGA TTGAGGATCC CTCGAG
                                                                       406
(2) INFORMATION FOR SEQ ID NO:692:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 263 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:692:
GTCCTGGAAG AATGTGTCCA GCAACCCAAA AACTAATAGA AGAGTCACAG AGAAAAATGA
ACGCTTTATT TGAAGGTAGA CGCATCGAAT TTGCAGAACA AATAAATAAA ATGGAGGCTA
                                                                      120
GGCCTAGAAG ACAATCAATG AAGGAAAAAG AGCATCAGGT GGTGCGTAAT GAAGAACAGA
                                                                       180
AGGCGGAACA AGAAGAGGGT AAGGTGGCTC AGCGAGAGGA AGAGTTGGAG GAGACAGGTA
                                                                       240
ATCAGCACAA TGATAGACTC GAG
                                                                       263
(2) INFORMATION FOR SEQ ID NO:693:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 404 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEO ID NO:693:
GCCGCCGAAG AAGCATCGTT AAAGTCTCTC TTCACCCTGC CGTCATGTCT AAGTCAGAGT
                                                                       60
CTCCTAAAGA GCCCGAACAG CTGAGGAAGC TCTTCATTGG AGGGTTGAGC TTTGAAACAA
                                                                       120
CTGATGAGAG CCTGAGGAGC CATTTTGAGC AATGGGGAAC GCTCACGGAC TGTGTGGTAA
                                                                       180
TGAGAGATCC AAACACCAAG CGCTCCAGGG GCTTTGGGTT TGTCACATAT GCCACTGTGG
                                                                       240
AGGAGGTGGA TGCAGCTATG AATGCAAGGC CACACAAGGT GGATGGAAGA GTTGTGGAAC
                                                                       300
CAAAGAGAGC TGTCTCCAGA GAAGATTCTC AAAGACCAGG TGCCCACTTA ACTGTGAAAA
                                                                       360
AGATATTTGT TGGTGGCATT AAAGAAGACA CTGAAGTCCT CGAG
                                                                       404
(2) INFORMATION FOR SEQ ID NO:694:
     (i) SEQUENCE CHARACTERISTICS:
```

- (A) LENGTH: 299 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:694: GAATTCGGCC TTTCATGGCC TACTGGATGG CTTTTTATCT TTTGCTTTTC TTTTATGGCA 60 GATGCCTTTC CATCGGCATC CCAGCTGTGG CTGGGGACGT TTTGGGAAGT GTGTTTGGCT CACTCCGAGA GAACGAGGTC TCAAGAGGAA GTGTGTCTGG CTTGCAAAGA TGTCCCTGGG 180 CCTGGACAGG ACCCCGCTGT GTTCTGCAGC CCTCGACGCA GTGGGTGAGT GAGGCCTTCC 240 TCTCCTGCTG GCTGCCCTGG AGGATTTCAA CATGTCCCAG GATTTGCTCC ACCCTCGAG 299 (2) INFORMATION FOR SEQ ID NO:695: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 468 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:695: GAATTCGGCC TTCATGGCCT ACCTGTTGAA AACTCTCCAA TGACTTCCCA CTCCATCATC 60 CTGTGGGATG GGTCCACCAT GCTGGACCAC AAGGCTCTGC ACAATGCGGC TCCCACCAGC 120 CTCTCCCCTT GGCCCAGATT GCTTCCTCCT ACCCCTTTCT CTAGCTGCCA GGCCCCCCAA 180 CCCCCGCATG GAGCCCTTCA GCAGCTCTGT GAGCTCCCTG CCTGTTGGCA GCCATCACAG 240 CAACGGGCTC TGGTGTGCCC CTTGTTATCC CTGTATTCAG GCCATTATCT GTAATGACAG 300 CCTGGCATAA TTTTATTTC ACAATTTGTA TAATTATATT CTATTGAGCT AAATGATCAT 360 TATAATCATT ATTAAATATT TATTAAGCAC TTCTAGCTGT GCAAACATAA TAAGATGTGG 420 CCTCAGCTCT TAAAATCTTT CTTCCTAATT CCAACCCAAA TACTCGAG 468 (2) INFORMATION FOR SEQ ID NO:696: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 309 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:

GAATTCGGCC	TTCATGGCCT	ACAAGGGAAC	ATGTAAACTA	ACATAACCAA	TTGTCAGTTC	60
TCCATGTATT	CCTCAAAAGA	ATGTCAGAGT	AAATGTATTA	GAAATACAGT	ATCCAGACTG	120
CTAGTCCTTG	CCAGAGACAT	TCTTACCTCT	GCCCTGTGAT	AATATTTTAT	GCTTGACAGT	180
GAAAACAAGT	GTGGCCCCTT	GCACCGGTTA	GCTAGAAGTA	CAGCCAGATT	TCAAGCTAGT	240
GCAGTCACCT	CTTCCGTCAT	TCTTCACAAA	TCTTGTCAAC	CTGGATCTTA	GACTTCATCT	300
GAACTCGAG						309

- (2) INFORMATION FOR SEQ ID NO:697:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 464 base pairs

(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:	
GAATTCGGCC TTCATGGCCT ACACGGATCC GTGTGAAGAC CTACACAGAT GAGCTGACGC CCATTGAGTC TGCTGTCTCT GTGTTCAAGG CAGCCAACTG GTATGAAAGG GAGATCTGGG ACATGTTTGG AGTCTCTTT GCTAACCACC CTGATCTAAG AAGGATCCTG ACAGATTATG GCTTCGAGGG ACATCCTTTC CGGAAAGACT TTCCTCTATC TGGCTATGTT GAGTTACGTT ATGATGATGA AGTGAAGCGG GTGGTGGCAG AGCCGGTGGA GTTGGCCCAA GAGTTCCGCA AATTTGACCT GAACAGCCCC TGGGAGGCTT TCCCAGTCTA TCGCCAACCC CCGGAGAGTC TCAAGCTTGA AGCCGGAGAC AAGAAGCCTG ATGCCAAGTA GCTCCAGGGA ACGCATGTGG ATCCTAGACA GCGCCTTATC TATGATTGAG TGCCCATTCT CGAG	120 180 240 300 360 420 464
(2) INFORMATION FOR SEQ ID NO:698:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 412 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:	
GAATTCGGCC TTCATGGCCT ACGGTGGTGA ACGAGTCTCC AGCACCATGT CTGGTTTGTC TGGCCCACCA GCCCGGCGCG GCCCTTTTCC GTTAGCGTTG CTGCTTTTGT TCCTGCTCGG CCCCAGATTG GTCCTTGCCA TCTCCTTCCA TCTGCCCATT AACTCTCGCA AGTGCCTCCG TGAGGAGATT CACAAGGACC TGCTAGTGAC TGGCGCGTAC GAGATCTCCG ACCAGTCTGG GGGCGCTGGC GGCCTGCGCA GCCACCTCAA GATCACAGAT TCTGCTGGCC ATATTCTCTA CTCCAAAGAG GATCCAACCA AGGGAAAATT TGCCTTTACC ACTGAAGATT ATGACATGTT TGAAGTGTGT TTTGAGAGCA AGGGAACAGG GCGGATACCT GACCAACTCG AG	60 120 180 240 300 360 412
(2) INFORMATION FOR SEQ ID NO:699:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 139 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:699:	
CAGCTCCTGT GACATTTGAA GTTTCTTTTA AAGGGGTTTT TCTTAATCAA AGTTTTACAT TTGGTAGCAT AAGTAGTTCT TTATGCTTCA CAGGACATTG TCTTCAGAGT AATCTCTCTG CTAAAATGGT ACATGTGGG	60 120 139
(2) INFORMATION FOR SEQ ID NO:700:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 406 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:700:

GAATTCGGCC	TTCATGGCCT	ATGAAATGAT	ACCTATGGAG	TGTGATTCAT	TTTGCAGTGA	60
CCAAAATGAA	TCTGAAGTTG	AACCATCTGT	AAATGCTGAT	CTTAAACAAA	TGAATGAAAA	120
TTCTGTGACA	CACTGTTCTG	AAAATAATAT	GCCGTCTTCT	GATCTTGCGG	ATGAAAAGGT	180
TGAAACTGTT	TCTCAACCAT	CTGAAAGCCC	AAAAGATACC	ATAGATAAAA	CCAAAAAGCC	240
TCGTACTCGA	AGATCTAGAT	TTCATTCTCC	ATCTACAACT	TGGTCACCCA	ACAAAGACAC	300
TCCACAAGAA	AAGAAGCGGC	CCCAGTCTCC	ATCTCCCAGA	AGAGAAACTG	GGAAAGAAAG	360
CAGGAAGTCT	CAATCACCAT	CTCCTAAGAA	TGAGTCAAAC	CTCGAG		406

- (2) INFORMATION FOR SEQ ID NO:701:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 511 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:

GGCAAGATGG	TGTTGCAGAC	CCAGGTCTTC	ATTTCTCTGT	TGCTCTGGAT	CTCTGGTGCC	60
TACGGGGACA	TCGTGATGAC	CCAGTCTCCA	NACTCCCTGG	CTGTGTCTCT	GGGCGAGAGG	120
			GTTTTGTACA			180
			CCTCCTAAAC			240
ACCCGGGAGT	CCGGGGTCCC	TGACCGATTC	AGTGGCAGCG	GGTCTGGGAC	AGATTTCACT	300
CTTCACCATC	AGCAGCCTGC	AGGCTGAAGA	TGTGGCAGTT	TATTACTGTC	AGCAGTATTA	360
TAGTAGTTGG	ACGTTCGGCC	AAGGGACCAA	GGTGGAAATC	AAACGAACTG	TGGCTGCACC	420
ATCTGTCTTC	ATCTTCCCGC	CATCTGATGA	GCAGTTGAAA	TCTGGAACTG	CCTCTGTTGT	480
GTGCCTGCTG	AATAACTCCT	ATCCGCTCGA	G			511

- (2) INFORMATION FOR SEQ ID NO:702:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 456 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:

GAATTCGGCC	TTCATGGCCT	AGGGATGGTC	TTAACAGGGA	ANAGAGAGGG	TGGGGGAGAA	60
AATGTTTTTT	TCTAAGATTT	TCCACAGATG	CTATAGTACT	ATTGACAAAC	TGGGTTAGAG	120
AAGGAGTGTA	CCGCTGTGCT	GTTGGCACGA	ACACCTTCAG	GGACTGGAGC	TGCTTTTATC	180
CTTGGAAGAG	TATTCCCAGT	TGAAGCTGAA	AAGTACAGCA	CAGTGCAGCT	TTGGTTCATA	240
TTCAGTCATC	TCAGGAGAAC	TTCAGAAGAG	CTTGAGTAGG	CCAAATGTTG	AAGTTAAGTT	300
TTCCAATAAT	GTGACTTCTT	AAAAGTTTTA	TTAAAGGGGA	GGGGCAAATA	TTGGCAATTA	360
GTTGGCAGTG	GCCTGTTACG	GTTGGGATTG	GTGGGGTGGG	TTTAGGTAAT	TGTTTAGTTT	420
ATGATTGCAG	ATAAACTCAT	GCCAGATATT	CTCGAG			456

(2) INFORMATION FOR SEQ ID NO:703:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 439 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:

GAATTCGGCC	TTCATGGCCT	AGTCCTTTGC	TCTACTGTTG	AATGGAGGAG	GATTTTTTT	60
TTTTTCCCTC	NACACAGGGG	TTTTCTTGGA	GCTCAAGTTT	GGATGACCCC	AGACAGTAAG	120
	CATGGTAAAG					180
GGCCAGGATC	AGCAGGTTTG	AGTGGATAAT	TGGCTTGTGG	TCATTTTCTC	ATAGGATTTT	240
TCTTTTAGTA	GTGGAAACTG	TTTTTCAAAT	CAAATTTGGA	TGCCAACTAT	GTGGAACAGA	300
AGTGTGGCTG	CTCTGGTGGA	AGTGGCAATG	GTAGTCCTAG	AGTCTCCCTG	TCAGCCACAC	360
CCTTTGTCTC	CCCCTACCCA	AGGGACCCTG	TGGCCTGGAA	CCGCAGTGTG	AAATGCTATA	420
TAGTGCAATG	AAGCTCGAG					439

- (2) INFORMATION FOR SEQ ID NO:704:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 437 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:

GAATTCGGCC	TTCATGGCCA	ACAGCTGAGA	TAACGAGGAA	ATATTCTGAA	ATGGATCCCA	60
AATATTTCAT	CTTAATTTTG	TTTTGTGGAC	ACCTGAACAA	TACATTTTTT	TCAAAGACAG	120
AGACAATTAC	AACAGAGAAG	CAGTCACAGC	CTACCTTATT	CACATCATCA	ATGTCACAGG	180
TATTGGCTAA	TTCTCAAAAC	ACAACAGGGA	ATCCTTTGGG	TCAACCAACA	CAATTCAGCG	240
ACACTTTTTC	TGGACAATCA	ATATCACCTG	CCAAAGTCAC	TGCTGGACAA	CCAACACCAG	300
CTGTCTATAC	CTCTTCTGAA	AAACCAGAAG	CACATACTTC	TGCTGGACAA	CCACTTGCCT	360
ACAACACCAA	ACAACCAACA	CCAATAGCCA	ACACCTCCTC	CCAGCAAGCC	GTGTTCACCT	420
CTGCCAGACT	ACTCGAG					437

- (2) INFORMATION FOR SEQ ID NO:705:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 403 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:

GAATTCGGCC	TTCATGGCCT	ACATTCACAT	GTTCCCAATC	ACTTCCCTCA	CACACATATG	60
CTCACTGATT	TACACAGCCA	TTCGCACTTA	TACATACTCG	NTCACATTCA	CACAGGGTCA	120
CCCATTCACA	CACACTCGAC	ACATTTACCC	TCACATTCAC	CCACTCACCA	TTCCCACTCA	180
CCAGTTCACA	TGCACTCACC	CAAGCTCACA	CTTGACCACG	GACACACCCT	CAAACATAGG	240
TGCTTACACA	CAAGCCNACA	CACACTCACC	TAGCCATTCA	TACTCACGTG	CACCTATACC	300
TTCACACACA	TCCTCACATA	CCCACACAGC	TCTACACATA	CCCACTTTCT	TACACATTCA	360
CACACATACC	TATAGACACA	TTCAAACACA	CCCNACGCTC	GAG		403

- (2) INFORMATION FOR SEQ ID NO:706:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 501 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:

GAATTCGGCC	TTCATGGCCT	ACTCAGAATC	ATAATGAAGT	CCAGTCTACC	ACACCACCCT	60
TCACTACTGT	TGATTCACAG	AAAGACTGTA	GAAAATTTCC	AGTTCCACAG	AAGGATGGTA	120
GTGCTTTGGA	GGATTCTAGC	ACTTCAGGGG	CATCCTGTTC	CAAGTCAAGA	CCACATTTAG	180
CTGGGACACA	TACTTCTCTT	AGACTTCCGC	AGGAAGGAAA	AGGAACCTGT	ATTCTTGTAG	240
GTGGTCATGA	AATCACTTCT	GGATTAGAAG	TAATTTCTTC	CCTAAGAGCA	ATTCATGGGT	300
TGCAAGTAGA	AGTTTGTCCT	CTTAATGGCT	GTGATTACAT	CGTGAGTAAT	CGCATGGTGG	360
TGGAAAGGAG	GTCTCAATCT	GAGATGTTAA	ATAGTGTCAA	TAAGAACAAG	TTCATTGAGC	420
AGATCCAGCA	CCTGCAGAGT	ATGTTTGAAA	GAATATGTGT	GATTGTGGAA	AAGGACAGAG	480
AAAAAACAGG	CGAAACTCGA	G				501

- (2) INFORMATION FOR SEQ ID NO:707:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 403 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:707:

GAATTCGGCC	TTCATGGCCT	AGGACAACTG	TGATATTTCA	GTTCCTGATT	GTAAATACCT	60
CCTAAGCCTG	AAGCTTCTGT	TACTAGCCAT	TGTGAGCTTC	AGTTTCTTCA	TCTGCAAAAT	120
GGGCATAATA	CAATCTATTC	TTGCCACATC	AAGGGATTGT	TATTCCTTTA	AAAAAAAACC	180
AATACCAAAG	AAGCCTACAA	TGTTGGCCTT	AGCCAAAATT	CTGTTGATTT	CAACGTTGTT	240
TTATTCACTT	CTATCGGGGA	GCCATGGAAA	AGAAAATCAA	GACATACACA	CAACACAGAA	300
CATTGCAGAA	GTTTTTAANA	CAATGGAAAA	TAAACCTATT	TCTTTGGAAA	GTGAAGCAAA	360
CTTAAACTCA	GATAAAGNAA	ATATAACCAC	CTCAAATCTC	GAG		403

- (2) INFORMATION FOR SEQ ID NO:708:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 348 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:

GAATTCGGCC	TTCATGGCCT	AGGTGGGGGG	CCTTCTGCAC	AAAAAGGGAG	TAAGTCCACG	60
CTATACCTGT	GCTCAAATAA	CAGCGCCATT	GATGTCTTGG	CANACTTGGG	ANGACATTCC	120
TTCTGCAAGA	CTTGNTGAGC	ATATTTCTGA	GCTCTCTTTA	CATGGTCAGG	GTCCACATAA	180
TGCATTTTTT	TCATGTCACA	TTCTTCAGTA	GTATAATTTA	ACTTGAGGAT	ATAAAGGATC	240
CACACTCCAA	ACACAAGCAA	TGTACATTTG	AGGATGTCTT	TTAATNACAA	GCTGGGCCTT	300

348

CTCATCTTGC TTTGAGCTCG GGTGTACCAT TGCAGGGAGG GCCTCGAG

(2) INFORMATION FOR SEQ ID NO:709:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 322 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:	
GAATTCGGCC TTCATGGCCT ACAGAATTGG CAGCACAAAG AAAACGCCCT CTCCTGACTT GTATTGTGGC AGTCTGAACG CCCCCAGAAA ATTGTGCCAA AGAGTTTAGA AAAATAAATA TACAATAAAA GTAAACACAT ACACACAAAA CAGCAAACTT CAGGTAACTA TTTTGGATTG CAAACAGGAT AATTAAATGT TCAAACAATC TGATAAAATA ACCATTTGGA AACTGCTTGG CCTTCTGTTC TTTTATTTGA TTGACTACAA TGCGGTATTG GTCTCTTGCT GCACTTCAAA AGCAACCAAC AAAACCCTCG AG	60 120 180 240 300 322
(2) INFORMATION FOR SEQ ID NO:710:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 367 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710:	
GAATTCGGCC TTCATGGCCT AGCCATAGAA ACTGCCTCTT TTCATGTGGG ATGAAGACAT CTGTGCCAAG AGTGGCATGA AGACATTTGC AAGTTCTTGT ATCCTGAAGA GAGTAAAGTT CAGTTTGGAT GGCAGCAAGA TGAAATCAGC TATTACACCT GCTGTACACA CACTTCCTCA TCACTGCAGC CATTGTGAAA TTGACACAT GGCGGTAATT TAAGTGTTGA AGTCCCTAAC CCCNTAACCC TCTAAAAAGGT GGATTCCTCT AGTTGGTTTG TAATTGTTCT TTGAAGGCTG TTTATGACTA GAATTTTATA TTTGTTATCT TTGTTAAGGA AAATAGAGGA ANNCAAAGGG ACTCGAG	60 120 180 240 300 360 367
(2) INFORMATION FOR SEQ ID NO:711:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 318 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:	
GAATTCGGCC TTCATGGCCT AGACTTCCAC AGAGACCTAT CTGGAACTCC TGGTTCCTTA CCTCTGCTTC TGTCAGAGCA GCTCTGGGTT TTGGTTTGTT ACTATTGTAC ATATTAGGCT TCTATACAAG AAGAACTGGT CCCATTGGTT TAAAAATAAG TTTGAAAATC CTAGAAACAG TGAGAGTCAG AAAAAAAAAC TGTTTTTATA TACATTATTCT CTCCCCCACC CCCTTTCTCT CCAGTTGAAA TATGTTGCAG AGCTCTAAAT TTAGGGATGC TTTTGGCGTA TTTCTTATAC ACTCCAGAGG CACTCGAG	60 120 180 240 300

- (2) INFORMATION FOR SEQ ID NO:712:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 468 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:712:

GAATTCGGCC AAAGANGCCT GAGTTCTTAT TGTTATTCTC TACCAAGCAC TGTTTATTAG CTAATAATCT CCTCAAGCAA AAACCCAGGG AATCAGATTG TTCTGGGTTC TCCNTTTTTT GGAACTTCTT ATTCTCTTAA	AGGTTAGGAG TTTCTGGCCT AGGCACCATG TTTTTTTTTT	TATTGTCCTT TAGGGGCAGG AATAGAATTA TCCATCGCCT GCCCAACTGA	TATTTACTGA TGATTAAAAA TAGTAGACAG TGAGAATTAA GTCTTTCTGT	ACACAGTGAA AACAAAAAAG TGAAGTATCT TAGGCTGCAT	60 120 180 240 300 360
				GGACTTACAT TTTGGAGAAA	360 420
CTGGATGTAG GGCCGTATGA	AAAAATCATT	CGAAATCAGA	ATCTCGAG		468

- (2) INFORMATION FOR SEQ ID NO:713:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 297 base pairs .
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:713:

TTGGGAAAAT TTAGTTTCGG ATGAGGATT TTCTGCACTG TCCTTGGAAT CAGCAAATGT GGAAGATTTG GAACCTGTTA GAAACCTCTT TAGAAAGTTG CAAAGCACAC CTAAGTATCA GAAACTTCTA AAGGAAAGAC AACAGCTACC TGTATTTAAA CATCGGGTGG TCTCCAAG	60 120 180 240 297
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- (2) INFORMATION FOR SEQ ID NO:714:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 327 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:714:

ATTATTATAG ATGTTTATTG GCTTCTGCTT	GGCACACATT CTATGTCCAT	TTCAACTCTC TTTTTACATTT TGTTTTCCTT TTCTCCATTA	TTGAATCTAA GATTTAACTT	TTAGTATTTT GACCAAAATT	GTGACTTAAA TGTGTCATTT AAATGAGCAA AGGAGCCATG TTCCCCATCC	60 120 180 240 300 327
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(2) INFORMATION FOR SEQ ID NO:715:

(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 324 base pairs(B) TYPE: nucleic acid

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(C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:715:
GAATTCGGCC AAAGAGGCCT ACTTCTCCAA GCATTCATGT ACATCCTTGG GATCTGCCTC
                                                                       60
ATCATGGAGC TCATTGGTGG CGTGGTGGCC TTGACCTTCC GGAACCAGAC CATTGACTTC
                                                                      120
CTGAACGACA ACATTCGAAG AGGAATTGAG AACTACTATG ATGATCTGGA CTTCAAAAAC
                                                                      180
ATCATGGACT TTGTTCAGAA AAAGTTCAAG TGCTGTGGCG GGGAGGACTA CCGAGATTGG
                                                                      240
AGCAAGAATC AGTACCACGA CTGCAGTGCC CCTGGACCCC TGGCCTGTGG GGTGCCCTAC
ACCTGCTGCA TCAGGAATCT CGAG
                                                                      324
(2) INFORMATION FOR SEQ ID NO:716:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 495 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (x1) SEQUENCE DESCRIPTION: SEQ ID NO:716:
GAATTCGGCC AAAGAGGCCT AAAGGGATTT AAAACCTCTG TAGAGGCTGG GCGCGGTGGC
TCACACCTGT AATCCCAGCA CTTTGGGAGG CCAGGGCGGG CAGATCACCT GAGGTCGGGA
                                                                      120
GTTCGAGACC AGCCTGACCA ACGTGGAGAA ACCATGTNTC TCTACTAAAA ATACAAAATT
                                                                      180
AGCCAGGCGT GGTGGCACAT GCCTGTAATC CCAGCTACTC GGGAGGCTGA GGCAGGAGAA
                                                                      240
TCACTTGAAC CTGGGANGTG GAGGTTTTGG TGAGCTGAGA TCGTGCCATT GCACTCCAGC
                                                                      300
CTGGGCAACA AGAGTGANAC TCCATCTCNA AAAAAAAAA AGAAGAGTTT ACACGAAGTC
                                                                      360
ACCTCTATTT CAGAAGATAA TCTAGACTCT ATTCCCTCAG AGTCTTTTTT CTCCCCAAAG
                                                                      420
ATAACACTGT CCTAGGTATT TCCTCATACC CCCAGGCCCA CAGTTCATGG CCCACATGTC
                                                                      480
CCCTGTAAGC TCGAG
                                                                      495
(2) INFORMATION FOR SEQ ID NO:717:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 414 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:717:
GAATTCGGCC AAAGAGGCCT ATTTTTTAGA TCATCAGCTA TTGTTAGTGT TTGTGTATGT
                                                                       60
TATGTGTGGC TCAAGACAAC TTTGCTTCTT TTAATATAGG CAGGGAAGTC AAAAGATTGG
                                                                       120
ATATCCCTGC TTTATACCAA GAAAGACAAC ACCCCACATT TGCAGTGCCT GAAAACACTA
                                                                       180
CCAGCCATCT GAAAAACATG TGACTTCTAA CTTCTGTTCT TTTTTGTAGC AGTGGAATCC
                                                                       240
CACGGTGATA TCTGAGGGAT GTGGTTACCT TTTGGAGGAG GTTGACGGTT TCTAAGGATG
                                                                       300
ATTCTTTCTG AGTGAAATAT TGTCAGTGTC ATTGACCTTT TCATTATTTC AACTATTATT
                                                                      360
ATTCCAGGTT ATCAATACTC TGGCTGACCA TCATCATCGG GGGACTGACT CGAG
                                                                       414
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## (2) INFORMATION FOR SEQ ID NO:718:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 457 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:718:

GAATTCGGCC	AAAGAGGCCT	AGGATGAGAA	TGACTGTGCC	TCATTGCATC	TTCCTGGCTG	60
CCTGATGGGC	AGAAAACCTG	GGTCTCCTCC	CCATTTTAGG	AATGGGAAGG	CTGAGTCTCT	120
GCGATGAGCC	TTCCTCAGGG	ATGGTGAGGG	GCCGGCCCGG	CACTAAGCCC	CATTCTCTGA	180
GTTAGGACCT	GTAGGAGGGT	GGCAGGGGCA	AGCGGGGCAG	GTGGGTGGCC	CAGGCAACTT	240
TGCAAACATC	TTCCCTTTTT	CCGGGAGAAG	CAAACGCGCT	GTGTGGAAAG	GCACATTCGG	300
AAGATGGAGT	TTCACATCAG	CAAGGTCAGC	TGGCTCGTGG	ATGTTGCAGG	GTGGGGTGGG	360
GCAGTGCCAG	CTTGCTGGGC	CTCAGCTAGG	TTAGCAGGAG	CTGGGGAGGT	GCCCTCGAAG	420
CAGGGATCAG	GGCCTCTGGG	TATGGTGCAG	GCTCGAG			457

- (2) INFORMATION FOR SEQ ID NO:719:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 509 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:719:

GAATTCGGCC AAAGAGGCCT	AACTTGCAGA	AGCTGTTTTA	TGCAGAGATA	AATTGGAAGA	60
ATGGTCAGCC TCTTAAGCTA	GCTTATTCGA	AGAGGTACTG	GAAAAAATAT	GGCAAAGACT	120
TCAACGACAT ATGCCAAAAC	TTTTTCCCTT	GGAAATCATT	GACTAGCATC	ACTGAATGTT	180
ATTTCTTGTG GAGAACTACT	GACAGATATG	TGCAACAGAA	ATGGTTAAAA	GCAGCAGAAA	240
CTGAGAGTAA GCTGAAACAA	GTATATATCC	CAATTTACAG	GAAACCAAAT	CCCAACCAAA	300
TATCTACCAG CAATGGCAAG	CCTGGTGCTA	TGAGTGAAAC	CATGAGGTTG	ACATTCCTGC	360
CTCAGAATCC CCTTGTAGTG	CAAGCCTGGG	AGGGCTGCTG	TGCTACACAG	TCTAACCAGT	420
AGTATTCTTG GGGCCCACCT	AATATGCAGT	GCAATTTGTT	GGCTTTATTG	AGAAAAATAT	480
GGAGACCTGA AAATGCCCAC	CCGCTCGAG				509
					505

- (2) INFORMATION FOR SEQ ID NO:720:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 344 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:

GAATTCGGCC AAAGAGGCCT	AATGTGTAGT	CATCTGGGAT	ATGCTAGCAT	CACAGTTACC	60
TGGAGTCATC TTGAATATGG	AGATGACAGG	GACTGATTTT	GCAGATTCGT	TGAGTTGGTG	120
GGATATGTAA ATATGTTTTT	CACCAACAAA	TCAGATATTT	CTGTTGGGCA	GCCAAGTGTA	180
ATAACCATTG CTGTAAATGA	TCTCTGTCCT	CTCCAAATCA	CATGATTAAT	TAAATTATGT	240

GAATGCCTAG TTGACTGCTA GGGAATGCTT GTACTTTGGA AATATTTTAA CCAAGGACAC TCTAGAAATT CTCTTGCTCT CCCACCTCAA CAGTGCAACT CGAG	300 344
(2) INFORMATION FOR SEQ ID NO:721:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 335 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:721:	
TTCTCTGCAA GGCGATTCCA TGACAGAAAC CGTAGCAGAA AACATCGTTA CCAGTATCCT GAAGCAGTTC ACTCAGTCTC CAGAGACAGA AGGCATCTGC TGATTCTTTT CCAGACACAA AAGTCACTTA CGTGGACAGG AAAGAGCTTC CTGGGGAAAG GAAAACAAAG ACTGAAATAG TTGTGGAGTC TAAACTGACT GAGGATGTTG ATGTTTCCGA TGAAGCTGGC CTGGACTACC	60 120 180 240 300 335
(2) INFORMATION FOR SEQ ID NO:722:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 348 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:722:	
CCGCAGATTA ATGACCCTGC ACCCTCCAGG CCCCTACTCA CATCCTCCCC CAACCGGCTT	60 120 180 240 300 348
(2) INFORMATION FOR SEQ ID NO:723:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 275 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:723:	
GAATTCGGCC TTCATGGCCT AGTAGTTGTT CCATGCTGTT GTTTTTGTT TTATCTTTCA TTGCCTTTCC CTCTGCAGTC AACATTATGA CCTGGGGACT CCAGCATCCT TCAAGCAAGC CATTTCCGAA GAAGGTGAAA AGAAGCCAGG ATGATTGGCA CCTCCTCCTC TCTTCCTCTT CCCTTGCCCA GCCCCCTCCT GTGCGTGTGT TTCAGACAAC ACAGGAGCCA GCACAGGAGT GGAAAATCCT GTAGCGCAAC TCGAG	60 120 180 240 275

(2) INFORMATION FOR SEQ ID NO:724:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 317 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:724:	
GAATTGGCAT CTTTTCATTG CTTTTGCCCT TTGAGAGTTG TTTAGTTTTT TAAAAGTCAG ATAATTTTGG ATTATATTCT AGACCTTTTG AATATTATGT TATAGGACTC TGGAGTCTGT TAAAATCTTT AGGAAGACAT TAATTTTTTG AATTTTAACA GACAGÁAGTC CTTGTTATAT TGATCCATTG GTTTGTTCTA CACTTGTGCA CCTTGGAGAT GAGTCTGACT TCATATGCAG AATTTAGTAT CCCTTTCTTG AGCTCCCTCC CCTCTGTGAT CCTCCCCATT CTTCCTTTCT CCCAAGAACT TCTCGAG	60 120 180 240 300 317
(2) INFORMATION FOR SEQ ID NO:725:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 288 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:	
GAATTCGGCC TTCATGGCCT AGGGTCAGTG AATCTGCATT ATTACATAAA AAATAAGGCA GAGGAAGCAA TCAAATATGC GTTTGTCTCT GGTGAGCCTC AGCAGGGATG ACTTTGAGTT CTGTCTGTCC TTTGTCCACA AGGAATTTCC TTGTGGAAAA TTGTGAAGGA GGTATGTCGC TTCTTAACTC TGTACCTATC TTATTTAGGA ATAAAATGGG AGGCAGGTCT GTCTGACATA GTTCCCAGTT TGACTTTCC CCTGACTTAG TGATTTTGAG GTCTCGAG	60 120 180 240 288
(2) INFORMATION FOR SEQ ID NO:726:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 247 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(11) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:	
GAATTCGGCC TTCATGGCCT ACACACTAAT AGGATTGGAT TTATGTATGT CCAGCTTGGG AATTATTACA GGAATTAAAA ACAACTTTTT AGAGTGCTTT CCTGAGCTCT CTTTCTATTT GTTCCCCCTT CTACTTTTTG CTTCCCTGTG GCTGCTGTTT CTATCCTCCA GCCAGAGAGC TAGTGTTTAT TTTCTCCATT GTGTTACACA CTTGTGCAGC TGCAACCACC ATATCCAGGG GCTCGAG	60 120 180 240 240
(2) INFORMATION FOR SEQ ID NO:727:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 256 base pairs	

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:727:	
GAATTCGGCC TTCATGGCCT AGAATTCTAG ACCTGCCCCG GTCTTCCTCC TCGTCCTGCC GCAGGGCCAG AACCCCTGAC GGTATTCAGC TGCGCGTAAG TCTGGCCGGT GCCATCTGTC TCCGCAATGC CCCCCAAGAA ACAGGCTCAG GCCGGGGGCA GCAAAAAGGC GGAGCAAAAA AAGAAGGAGA AGATTATCGA AGACAAAACT TTCGGTTTGA AGAATAAGAA AGGAGCAAAG CAACAGTTAT CTCGAG	60 120 180 240 256
(2) INFORMATION FOR SEQ ID NO:728:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 279 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:728:	
GAATTCGGCC TTCATGGCCT AAGTGCTTGC GCTCTAATAA CCATGTTTAT CTCATGCCTT TGGGCCTTTG CATATGTGTT TCCTCTGCTG ACACCAACCT CCTCCTCCTC CTCCTCCTCC TCTGCTTGGC TGGCTTCTCT CAGTCTCAGT TGCGATACCT TCTCTTCTAG GAAAGCTCCC CTGACCACTC TTTCTTTGGG CTTCTATAAC CCCCCTGTCT GCCCCCATCA GGGCACCTCC CAAATTTCAG TGTTTCCTTT CCTCCCCC AATCTCGAG	60 120 180 240 279
(2) INFORMATION FOR SEQ ID NO:729:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 231 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:729:	
GAATTCGGCC TTCATGGCCT AGAGAAACCT ATTTTTCAT TTAACCTGTT CTTTAAATCC AGTATGTTCC AGAACATACA AAAATGTTTA AATGTTCCAT TTGTAAGAGG ATATCATGTA TTTTATATCA ATTTAAATGC AGTTATCCTA ATCATTTTC TTTCATTTTT ACCCTTTATT AACTCTTCAT TTGTTTACAA AACAAATCCA CTCTATAAAC GCAATCTCGA G	60 120 180 231
(2) INFORMATION FOR SEQ ID NO:730:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 253 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:730:

GAATTCGGCC AAGAGCAAGT	TTTCACAGG	ACACACATAA	TTAGTTATTT	TACCATTCTT	TCATAGTTTT TTAAAAATCG	60
TTTTCTATTA	TTCAAATATA	GAATGTTATT	AAATTTTTTG	GTATCGCTGG	TTAAGTGCCT	120 180
AGAACTTGAT AAGTATACTC		TTCTTTTTCC	TTTTTGCTAT	GAGAAAAATA	ATGCTCAGAG	240 253

- (2) INFORMATION FOR SEQ ID NO:731:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 239 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:731:

GAATTCGGCC TTCATG	GCCT AAGAGACTTA	ATTATTAACA	AAGTATTAGA	AGCTAGAAGT	60
AGGTAAAATA AGTGAT	AAAAATT TTAT	TTATCCTTAC	TTTACAAAAT	CCATATTAAC	120
CTCACTTGAA ATTTTA	TGAG CTTTTCCTAT	AAGTTTAAAG	AGATAGAAAT	CAGTGAAAGA	180
CCTCAGTAAT TCCTGC	AATG ATCTTAATAG	AAAATATTTT	ATACCTTCTC	TCCCTCGAG	239

- (2) INFORMATION FOR SEQ ID NO:732:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 262 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:732:

GAATTCGGCC	TTCATGGCCT	AAATAAATAT	CTCATTTTAA	TTGTTACTTT	GTTGGACTTG	60
ATTACTGCAA	ACCTATCACT	AATTCTTTCT	GAGTTCACCG	AAAGAAGTGC	AAAACCCTTC	120
AATATATTAC	CATCATGTGC	TTCTTCTGTC	CCACTCTTTT	CCTTAGAGAC	ATTTTGTTTT	180
TGTTGTTTTT	AATTGGTATT	GTATTGTTTT	TCAAATCTTT	GTCCCCCACG	GCTCGACCTA	240
TAGTGAGTCG	TATTAATTTC	AG				262

- (2) INFORMATION FOR SEQ ID NO:733:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 253 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:733:

GAATTCGGCC	TTCATGGCCT	ACACACATAA	TTAGTTATTT	TACCATTCTT	TCATAGTTTT	60
AAGAGCAAGT	TTTCACAAGG	GCGATTTGAA	TTAGAGGGTA	GAATAATATT	TTAAAAATCG	120
TTTTCTATTA	TTCAAATATA	GAATGTTATT	AAATTTTTTG	GTATCGCTGG	TTAAGTGCCT	180

AGAACTTGAT CATCTTCTAT TTCTTTTTCC TTTTTGCTAT GAGAAAAATA ATGCTCAGAG AAGTATACTC GAG	240 253
(2) INFORMATION FOR SEQ ID NO:734:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 301 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:734:	
GAATTCGGCC TTCATGGCCT AGTATCACAG GCTTTCTTCA AATAACCAGT TCCTCTAAGA CATTGAAAAT ATAATTCGGT GTTTAAAATA AATTCATACC CGTTTTGTGT GCTGTGCATA AATAGCAAGT ATATGTGTAC CTTACCAAAC TTATGGTCCC CAGTCCCCAA ATTCCAAAAT TATGCAGGAG GGAAGGTTAG CCATTGCAGT AAACAATTTC TCCCTATTGA CCCATGCTCT CCAGCTGATT ATGATGTGGG CAGTACTCAT CCAAGGCTAT ACAGACCAGC CGGGTCTCGA G	60 120 180 240 300 301
(2) INFORMATION FOR SEQ ID NO:735:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 241 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:735:	
	60 120 180 240 241
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:735:  GAATTCGGCC TTCATGGCCT AGAGACACAA TGGGCTCCAA GAATTTGAAA TCCCTCATCT GTGAAGGCAG AAATACTAGG AGAATGGGTA ATGTTTATAC CATCAATGAA GAAACTCTTG TAACCTAGGG TTTTCAAATT ACAGAAGAGG AAGAACAATG GAGGCTGATC TCCAGTTTGT GACAGTCTAG ATAGGTGGCC TCAGTCTTGC TCTTATAAAT TCTAATTCCC AGAAGCTCGA	120 180 240
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:735:  GAATTCGGCC TTCATGGCCT AGAGACACAA TGGGCTCCAA GAATTTGAAA TCCCTCATCT GTGAAGGCAG AAATACTAGG AGAATGGGTA ATGTTTATAC CATCAATGAA GAAACTCTTG TAACCTAGGG TTTTCAAATT ACAGAAGAGG AAGAACAATG GAGGCTGATC TCCAGTTTGT GACAGTCTAG ATAGGTGGCC TCAGTCTTGC TCTTATAAAT TCTAATTCCC AGAAGCTCGA G	120 180 240
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:735:  GAATTCGGCC TTCATGGCCT AGAGACACAA TGGGCTCCAA GAATTTGAAA TCCCTCATCT GTGAAGGCAG AAATACTAGG AGAATGGGTA ATGTTTATAC CATCAATGAA GAAACTCTTG TAACCTAGGG TTTTCAAATT ACAGAAGAG AAGAACAATG GAGGCTGATC TCCAGTTTGT GACAGTCTAG ATAGGTGGCC TCAGTCTTGC TCTTATAAAT TCTAATTCCC AGAAGCTCGA G  (2) INFORMATION FOR SEQ ID NO:736:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 251 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	120 180 240
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:735:  GAATTCGGCC TTCATGGCCT AGAGACACAA TGGGCTCCAA GAATTTGAAA TCCCTCATCT GTGAAGGCAG AAATACTAGG AGAATGGGTA ATGTTTATAC CATCAATGAA GAAACTCTTG TAACCTAGGG TTTTCAAATT ACAGAAGAG AAGAACAATG GAGGCTGATC TCCAGTTTGT GACAGTCTAG ATAGGTGGCC TCAGTCTTGC TCTTATAAAT TCTAATTCCC AGAAGCTCGA G  (2) INFORMATION FOR SEQ ID NO:736:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 251 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	120 180 240
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:735:  GAATTCGGCC TTCATGGCCT AGAGACACAA TGGGCTCCAA GAATTTGAAA TCCCTCATCT GTGAAGGCAG AAATACTAGG AGAATGGGTA ATGTTTATAC CATCAATGAA GAAACTCTTG TAACCTAGGG TTTTCAAATT ACAGAAGAG AAGAACAATG GAGGCTGATC TCCAGTTTGT GACAGTCTAG ATAGGTGGCC TCAGTCTTGC TCTTATAAAT TCTAATTCCC AGAAGCTCGA G  (2) INFORMATION FOR SEQ ID NO:736:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 251 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA	120 180 240 241

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 313 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:737:	
GAATTCGGCC TTCATGGCCT ACAGGGTTGC TGGGATGATC AGTGATTTTG CTAATATCAA AAGTGCCCAG CACAGTGCTT GGGTTGTTGG AGGCATTGAA CACACGGCAT TGTTATTATT TATATGCCTT GTAACTGGAA GAGCCTGTGG GCAAACAGTG GATGCTAAAA TTCAGTTTGT GGAAGAACCA GGTGCACAAA CTCCTGTTCT ACCTGTGGTT GAGTCTACAC TCCCCCACCA CACCCCAGCT GCTCTGATCT ACCTCCTGTT CCTTGAGCAG GCCATTTTCT TTCTTGCTTC AGGGCAACTC GAG	60 120 180 240 300 313
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 302 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:738:	
GAATTCGGCC TTCATGGCCT AGTGTCGTTG TTCCATCTGG TTTTCTTCTT TCAAATTCGC ACTGACTGTT CACAAGCCGC CTGGTCAGCT TTCCTCCAGA TTCCTTCACG ATGCGGTCAA GCTGCTCCTG CTCTCTCTT AAATTATTGC TTTTAAACTT ATCTTCAAGC ATATCTTTGT CTTTCTTTTT ATTTCTTTG CTGGGACTCT TGAAGGCGTG TGCTTCGGCA TCTCCAGAGT CCTCTCTCTC TCTCTGCCAG CAGCCTCCGT CCTCCCCACT CTGTGAGGTG TCTGTTCTCG AG	60 120 180 240 300 302
(2) INFORMATION FOR SEQ ID NO:739:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 196 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:739:	
GAATTCGGCC TTCATGGCCT AGGACTGTAC CAGCGCTATA CTGTAGTTAT TTTTTTAAAT GAACTTCACA TATTTTTGTA TTCTTTCAAA TTGTTTGCTA TATATAAAAG AAGCTCACTG CAAAATGCTT GAAGGAAAAAA AGGAAACAAA AGAAATTCAG AACTTCCCAG AAATGTACAG CTTTTCGGCC TTCATG	60 120 180 196
(2) INFORMATION FOR SEQ ID NO:740:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 309 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:740:

ATGGCCTATG CCTCCCCACT	CCACCCACCT	CTGCCTTCCT	TACTGCTGTA	TCTGCTGCTT	50
GAACTGGCAG GAGTCACACA	TGTGTTCCAT	GTGCAACAAA	CGGAGATGTC	ACAGACTGTA	120
TCAACTGGGG AGTCAATCAT	CTTGAGTTGC	AGCGTACCCG	ATACCTTACC	AAATGGACCT	180
GTCTTGTGGT TCAAGGGAAC	AGGGCCAAAC	CGGAAATTAA	TCTACAATTT	CAAACAAGGT	240
AACTTTCCCA GAGTAAAAGA	GATTGGAGAC	ACCACCAAGC	CTGGCAACAC	AGACTTTTCC	300
ACACTCGAG					309

- (2) INFORMATION FOR SEQ ID NO:741:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 295 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:741:

GAATTCGGCC	TTCATGGCCT	ACTGAAGGTA	GGTGAGTTCA	TCCTCTTCAT	AGTAATGCTG	60
TTTTACCAAG	ACTTTATAGC	AGATGGACCC	AGAAAGAATT	TTCTGCTATT	GTGTTCACTA	120
CAACAGGATA	GGGACATCAG	ACAGCCCCAG	AAACCCCTTC	CAGATCTGAT	ATGGGACTAT	180
TAATTTTTAT	GCTGTTAATT	GGTATTCATT	CACAATGCAG	TTGAAGGGGG	AAGGCTCCAC	240
TGCATTCTTT	GGCTAAGGCC	TGAATGCTTG	CTCATCTGTA	AGATCTATAC	TCGAG	295

- (2) INFORMATION FOR SEQ ID NO:742:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 371 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:742:

GAATTCGGCC TTCATGGCCT ATAAAAAGTG GGCCAGTTTA A	AGAAAAATT T	TATCTAAGC 6	0
AGTAGTACAG CTGGCTTTCC AATATGGCAA AATAAGTCTT T	rctgtaggag á	TATCACCAT 12	0
TTTGGCAGGA TTGAAAAGCC TCTTGTTTTG TGCCATATAA T	CAAACTATA T	CTGTGATTT 18	0
GAAAAATGAC AAAGGGTATA ATAATTCCTA GAATTGGTTT T	TAAAATGAAG G	AAAATAGTA 24	0
TCCTAGTTCA AAAGTTATGG CTCATTGTAA GTGCTGGTCT G	GTATAACCA T	ACAGATTGT 30	0
TTAAAATCTT TAAATAAATA CTTGGCCCAA TCCCTTTTGT T	CCCCCTTTC T	CGCTGCCCT 36	0
GTAAACTCGA G		37	1

- (2) INFORMATION FOR SEQ ID NO:743:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 300 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:743:

GAAATGACTC TAGCCTGTGG AAAGAGAATC ATAATTCTAC GGACCTTTTA AATCCGCCAG
GAACCCTGAA TATCTATCTT TTTTGCTTGA CATGTCTCAT GACTTTTGCA GCCTTGGTGG 120
GCAGCATTTA TCACTAATT TCCCTGCTGA AAATGCAGAA CAGAACTGTT GTGTCCATGC 180
TTGTGGCTTC CTGGTCTGTG GATGATCTCA TGAGCGTCCT GTCGGTGACC ATCTTCATGT 240
TTTTGCAGTG GCCAAACGAG GTCCCCGGTT ACTTCCAATT TCTGTGCAAC ACCTCTCGAG 300

- (2) INFORMATION FOR SEQ ID NO:744:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 450 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear.
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:744:

GAATTCGGCC TTCATGGCCT	ACCCTAAGAG	AAACTTCCTG	GTGATAATCA	CAGGGTCCAA	60
AAGTAAAGGA AACCTGGCAG					120
AATTTGAGAT GCCTTCTAGT	AAGGAATGGA	CCTTAGTGGT	GATGGTTAGT	TGCGTTATGA	180
TGACAGCCAC TGGGTTGGAG					240
CTTCAAAAGT ATCCATGGGA	TACAAAGGCT	TAGGATCATT	GAGACACTGA	ATCAAGGGCT	300
CAATCTGGTA AAAATCTGCT					360
AGGTCAATTC TGAAGTTCTT					420
CAATAAAGTA ATTGCCTTGA					450

- (2) INFORMATION FOR SEQ ID NO:745:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 278 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:745:

GAATTCGGCC	TTCATGGCCT	ACTTATTAAC	CCCAATCAAT	AGAGTTGAGA	GACTATGGCT	60
TTAAAAAATT	AATGCAAACC	TGGCTTTAGC	TGTAATAACA	CCCACCGTAA	GCACTTGGAC	120
TTAGTTATTA	TAGACAAATG	TAAAGAAAAT	TTAATGAAAA	ATAACACCCT	CTCTCTTAAA	180
AAAAAGAAGT	CTCAGGCAAT	AGATGCCTGG	TACTATGAGG	AAGAATGTTA	GAAATAGAAG	240
TGAAATCCCA	GAGAAGCCCN	AAACCCCCCA	ATCTCGAG			278

- (2) INFORMATION FOR SEQ ID NO:746:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 267 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:746:	
GCAATATCAA ATAGCTAACT TCACCCCAA CCACAGTCCT TGCTGTTGGC ATTTACTCAA CTAGTCTTTA ATTCCTGTTT GACAAACTTT ATAAGGTGCT ACAAGACAGA TGATTTTTCA CCATCTACCA TAATGTGGAA CAGATATTTT GTCTTCTATC TCCTGCTTTT GTCAGCGTTT ACGAGTCAAA CAGTATCCGG ACAAAGAAAG AAAGGACCAA AATCAAATTT GCTTGCAAGG AAAAGTGATG TCCAGGGGCA CCTCGAG	69 129 189 249 269
(2) INFORMATION FOR SEQ ID NO:747:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 287 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:747:	
GTTCTACCTG GAATATGGTC CTTCTACCTG GAATATTTTT TCCTCAGGCC TTCTCTGGCT TCTTCTTCCT TTATTCCTTG GATCTCAGCT TAATCATCTC TTTGGCAAGT ATCCATGATC CAAACTGGGT TAGTGCCGCT CCCAAGACCC CCTTTATTAA CCCTGTACTG GCACTTAAAA CATACTCTAT TGTATTTGCC AGCTCCTTGG CCTGTCTGCA AGTTCCTTCA GGCATGCTGC CATCATTCTC ATTTATCACT GTATCTCCTG TGCCCAGCAG TCTCGAG	60 120 180 240 287
(2) INFORMATION FOR SEQ ID NO:748:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 274 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:748:	
GAATTCGGCC TTCATGGCCT ACTTTATCTG CCTCTACACT CTCTTCTGGT TATTCAGGAT ACCTTTGAAG GAATATTCTT TCGAAAAAGT CAGAGAAGAG AGCAGTTTTA GTGACATTCC AGATGTCAAA AACGATTTTG CGTTCCTTCT TCACATGGTA GACCAGTATG ACCAGCTATA TCCCAAGCGT TTTGGTGTGT TCTTGTCAGA AGTTAGTGAA AATAAACTTA GGGAAATTAG TTTGAACCAT GAGTGGACAC AAGAAAAACT CGAG	120 180 240 274
(2) INFORMATION FOR SEQ ID NO:749:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 345 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:749:	

TAGCAACTCT GAGTAACCTT CTCCCAGGTT TATTTGTATT TGCTCATTGC TTATTTATTT

ATTACTAGCT GGGTTTTTTT AGTGGCACCT ACTCCTCTCC CCACTTAACC CTCTGATGTT

ATGCTTGTTA TGCCTGATCA GGGCAGTTAC GGATTGAATT GTGTCCACTC AAAATGTATA

TGCTCATGCA CTGACCTCCA GTGCCTCAGA ATGTGACACC TCGAG

180

240

300

345

(2) INFORMATION FOR SEQ ID NO:750:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 289 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:750:	
GAATTCGGCC TTCATGGCCT ATAGAGTAGT GATTTTGGTC AGCGTGTGTG CTATTTCGGT GTTTCAGTTT TTCAGCTGGT GGAATAGCTA CAATAAGGCA ATCAGCTACC TAGCCACAGT GCCCAAGTAC CGTATCCAAG CTACAGAGAT TGCCAAGCAG CAGGGACTGC TCAAAAAAGC CAAAGAAAAA GGCAAAAACA AAAAGTCCAA AGAAGAAATT CGTGACGAGG AGGAGAACAT CATAAAAGAAC ATTATAAAAA GTAAAATAGA TATAAAGGGT GAACTCGAG	60 120 180 240 289
(2) INFORMATION FOR SEQ ID NO:751:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 336 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:751:	
GAATTCGGCC TTCATGGCCT ACGTAGGCAG ATGGAGCTTG TTATAATTAT GCCCCATAGG GATAGTACAA GGAAGGGGTA GGCTATGTGT TTTGTCAGGG GGTTGAGAAT GAGTGTGAGG CGTATTATAA CAAGCTCCAT CTGCCTACGA CAAACAGACC TAAAATCGCT CATTGCATAC TCTTCAATCA GCCACATAGC CCTCGTAGTA ACAGCCATTC TCATCCAAAC CCCCTGAAGC TTCACCGGCG CAGTCATTCT CATAATCGCC CACGGGCTTA CATCCTCATT ACTATTCTGC CTAGCAAACT CAAACTACGA ACGCACCCTT CTCGAG	60 120 180 240 300 336
(2) INFORMATION FOR SEQ ID NO:752:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 280 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(x1) SEQUENCE DESCRIPTION: SEQ ID NO:752:	
GAATTCGGCC TTCATGGCCT AAGGAAAGAA GAGCAACTTT GTCAGCTTGA GAAGGAACAG AAAGCCGCCC TTCCCAGCTA TTTCCAAAAT AGAGTCTGCC TTTAACTGTG GATGTCCGAG GTTGCGCTGA TTTTCAGGGC TATTCTCAAA GAGAAAGGCA GAGTCAGTCT TCCTGCCTTT CTACTCTCAG GCCTCTTCC TGAGTGCTAG AAGGAGCTCT TTTAGTTGGT TTATACCTCG GGACCCTTAT TTCCCTCTCA CCCTCGGCCC CAATCTCGAG	60 120 180 240 280

- (2) INFORMATION FOR SEQ ID NO:753:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 366 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: CDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:753:

GAATTCGGCC	TTCATGGCCT	AAGAAGAAGT	AAACTGCCTT	GCCTGGACTA	TTTCCAATGA	60
TGCCAAACAA	TAATTGTTGC	CCCTTGTCTT	TCTTAAAAGG	AGACTGCATC	CATTTAACCA	120
AACTAAGAAA	TTTTCAATTA	GTCCTCTGCT	GAAGTCATAC	TATACACATC	TACTTAATTA	180
AAGATACATT	TATTGAAGAG	AACAGGTCTC	CTCCGGGTTT	ATCTGCTATA	GCCTTGCTTA	240
GGAAAGGAAT	AATAGTCTGT	CTTTTAATTA	GGTGTGGCTA	TTGATTGGAG	CAAATGTTGT	300
CAGGTGGCCC	AAGCATGAAT	CAATGAGTGA	CCATGAGGTC	ACCCATCAGT	GAGGGCACCC	360
CTCGAG						366

- (2) INFORMATION FOR SEQ ID NO:754:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 370 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:754:

GAATTCGGCC	TTCATGGCCT	AACCTATTTG	CCTCAGTCCT	ATCTGATTCA	TGAGCACATG	60
GTTATTACTG	ATCGCATTGA	AAACATTGAT	CACCTGGGTT	TCTTTATTTA	TCGACTGTGT	120
CATGACAAGG	AAACTTACAA	ACTGCAACGC	AGAGAAACTA	TTAAAGGTAT	TCAGAAACGT	180
GAAGCCAGCA	ATTGTTTCGC	AATTCGGCAT	TTTGAAAACA	AATTTGCCGT	GGAAACTTTA	240
ATTTGTTCTT	GAACAGTCAA	GAAAAACATT	ATTGAGGAAA	ATTAATATCA	CAGCATAACC	300
CCACCCTTTA	CATTTTGTGC	AGTGATTATT	TTTTAAAGTC	TTCTTTCATG	TAAGTAGCAA	360
CGGGCTCGAG						370

- (2) INFORMATION FOR SEQ ID NO:755:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 286 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:755:

GAATTCGGCC	TTCATGGCCT	ATGGAAAACT	ACTCATTCAT	TCTTCAGAAC	TGTTTTCAGG	60
ACTTCAAGGA	GGCCTTCCCT	AACCACCCTA	TTTAACATTC	CAGTTCTTGC	ACCATCCCCA	120
CCCCTACTCT	GCCCTCACTT	TTTTCTCCAT	GGCACTGGGC	ACCAGCTGGC	TAACTCTGTC	180
TTCAAAAAGT	ACTTTTCTTT	GGGGGAGGTT	TTTCTTTTGT	TTTTGTTTTC	TTTCTTTCAG	240
TCCTGTATCT	TCAGCACTTA	GAAGAGTTCA	TGGCACACAT	CTCGAG		286

(2) INFORMATION FOR SEQ ID NO:756:

(i) SEQUENCE CHARACTERISTICS:

```
(A) LENGTH: 348 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:756:
GCGCCGAGTG GGACAGCGCT GGTGCGGAGA CTGCTTCCGG ACTCCAGGTA CCGCGCTTGG
CGGCAGCTGG CCCCAGACTT CTGTCTTTTC AGCTGCAGTG AAGGCTCGGG GCTGCAGAAT
                                                                      120
TGCAACCTTG CCAATGGACC TGATCGGTTT TGGTTATGCA GCCCTCGTGA CATTTGGAAG
CATTTTTGGA TATAAGCGGA GAGGTGGTGT TCCGTCTTTG ATTGCTGGTC TTTTTGTTGG
                                                                       240
ATGTTTGGCC GGCTATGGAG CTTACCGTGT CTCCAATGAC AAACGAGATG TAAAAGTGTC
                                                                      300
ACTGTTTACA GCTTTCTTCC TGGCTACCAT AATGGGTGTG TTCTCGAG
                                                                       348
(2) INFORMATION FOR SEQ ID NO:757:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 300 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:757:
GCGAGGTCAG GAGCTATGGG ATGGTATTAA TACATTGGCA GAGCAACCCA AGGGGGCAGC
ACATGCAGTG AACTGCCATG CAGAACTCCC GACGGGCCTC TTCCCCATCC CAGAGTGGGG
                                                                      120
AACAACACGC CGTCACAGAC AAGGAAGTGG GTGCCCCCGT CCCCTCCCCG ACCCCGAGAC
                                                                       180
CCAGGAGTGC TGGGCTCCGA GCAAGTCTAT TGCATGCTTT CCTGGCCAAA GCTATATGGA
                                                                       240
AAGCGGGAAC AGCAGGCTGG GGAGATGATG CTGGGGGGTG GGGAAGGAAA GCGTCTCGAG
(2) INFORMATION FOR SEQ ID NO:758:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 393 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:758:
GAATTCGGCC TTCATGGCCT AGAATATTTT ATTATAAATA TAATATATGA TTTTTTAACC
TGTTTTGTTG CCTCATATGC TGTCAGGTTA ATTTGTTTTC CTTCGTGCCA GAGGTGGGGA
                                                                       120
GGAAGGCACT CTGTCTGCTG GGTAAATGCC TAAATTCACT CACCTTCATG GTTTGGGGGC
                                                                       180
AGCATGGTCA TTGTGGATAT TGGTTTTGTG GAGTTGAGGG AACTTAGGAT ATAAGTTCAC
                                                                       240
TCCCTCTATT TTTCTTGTG ATTCAGTTTT TCAAAAATCT TTTTTTCTTC CCTTTCTCCC
                                                                       300
CATTGTGGAA ATTACAAATC AAAGGCCTTT TTCTTTAATG TAAAGTGTAT TTATTTAAAA
                                                                       360
AAAATACAAA ATAAACTACA AGTCTATCTC GAG
                                                                       393
(2) INFORMATION FOR SEQ ID NO:759:
     (i) SEQUENCE CHARACTERISTICS:
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(A) LENGTH: 313 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:759:

GAATTCGGCC T	TCATGGCCT	AAGCACATTC	AAGATGCCCA	CNAGAACCAT	CGTGTTGGGC	60
TCATGTTTAT T	<b>FACTTAAGCA</b>	AGAGAGCTCT	TACCCAAATT	CCTTTGTTTC	CCCACTGTCA	120
GAAACAACAT A	AGTCTGGAAC	TGGAGGCCTA	GAACTCTGGT	TGTATTTCCT	GTAGTGGGTA	180
AAAGTCNACA A	AAGATAATGA	ATGAGGCAGT	GTCTCCTCAT	GCCTTCATAT	TTTCTTTTTG	240
TATTTTAATT 1	TTTTTTTTTT	TTTTATTTT	GTGGGTGATA	GTAGGTATAC	GTATTTGTGG	300
GGTACGACTC C	GAG					313

- (2) INFORMATION FOR SEQ ID NO:760:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 288 base pairs
    - (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:760:

GGAAAAAAAA	GGTAAGATGG	ATGAAAAGGA	GGAGAAGGAA	TTTAATACTA	AGGAAACCAG	60
AATGGATCTT	CAAATAGGAA	CAGAGAAGGC	TGAAAAGAAT	GAAGGTAGGA	TGGATGCAGA	120
AAAGGTGGAA	AAGATGGCAG	CAATGAAAGA	AAAGCCTGCA	GAAAACACTT	TATTTCAAGG	180
CATACCCAAA	TAAAGGAGTG	GGTCAGGCTA	ATAAGCCTGA	TGAAACTAGT	AAAACTAGTA	240
TTTCTGGCTG	TATCAGATGT	ATCTAGCAGT	AAACCAAGGT	CACTCGAG		288

- (2) INFORMATION FOR SEQ ID NO:761:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 482 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:761:

GCTCGAGGCA GGGGGA	AATG GCGGCTTCAG GAG	SAGAGCGG GACTTCAGG	GGCGGAGGCA	60
GCACCGAGGA AGCATT	TATG ACCTTCTACA GTO	BAGGTGAA ACAAATAGA	3 AAGAGAGACT	120
CGGTTCTAAC TTCGAA	AAAT CAGATTGAAA GAC	TGACCCG TCCTGGTTC	TCTTACTTCA	180
ATTTGAACCC ATTTGA	GGTT CTTCAGATAG ATO	CTGAAGT TACAGATGA	A GAAATAAAAA	240
AGAGGTTTCG GCAGTT	TATCC ATCTTGGTGC ATC	CAGACAA AAATCAAGA	r gatgctgaca	300
GAGCACAAAA GGCTTT	MTGAA GCTGTGGACA AAC	CTTACAA GTTGCTACT	GATCAGGAGC	360
AAAAGAAGAG GNCCCT	TGGAT GTAATTCANG CAC	GAAAAGA ATACGTGGA	A CACACTGTGA	420
AAGAGCGAAA AAAACA	ATTA AAGAAGGAAG GNI	VAACCTAC NATTGTAGA	G GNGGNACTCG	480
AG				482

- (2) INFORMATION FOR SEQ ID NO:762:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 83 base pairs

(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:762:	
GGGGGATGCC AACATTTAAA GCAAGAGGCA GAAGGGCTCC TGCAGGAGAC AGGGAATCGG GAAGGCAGCA GGTTAAACTC GAG	60 83
(2) INFORMATION FOR SEQ ID NO:763:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 296 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:763:	
GAATTCGGCC TTCATGGCCT AGGAATTGAA AAGAAAGGCA GAGGAGGAAA GGATTCGCCT AGAAAGAGGA AGCCCGAAAG CAGGAAGAAG AAAGAAAG	120 180
(2) INFORMATION FOR SEQ ID NO:764:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 289 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:764:	
GAAAAGAAAC TAACCAGGAT TCCCTCAGTG TTATTTACTG GGATTGGCAT ACGTGTTCAC AGGCAGAGTA GTTGATCTCA CGCAACGGGT GATCTCACAA AACTGGTAAG TTTCTTATGC TCATGAGCCC TCCCTTTTT TTTTTAATTT GGTGCCTGCA ACTTCCTTAA CAATGATTCT ACTTCCTGGG CTATCACATT ATAATGCTCT TGGCCTCTTT TTTGCTGCTG TTTTGCTATT CTTAAACTTA GGCCAAGTAC CAATGTTGGC TGTTAGAAGG GATCTCGAG	60 120 180 240 289
(2) INFORMATION FOR SEQ ID NO:765:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 306 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:765:	

GCACCAAGAG ATGTTTATTA GGGCAATCAA AAGATGATT ATTATTTTT AAAAAATCAA TGTGGCCTTC CCTTCTCTT TCTTTTGATT CCCCTCTTTG AGTTTTTATG IGTCTCTTTT GCCTTCCCTT CCCAGAGTGG AGGAGTTAGA CCTGCATTGT GGGATGAGAG GAGTTGTGGC TATGTGTCTG CTGGCACCAA GAGGGCTGAG GGTGAGGTGT GGAAGGGACA GGGGGAGGAG ATGGGCAGCA TTGTTAAGAG ATTGGTACCA CTGAGCAAAT ATGTTGAGAA TGATGATTGG CTCGAG	126 186 246 306
(2) INFORMATION FOR SEQ ID NO:766:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 195 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:766:	
GAACTTTGAC ACCTACACTT AAATTCTGAG TCATTAAACA GGCCTACATT TATCAACTGT GGAAAATATCA GCCAGTTTTT GCAAAACCTCT TCTTAGGACA CTAAGTTGTT TGCAGAAATC ACTAGCATTG ACTGACTCAG CAACAATGTG GTTATATTCT TTGATTAACT TAGTCCTTTT ICTTGGTCAA GAGTCAGTAG ACAGGACTGA AGCTTATGCC CCTTGCCCCC CCACCACCAC ICCCATTACTA CCACCTTGGT TTAGCCATCC TTTTCTTGAT CTGTTCTCC CACTTCTACT GTGCTACTCT ACAGACTTGC CCTGAATGTA AGAGCAACAA TTACCTTGTA AAGTCCAAGT IGGGGCCAGGT CACTCCCAAA CTCCACAACC TCGAG	60 120 180 240 300 360 395
(2) INFORMATION FOR SEQ ID NO:767:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 267 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:767:	
EAATTCGGCC TTCATGGCCT GCCTCGCTGC TTTCTTTTCT	60 120 180 240 267
(2) INFORMATION FOR SEQ ID NO:768:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 492 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:768:	

60

GAATTCGGCC TTCATGGCCT AGCATGTCTT CTGCCTCGGC CTCCCGGGTA GCTGGGATGG

CAGGTGTGCA CCACCACGCC TGATTTTTGT ATTTTTAGTA GAGATGGGGT TCCATCCATC

C1 000 C001 CC		001				
CATTCCTAGG	CCATGAAGGC	CGATCTTGTT	TTCCTGAAAG	TATGGCATCA	AAAATACTTG	180
TAGAAAAACC	TTCTCDCDAC	TCATTTCAAT				
TAGAAAAACC	Horana	TOATTIGAAT	GITCCTATTT	TCTTTTCCTT	TGACTTTGAT	240
ATTGGCTTGT	AATGTCTCTT	TTCATCATAT	CTAATATCAC	TCCNACACCC	1000000	
		TORTORIAL	GIAMINICAG	IGGMACAGGC	AGCGCTACTC	300
AAGTCCTAAG	GATTCCTCAG	TGATCAGTGA	TCCAGGGCCG	TTCATCAACC	NOTCOCCTOC	360
1 777770 1 07707					WC 1000C 100	360
ATTTGACTGT	TGAGTGTGGC	AGTTAATGCC	CCTCAAGAAA	TCAAAGGATG	ΤሮΤΤΔΤΔΔΩΤ	420
CTCCCCCAAA	******	3.000.000.000			101111111111111111111111111111111111111	420
GTCTTCCAAA	AMMAMGCAM	AIGCIGAAAT	CCTATTGGCA	AAGTAAACTG	AAATTGGCTG	480
CTACCACTCG	A.C.					
CINCCACICO	AG					492

- (2) INFORMATION FOR SEQ ID NO:769:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 327 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:769:

GAATTCGGCC TTCATGGCCT	AACGTGAGCT GCAGGAGCTC	GCCCGCAAGC	TGCAGGAGCT	60
GGCCGATGCC TCAGAAAACC				120
CATGGAGAGG AAACTGGAGG				180
CCACCCAAG CAGCCTGAGC				240
TGCCAATGTC AGCGCCACAC				300
TTTTAAATGA TATGAAGTAA				327

- (2) INFORMATION FOR SEQ ID NO:770:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 534 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:770:

GAATTCGGCC	TTCATGGCCT	AGTGGANTCT	TGGAGATAAG	CTGAGCTTGA	TGCATTGCTA	60
CCACACACTC	CAAACCATGA	AGAAGGTACC	GTTGGGCTTT	TTGTTGTTGT	GACAAAATCG	120
TAGGAAATGG	CGCCTGTATT	TCTTAATCTG	TTCTCTAATC	TTCTCATTAA	AAAGAACTTC	180
AGTTAGAACA	AGAGGGCCCA	TGGCTTTTAC	ATCCAGTCTT	TCTGCTTCAG	CAACGATTTC	240
TTTGTCAGAT	GAATCAATAA	CACCCTCTTC	TTTCTTTTTC	TTAACAAAAT	CAAAGAGGAT	300
ATTGACCCTC	TCCTCAATTG	TTCTTTCCAA	ATCATCACTG	AGTGTCAGAA	CTTTTGCATG	360
GTCACTGATT	TCATCCATTC	GACGCCTTTG	AGCTTCCTCA	GTTGTATCTT	CTCCCCAGTC	420
ATCATCCTCC	TCTTCTTCCA	TTGTATGTGG	AGGAGGATTA	ATTTCATTTG	GTGGTGGTGG	480
TGGTGGTGGT	GTCTCACTGC	TGGATACGGA	ATTGAATTCT	AGACCTGCCT	CGAG	534

- (2) INFORMATION FOR SEQ ID NO:771:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 408 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:771:

GAATTCGGCC TCATGGCCT ACTAGAATGT GTGACTCTGT GGGGACTGCA TAGGTTTGTT AATTGACCTA TAGCTAAACC TTAATGTGTT TGTGTGTCTA TACATTGCTT TCCGCATTTC AAGACATCCA GACGCTATTA CCAACATTTT CCTGTGCATT AACCTCTGCA TGTGAAAACT TTTAACAGTT ACTGAACTAT GTAAATATGT GAATTTTTTT ATTTAGGTGG ATGCATTTTT TGTCTGTTTTA CTGCTCTTCT CAGCTTTATT CAATAAACTT GCATTTTAAG GGTTGTATTG GCAATTTTAA CTTAAAATGT GCATCATGAT GGAAGGTGCA GACTTTTTTG GAAGTTCCG AGAGGAGGGT CTATAGACCA TTTGTCAGAA ATCAGATCAA CCCTCGAG	60 120 180 240 300 360 408
(2) INFORMATION FOR SEQ ID NO:772:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 288 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECILE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:772:	
GAATTCGGCC TTCATGGTGT CGTCTCCATT CTGATGCATC AGCTCAAACA GCTCTGAGTC CAGGATCTGG ATGAGGGAGC GCATGTTGGC AAAGTGGGTG TCCATGGCAC CCCCGTTGGG GAAGTTCTGG CTCATCCTCT TCATGAGGTG GCTGAAGCAG CTGTAGGCCA GCTGATCATT GTCGAGGGTG ACCAGGAGAG GCGCCAGCAG ATCGCACATG CCCTGCACAT AGCCCACGTC CAGGTGCTCC CACACGTAGC TGCACATGAC GTCTCTGAGC CTCTCGAG	60 120 180 240 288
(2) INFORMATION FOR SEQ ID NO:773:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 255 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:773:	
GAATTCGGCC TTCATGGCCT AATCCAGTGA CTGACAAAGC AAAATTGCAT GAAATTTACA TTTTTTTTCT TCTTGTAATT TAAAACTTGG TTCCTGTATA CCTTCCTGGA TCTTTATACT TTTGTATCTT TTCTACCATT TCTGTAAAAC CTCAACTGCA GGGTGCAATA ATGGGCCTTA TTTTCTATAT TTCAGCAGGA CAGTTGCTGA AAATGGGTTT AAACTCCACT GGCATTATAT CCCACACAAC TCGAG	60 120 180 240 255
(2) INFORMATION FOR SEQ ID NO:774:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 218 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:774:	
GCNTTCAGGC CNAAGGTACT TTAATCAGTC TAAATACTTG AACATTTTTA TTTCAGTGGT	60

120

AAAAAATAGA CTGAGGCAGA GTGAAGTTAT AAATTAGAAT CTAAAAATTT ACCCTTCAAC

ATTAATATT TTTAGTGCCT CTAATATAAA ACACAGAAAA CCTATCTCAA ATATAAAAGA TGAATATAAA ATTATTAATT AAACAACNGG CGCTCGAG	180 218
(2) INFORMATION FOR SEQ ID NO:775:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 257 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:775:	
GCCTTCATGG CCTAGAAAGG AGCATCCCTG TTTTTGGAGT CAGGACCATT CAGGGGGTGA ACGAGGCCCA GGCCAGGTGC CTTTTTGGAG CCTGGAATAT TAAAACCAGG ATGCCAAAAT TGTAGTGTGA TCTCAGTCTT TACATTTAAC AATTATATAC ATTTTTAACA TGGAAGATTA CAGTATAATT TATTTAGGCT AATCAGAAGC TAATTATAGG CTATTTAAAA ATGTTAATTT GTAACACANT ACTCGAG	60 120 180 240 257
(2) INFORMATION FOR SEQ ID NO:776:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 257 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:776:	
GAATTCGGCC TTCATGGCCT AAAGAAACAA AGAAACAAAC CGTATATATA TATCTTCAGA GTTAAAAAAT GGTGAGAACA AGAGCATTGT TTTATATATT TTTTCAACTC TCTTTAACTT CTGGCTTAAT AGAAGACAGC TGCATTCTCA TTATTATTTA TTTATTTTT TTTAGATGGT GTCTCGCTCT GTCACCCATG CTGGAGTGCA GTGGCGTGAC CTTAGCTCAC TGCAACCACC ACCTCCCCAG GCTCGAG	60 120 180 240 257
(2) INFORMATION FOR SEQ ID NO:777:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 243 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:777:	
AGCTTCATGG CCTAGTCTCA GGTTAAGTTT TTTGCAGTAA TCTTTCTTTC CCCTAGAAGT GAGTAAAACT TTCTGTATCC CTTTTTCTCC CCACCTATGT TCCCTAAATT AGTGATTCTC TTACAAGGAA TTATTATCGC CCCTGCAGTT TTGGAAGGAT ACCTCCAAAA TATATCTTGG GGACTTCGAT TTATAGAATT TGGTTTAAGC TTAGATTCTG AGTCCCAGGG TACCTGCCTC GAG	60 120 180 240 243
(2) INFORMATION FOR SEQ ID NO:778:	

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 309 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:778:	
GCTGACAGGA GCATTATGAA GCAAATGGTC ATTGATACAG TTTCACTGAG GGAGTATAAC ACTGGGATTT TGCAGCCTGT GGTGTTCAGT CTCCTGACCT CTATGCCAGC ACACAGACAG CAAGAAGCAG TGGGGAACTT TGAGCTTCAA GCTCTACATT GGTTTGACAA AATCAATTCA TCACTGTCTC ATTCATTAAT GTGCTGTCTG ATACTGACAT TTGTCAATGG CTTGTTTCTG GAAGCCCCTG GTCCTCAAGG CTGGTCAGCT CTACAGTCAC AGCCCCAGGG TGAACCCCAG CAACTCGAG	180 240
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 255 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:779:	
GAATTCTAGA CCTGCCTCGA GCCTGGGTGA CAGAGTGAGA CAATGTCTCA AAATAATAAT AATAATTTCA ACATGATTTT TGGTGCGGAC AAACAAACCA TATCCAAACC ATTTACTCAT CCTAGTTCAG GACAGTGTCC TGGGACTGAC ACAAGGGCTC ACAGCCAGCT AGCACTGTGG GCTCTCACGG GTCCCTTCTG CTGTTTTATT TTAGTAGTTA TTTATTTCCA TTCCTCACTT CCACTACCAC TCGAG	60 120 180 240 255
(2) INFORMATION FOR SEQ ID NO:780:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 156 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:780:	
GAATTCTAGA CCTGCCTCGA GCTAATGGGT GCATGCTACC ACGCCCGGGT AACTTTTTTT TTTNCTGTTT TGTTTTGTGT ATGGAGTCTC ACTCTGTTGC TGAGGCTGGA GTGCAATGGC ACGATCTCGG TTCACTGCAA CTCGAG	60 120 156
(2) INFORMATION FOR SEQ ID NO:781:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 280 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: cDNA	(ii)	MOLECULE	TYPE:	CDNA
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:781:

GAATTCGGCC	TTCATGGCCT	ACTCCACACA	TTCATCTCCC	AAAGGACTCC	TTGAATATTT	60
GCCCCAAAAC	ATCAGCTCCC	AGAAAACACC	CCTCCCAGTC	ACACACACAC	CCAAATTCTC	120
CGATGTATTT	TCATTTTTTT	TCTCCTCTTC	TCTTCTCTTT	TTCCTTCCTT	CCTTCTCTCT	180
TTTCTCTCTT	NCCATCCCTC	CCTTCCTTCC	TCCCTCCCTT	CCTTCCTCCC	TCCCTTCCTT	240
CCTCCCTCCC	TCCTTTCCTT	CCTCCCCCA	CCCACTCGAG			280

- (2) INFORMATION FOR SEQ ID NO:782:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 290 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:782:

GAATTCGGCC	TTCATGGCCT	AGCCGTGTTG	TTACTTGGTG	AATGATAAGG	CCTAGATCTG	60
GTAGTGCTTT	TGTTTGCTCT	AAGGTCTATT	AATTTAATGT	AGCAATCTTT	CTTTTCCCTT	120
TTTCTTTTCT	AACTTCACAT	CAACCTAACT	GGCTACCTAA	ATGTTCATTG	AATGACTGTT	180
TTTGCTTTGG	GATAGAATCC	TCCTTTTTTA	TTTTTAGGGT	GTTAAATTGA	TATAGTATTG	240
TTTAATAGCT	<b>AATAAGATAC</b>	ATTTTGGGCT	<b>AAGTTTCTTA</b>	GGCCATGAAG		290

- (2) INFORMATION FOR SEQ ID NO:783:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 120 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:783:

GAATTCTAGA CCTGCCTCGA GAATGGCTTT GCAGATCTGG GATCTTGTGT TCCTTCTTTC 60
TGGGTTGGTT TTATACGTTA ACTGTCAGAG GCATATGCCA CTTTATTCAG GTTCCTCGAG 120

- (2) INFORMATION FOR SEQ ID NO:784:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 276 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:784:

GAATTCGGCC	TTCATGGCCT	AGTTTAGGTC	AGTAGCAAAT	GGGCCCAGTG	GGAGAGAGTA	60
TGCCCAGAGT	TTGGAGAGGG	TCAGGGTGTC	GGGTGCTGGG	ATGAGGGCTT	CATGTTTGGA	120
AGACGCAAGG	TAGAGAGCAA	GAGAGGAGGA	AAGGTAGAAC	AGGATGGAGG	GCAAGACCTG	180

240

TGTAAGAAGA AGTCTTAAAC TGTAAACATG GGTGTAGTGA GGGTAGTGTG GCTAAGAGGA AATGGATCCA GATGGGCTTG ATGGGTAGCA CTCGAG	240 276
(2) INFORMATION FOR SEQ ID NO:785:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 233 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:785:	
GAATTCTAGA CTTGCTCTCA GGCAGTGAAG GACTGGCACA TTGTGTAATA AACAGAATCA AAGGCAGAAA TTAGATTACA AGCCACCTGA TGATGATAAA ATCAATCACC CTCATCAAAG GGATTTGCTT TGTGTGTGTT TTTCTCTTTC ATTCTTGTGG ATGCAGACAG GATATTGAAC AGCAGCTGGG CTCCTTGATC TTGGCAACAG ACATCAACAG GCAGCGTCTC GAG	60 120 180 233
(2) INFORMATION FOR SEQ ID NO:786:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 203 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(II) MODECULE TIPE: COM	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:	
	60 120 180 203
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:  GAAGATTTTG CCACTCTAAG GAGAGGTGAT ATTTGTATTT TTCTTTTTAC TGAAACCAGA TCGTGAGACA CGCTTTTCAT TCATACTTGA AACTTGATAA AATGTTTGGC TTTATATTAA TTTTCTCAAT TATAAGTGTG GGAAATGAAT TCGTTGATAA CCCTTTTCAA GTAAATGAAC	120 180
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:  GAAGATTTTG CCACTCTAAG GAGAGGTGAT ATTTGTATTT TTCTTTTTAC TGAAACCAGA TCGTGAGACA CGCTTTTCAT TCATACTTGA AACTTGATAA AATGTTTGGC TTTATATTAA TTTTCTCAAT TATAAGTGTG GGAAATGAAT TCGTTGATAA CCCTTTTCAA GTAAATGAAC TGATTAGAAC CAGTAAGCTC GAG	120 180
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:  GAAGATTTTG CCACTCTAAG GAGAGGTGAT ATTTGTATTT TTCTTTTTAC TGAAACCAGA TCGTGAGACA CGCTTTTCAT TCATACTTGA AACTTGATAA AATGTTTGGC TTTATATTAA TTTTCTCAAT TATAAGTGTG GGAAATGAAT TCGTTGATAA CCCTTTTCAA GTAAATGAAC TGATTAGAAC CAGTAAGCTC GAG  (2) INFORMATION FOR SEQ ID NO:787:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 262 base pairs  (B) TYPE: nucleic acid (C) STRANDEDNESS: double	120 180
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:  GAAGATTTTG CCACTCTAAG GAGAGGTGAT ATTTGTATTT TTCTTTTTAC TGAAACCAGA TCGTGAGACA CGCTTTCAT TCATACTTGA AACTTGATAA AATGTTTGGC TTTATATTAA TTTTCTCAAT TATAAGTGTG GGAAATGAAT TCGTTGATAA CCCTTTTCAA GTAAATGAAC TGATTAGAAC CAGTAAGCTC GAG  (2) INFORMATION FOR SEQ ID NO:787:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 262 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	120 180
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:  GAAGATTTTG CCACTCTAAG GAGAGGTGAT ATTTGTATTT TTCTTTTTAC TGAAACCAGA TCGTGAGACA CGCTTTCAT TCATACTTGA AACTTGATAA AATGTTTGGC TTTATATTAA TTTTCTCAAT TATAAGTGTG GGAAATGAAT TCGTTGATAA CCCTTTTCAA GTAAATGAAC TGATTAGAAC CAGTAAGCTC GAG  (2) INFORMATION FOR SEQ ID NO:787:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 262 base pairs  (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA	120 180
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:  GAAGATTTTG CCACTCTAAG GAGAGGTGAT ATTTGTATTT TTCTTTTTAC TGAAACCAGA TCGTGAGACA CGCTTTCAT TCATACTTGA AACTTGATAA AATGTTTGGC TTTATATAA TTTTCTCAAT TATAAGTGTG GGAAATGAAT TCGTTGATAA CCCTTTTCAA GTAAATGAAC TGATTAGAAC CAGTAAGCTC GAG  (2) INFORMATION FOR SEQ ID NO:787:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 262 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:787:  GAATTCGGCC TTCATGGCCT ACGAGATTGT CCTGGGTCAC ATAATGCCAG CTGAGCGTAA AAAGCCAGCA AGTATGGAAG AAAAAGACTC TTTACCAAAC AACAAGGAAA AAGACTGCAG TGAAAGGCGG ACAGTGAGCA GCAAAGACA GCAAAGACA GAAGAGAGAA CTGGAAGATG ATAAGAGAAAA GAAGAGGAGAA CTGGAAGATG ATAAAGAGAAAA	120 180 203 60 120 180 240

(A) LENGTH: 259 base pairs

(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:788:	
GAATTCGGCC TTCATGGCCT ACAAACAGCT GGGAATGTCT CCAAGCCAGA GTGGACTACT AGTAGGTATT CGTTACTTCA TTGAATTCTG CAGTGCCCCC TTTTGGGGTG TAGTTGCAGA CCGCTTTAAA AAAGGCAAAA TTGTCCTCCT CTTTTCTCTT TTGTGTTGGG TTTTATTCAA CCTGGGCATT GGATTTGTCA AACCTGCTAC CTTGAGATGT GTACCAAAGA TTCGCCCAAC AACTCACCCC CAACTCGAG	60 120 180 240 259
(2) INFORMATION FOR SEQ ID NO:789:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 152 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:789:	
ATACTITAAG TTCTGGGATA CGTGTGCAGA GCATGCAGNT TTNTTACATA GGTATACACG TGCCATGGTG GTTTGCTGCA CCCATCAACT CCTCATCTAC ATTAGGTATT TCTCCTAATG CTATTCCTCC CTTAGTCCCC CGTCCCCTCG AG	60 120 152
(2) INFORMATION FOR SEQ ID NO:790:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 241 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:790:	
GAATTCGGCC TTCATGGCCT AGGCAAATTT GGCACTGAAT ATGTACTGGA CTGTGATTAT TTTTATTGTT TTTAAAGTCA GCTTCCCTCC CTCCTTCCTC CTCCCTCCTT CCCAAGCTGA ATCTGAACCA AGGAAGTCTT CCTACAGAGC CACTGACTGG TCCCCACTAA GGCAGGGGTG GAGGGAGGGG CAGGATGTTT TCCTCTCCAG CCTTTGTCTT GCAGCAGATC CCCAACTCGA G	60 120 180 240 241
(2) INFORMATION FOR SEQ ID NO:791:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 182 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:791:

GTATTTGACT CAAAGTATTT TTTGACTGAT AGCAGTATAG CTCCCTCATT CCCTGCTCTC TTTTTGGTTAT CATTTGCATG AAATATAATT TTCTATCCCT TTACTTTTAC TGTGTCCATA AAAGTGAAAT GAGTCTCTTA TGGGCAGGAT ATAGTTGGGC AATTTTTATA CTAATTCTGC  (2) INFORMATION FOR SEQ ID NO:792:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 274 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA	50 120 130 132
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:792:	
GAATTCGGCC TTCATGGCCT ACAATCTTCT TGGCCTGGCA CTAAGGACCT ACTACAGACT GGCACTGAAA TATCTTCCCT ACCTTATCAT TCCTTGTGCT TCTCCACAAG CCCACTCTTC CCCTTCATCA TACATGTGCC GACCTTTCCT GTCTCTTTTA CTTTGCAGCA CCAAATGCTT TCTACTTTGT GGTCTAGGAG GAACACATGT CACTTTTGTA AGCTGCTCGA AAGCAGGGGC CACACCTTCA TCCTTGTTTT CCACACAACA CCAA	60 120 180 240 274
(2) INFORMATION FOR SEQ ID NO:793:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 416 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:793:	
AATTCGCCTT TCANGCCTAG TGAGTAGTTA TCAACACCGG AGATGCATTA GATCAATCTC TGGGGGGCTTC TTCCTGGACC TGCTTCCATA TACACTTATT CATTTTGTCT TCACCGGACA TGTTAAACTT CCAGAGTGAC TCTAATGTGC AGACATGGTG AACATCATTC GCTTAGCTGC ATGTCAGCGC TCACTCAATG TCTGTGAACA GTGAAAGCTA CTTATTCTAC TTATAAGTTC ATTAAGTCTG TGTATAACTA TTGCAAAGCA GAATAGTTGT CCCAGCCACC TGTGTTTGGG GAGATGAAGC TGGGAGGCCA TCAACCTTCT TTGCAATAAA TTTCCTCACG TTTTGTCAAG CAACCTGTTT TTTGTATTCT CAGCTAGAGG CTTTCATTCT CTATCCCCCA CTCGAG	60 120 180 240 300 360 416
(2) INFORMATION FOR SEQ ID NO:794:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 324 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:794:	
GAGATGGATG TCTCTCTTTG CCCAGCCAAG TGTAGTTTCT GGCGGATTTT CTTGCTGGGA AGCGTCTGGC TGGACTATGT GGGCTCCGTG CTGGCTTGCC CTGCAAATTG TGTCTGCAGC AAGACTGAGA TCAATTGCCG GCGGCCGGAC GATGGGAACC TCTTCCCCCT CCTGGAAGGG	60 120 180

240

CAGGATTCAG GGAACAGCAA TGGGAACGCC AGTATCAACA TCACGGACAT CTCAAGGAAT ATCACTTCCA TACACATAGA GAACTGGCGC AGTCTTCACA CGCTCAACGC CGTGGACATG GAGCTCTACA CCGAACTTCT CGAG	240 300 324
(2) INFORMATION FOR SEQ ID NO:795:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 430 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:795:	
GATTCGGCCT TCATGGCCTA GCAAAAGGGA CAAGGGAGA AACAGGAGTA GCAAAAATAA AATAAGAAAT TATGATGCTG CTTTTACCAG AGACAAGCTG CTGCCACCAC TAGGCTGGAA CCTACAGGCT GCACCTGTCC CTAATTAGGG TATTGGATAC TATTCACACT GCTCCTGCAA CAACTGCTAG CCTGTCTAA TCAGTAACTT CTCTCTTCCT CCTGTCTTCT CACCCTCCAG TCCTCCTCAA CAGGAACCCA GCTGGCAAAG ATGTCTGGGA AATGTCATTT GCATTCCTCAG CCCCAGCAGT GCAGAAAGGT AGGAGTGGGG CTGCGAAACA ACAGAAAAAT AAGGACCATA GGTGACAAAG GAAATGCATA TACACTTCAC AGATGGCCCA TAAACATATA ATACAAAGAG GTGCCTCGAG	60 120 180 240 300 360 420 430
(2) INFORMATION FOR SEQ ID NO:796:	430
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 275 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:796:	
GAATTCGGCC TTCATGGCCT ACTCATGAAA TGTCCCAAAG TCTTCTCATT CTGTTCTTCC CTCTCCTTTT CTTTGGTCTT ACTTCTGTAG ACTCTAGCAG AGATGGCATC CTGGGATGGA ATGGCAGAGAA TCTGATGCAG TGGCATGCTC ATCCCAACCT CTTATCTGGT CGTCTTCTTC ACAGAAGAGA GTCTCCACTG GTAGAGTCAT TTTGGGCCAT GGATTTCAAG CTATGCTTTC CTTCTGGCAC CCCGAATGTA CGCAGGTCTC TCGAG	60 120 180 240 275
(2) INFORMATION FOR SEQ ID NO:797:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 157 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:797:	
GCACAATATT TCAAGCTATA CCAAGCATAC AATCAACTCC AAGCTCGGAA TTTTAATTAC GAGGAGGTTA GTTGTGGCAA TAAAAATGAT TAAGGATACT AGTATAAGAG ATCAGGTTCG TCCTTTAGTG TTGTGTATGG TTATCATTTG TTTCGAG	60 120 157

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(2) INFORMATION FOR SEQ ID NO:798:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 249 base pairs	
(B) TYPE: nucleic acid	•
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:798:	
GAATTCGGCC TTCATGCCAA ATGACCAGCC CCTACTGAAG TCCCCAGCAC C GCATGTAGCA GCCCTGGGCC AGAAGCAAGG GATCCTGGGA GCTCAGCCTC A CCAGCCTCAC CGGATTCCCC CACTCTTTCC TCAGAAGCCT CTGAGTCTCT T CCACACACTT CACCTGAGCC ACCTGAACAG ATTTCCTGCC CGGGGCCCTC A GGGCTCGAG	GTTGATCTT 120 CCAAACATC 180
(2) INFORMATION FOR SEQ ID NO:799:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 303 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:799:	
GAATTCTAGA CCTGCCTCCC CCCCCCCTT TCAGAATAAT TTACATAAAT A	CTCCTGAGT 60
TCAATTTTTT TNAATTTTTT TTCTGCTTTT ACTTATTACC CTTTAAGTGC T	
TCTCTGATAA TTTACTTTCT TCTACTCTGT GATTTCTTTT ACAAATCAAT G	
TGTCTTGTTT TCTCAAGTTT TTTCCTGTTA CCTTTCCTGT GGTCACCTGG A	
CCGTTTTCCA CACTCTCCCT CTACCTTCTC CCCCAGTTCT TTAAAGAGAC A	
GAG	303
(2) INFORMATION FOR SEQ ID NO:800:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 405 base pairs	
(B) TYPE: nucleic acid	

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:800:

GAATTTCGGC	CTTCATGGCC	TAGCCATGCA	ATATCTTTTG	CATTACAGTG	CAGTCTTTGA	60
GAAGAGCCAA	GTGGGTGAGA	GGTATATTTT	CGGTGGTAGT	TGAAGAGAAG	GACAAATTAG	120
CACAGGAACA	AGAACTTCAT	GTAGTTGTGT	TTGAAGGCAG	TAGAATTGCC	TTTTAAAAGT	180
CATATCTGGA	TGTTAAGCTC	TCTCTGGGAT	CCAGTTATTA	GGATGAAGAA	ATTCTGCCGT	240
TTAAGTGCCT	GCCATTTATA	GAGGTTGCTT	GTAACTTGTG	TGGCTAGGTA	ATTGTGCTGT	300
GTGAATTTTC	TACTCAAGGT	TGGTTTGGCA	GAAAGTAGAA	TTCTGAGTCT	GGGTATAAAG	360
<b>GGGTTTACTA</b>	ACATGGGAGA	GATTTGTGTG	GAACCCAAAC	TCGAG		405

(2) INFORMATION FOR SEQ ID NO:801:

(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 390 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double

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(D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:801:
GAATTGGCCT AATTAGCATC CTCAAGGACA CCAAAATCAC GTGTGAGGAG AAGATGGTGT
CAATGGCCCG AAACACGTAC GGGGAGTCCA AGGGCCGGTG AGGGAGGGTA TTGCCCTCCG
                                                                      120
TGAGCACAGA GACTCTCCAT GGGAGGGGGA GCAGTATTCT CCTGGATCCT GGGGCCTGGG
                                                                      180
TGGGCTGGGG GACAGCTGAG GATGGGCCTA GCAGATGAAG CTTGCCAGCA AGGCCAAAGC
                                                                      240
AAACGGTTTC TCCTGTGGAT AGTGGACAGA GACCTTTGTA ACCAATGGAA TTATTCATTT
                                                                      300
TTCTCTATCT TTTATTTTTT CAAAGATATT ATTTGACTCT ATCAAAAGTC TCTCCTTTTT
AAACCTTTTC TTATGGCGGG CTATCTCGAG
                                                                      390
(2) INFORMATION FOR SEQ ID NO: 802:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 231 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: CDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:802:
GAATTCGGCC TTCNTGGCCT ACTTTTGAC CTTCTGAGTT TTAGTTTGTC CACTGAGTTT
                                                                       60
TAGGTNAAAA AGAAAAAAA AAAGGAAAAA TTATCTGTAA CCTCAAGACT TTTTATGAGG
ATTATGATTT TACTGTGTTT GATAATAAAT GCCTTTTGCA TGCACTGGTT TTCAGCATAC
                                                                      180
AGTTATGAAC ATTTCCTAGT GGATGAGCTT AAAAAAGGGG AAAAGCTCGA G
                                                                      231
(2) INFORMATION FOR SEQ ID NO:803:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 492 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:803:
GGGACAAGGA CCTGTGCAGT GGCGTGACAT GACAGACGGA CCTGNTCAGC GTCCTATTTG
                                                                       60
CAGTGATGTT CGAGTTTAGC CACCGTACTG TGGACATGCA CCCAGACAGC GGATTAAACG
TTAGTGTGTA CCCTATTCCC AGAAGAAAGG GTCCAAGAAA CACCCACACA GATCCCAAAT
                                                                       180
GCAGCACACC TGTGTGGGG CCTTCATCTT TTGGAGCCCA CCAATGCCTG CCATCCCTAA
                                                                       240
CAACTGCCTT CGCACCCACC AGGGATCAAG GCATTCTGTT TTTCGGAACG TGCTCCGACA
                                                                       300
GTGGAGAAGT GCAGCATGGG AAGGTTGTAT CTAGGAACTT GAAGCAAATA AATTCCTTTT
                                                                       360
AATTCATGCT TGTGATCCCT GTTATTCTGT CTCTGAACTG TGCCTTTATG CTCCAGATTA
                                                                       420
GCTTTGAATC TTATTGCTAG ATTCTCCAAT CTGTTTACAA AATAAATGCA CCTAATCTTC
                                                                       480
GCCTGCCTCG AG
                                                                       492
(2) INFORMATION FOR SEQ ID NO:804:
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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 444 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:804:

GATACATAGT	TCAATTCAGT	TCAATCAAAA	CCATTCAATA	CATATTTACT	GAGTCCCTTC	60
TGCGTGTCAG	GCACTGTTTC	AGGCACTTGT	GATATATCAG	TGAAAAAAAC	AAAGGCCCCT	120
GCCCACATGG	AGCTTACATT	ATAGCCAGGG	GAAACAACAG	TATACAATAA	ACACAAATAT	180
GTGAAGTATC	TAGGGTGATA	GGTGATATGA	AAAACATAGA	GCAGGTGAAA	GGGGTATGGG	240
ATTTCTCGAT	CTGGAAGGTA	GACAGCTGCA	GTATTAAATA	GTATGGACAG	GATAGGCTTC	300
AGTAAGAAGG	CAACAATTGA	GCAAAGATGA	GTAGGTAAGG	GTATAGGGCA	TCTGCAACAG	360
CTAGTGAAAC	GGCCCAAAGG	TTAGAACAAG	GCTGGAGTTC	GGGAGAGGTC	TGGGCTGGAG	420
ATGTAGNCCA	TGAAGGCCGA	ATTC				444

- (2) INFORMATION FOR SEQ ID NO:805:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 352 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:805:

GAATTCGGCT	TTCATGGCCT	ACAAGAAGCT	GGAGGAAAAA	AATACGCTGG	CTCAGGGCTT	60
TCAGAGAAGA	GAGGAAAATG	GTACAGGAAG	ATGAAAAAAT	TGGCTTTGAA	ATTTCTGAAA	120
ACCAGAAGAG	GCAGGCTGCA	ATGACTGTGA	GAAAAGTCCC	TAAGCAAAAA	GGTGTCAACT	180
CTGCCCGTTT	CAGNTCCTCC	TTCTTACCCA	CCACCGCAGG	ACCCGTTAAA	CCACGGCCAG	240
TACCTGGTCC	CCGACGGCAT	CGCTCAGTCG	CAGGTTTTTG	AGTTCACCGA	ACCCAAGCGC	300
AGCCAGTCAC	CATTTTGGCA	AAACTTCAGC	ATGTTAACCC	CCATCACTCG	AG	352

- (2) INFORMATION FOR SEQ ID NO:806:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 272 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:806:

GCACCCCGGG	AGCTGAGTGA	TTGCAGAAAC	TGGCCTTCCA	TCTCTCTCAG	ACACCAAGCT	60
GCAGATCCAG	GCTTTTCTGG	GAAAGTGAGG	CCACCATGGC	TCTGGAGAAG	TCTCTTGTCC	120
GGCTCCTTCT	GCTTGTCCTG	ATACTGCTGG	TGCTGGGCTG	GGTCCAGCCT	TCCCTGGGCA	180
AGGAATCCCG	GGCCAAGAAA	TTCCAGCGGC	<b>AGCATATGGA</b>	CTCAGACAGT	TCCCCCAGCA	240
GCAGCTCCAC	CTACTGTAAC	CAAGGTCTCG	AG			272

- (2) INFORMATION FOR SEQ ID NO:807:
  - (i) SEQUENCE CHARACTERISTICS:

<ul><li>(A) LENGTH: 277 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:807:	
CCTAACCTCG CTCTCGCGGC CTACCTTTAC CCGCCCCACC CTCAGGAACT TTTGTTAGGA  AAAAATTGAA AGAACTTAAG TCTCGAATGT AATTGGAATC TTCACCTCAG AGTGGAGTTG  AAACTGCTAT AGCCTAAGCG GCTGTTTACT GCTTTTCATT AGCAGTTGCT CACATGTCTT  2	60 20 80 40 77
(2) INFORMATION FOR SEQ ID NO:808:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 279 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:808:	
ATGTTTATCT TCTTTGTCTA GTTTTTCAGC AGAAATATGC CCGTTTCCCC CTGATAATTC 1 CCTTCCTTAG AGACAGCATA ATTGTAGACC TGGCCAGAGA AATGCTGAAA ACAAAGGGAA 1 CCCCCTTGAG CCCAGCCCTT CACCTGCTCT TAGCACTTCT TCAGAGGTTT ACTCTGGAGT 2	60 20 80 40
(2) INFORMATION FOR SEQ ID NO:809:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 247 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:809:	
GGGCAATGGT TTGGCTTATG AAGACTTTAG TTTCCCCATC TTTCTTCTTG AAGATGAAAA TGAAACCAAA GTCATCAAGC AGTGCTATCA AGATCACAAC CTGAGTCAGA ATGGCTCAGC	60 120 180 240 247
(2) INFORMATION FOR SEQ ID NO:810:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 561 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:810:

GAATTCGGCC	AAAGAGGCCT	ACCCGGGCTC	AGTGTGCCGA	CTTCTGACTG	CAAATGATCT	60
			TTAAGAAAAA			120
GCCTCACAAA	CTTAGAAATG	CTTCAGAGTA	AGTATCTGAG	AAGCAAGCCC	ACCCCACATC	180
CACCATATAT	CATCGTTTCT	GTTAAGGGCC	ANCCCATTTC	TTCAGACAAA	TTCTATCTTC	240
TTCCTCCCAT	CCCACTTACT	TTTGACTTTG	AAGGTGGATT	ATCTCATCTC	AAATTTCCTT	300
NCCAGAATAG	NACCACATTT	CAGCAAAATA	TTGGGTGGCT	GGTTCTTTTC	TTCAAGACCC	360
ACCTGCATCT	GTGTTGGTCC	TCTATGTGAG	GAAGGTCCTC	TATGTGAGAA	GATCTGAGGG	420
GTAGGCAGGT	TTTAATGGAC	TAAGATTTTT	TTTATATGTA	TAAGGGGGGT	GGGAGGAGGA	480
TTTTAGAAAA	CTAGATCCAT	TGGCCTGCAG	TTAGAAGTCG	AACACTGAAC	TTGGGAAGGC	540
TTTCTGTGGC	CGAACCTCGA	G ·				561

- (2) INFORMATION FOR SEQ ID NO:811:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 310 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:811:

GAATTCGGCC	AAAGAGGCCT	ATCAATTNGT	TTTNTTACTT	GGTACTGTGA	TTTATTATNT	60
NTAATTATNG	TNAANTNNTA	AAGCTCAATT	TTACCAGCTT	CAGCAGTTTT	AAGTGTATAG	120
TTGCACAACA	CNACATAACT	CATCTAAGGT	GAATTATACT	GTAATTTTCT	TTTNGTGCCT	180
AGCTTTTTGC	NATTACCATA	GTATCCTGAA	GTTTTGTGAT	TGTNGTACCA	TGAGACAGGA	240
TGTTATAAGA	TTAATATTTC	AATGTATATA	TATGCCTAGC	ATATTTTCNT	TATGCATGCA	300
GCCACTCGAG						310

- (2) INFORMATION FOR SEQ ID NO:812:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 388 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:812:

GAATTCGGCC	AAAGAGGCCT	AGGCGGCAGG	AGGCAGTGGC	GTTGGTGGGA	AGCGCAGCTC	60
GAAAAGCGAT	GCCGATTCTG	GTTTCCTGGG	GCTGCGGCCC	ACTTCGGTGG	ACCCAGCGCT	120
GAGGCGGCGG	CGGCGAGGCC	CAAGAAATAA	GAAGCGGGGC	TGGCGGCGGC	TTGCTCAGGA	180
GCCGCTGGGG	CTGGAGGTTG	ACCAGTTCCT	GGAAGACGTG	CGGCTACAGG	AGCGCACGAG	240
CGGTGGCTTG	TTGTCAGAGG	CCCCAAATGA	AAAACTCTTC	TTCGTGGACA	CTGGCTCCAA	300
GGAAAAAGGG	CTGACAAAGA	AGAGAACCAA	AGTCCAGAAG	AAGTCACTGC	TTCTCAAGAA	360
ACCCCTTCGG	GTTGACCTCA	TCCTCGAG				388

- (2) INFORMATION FOR SEQ ID NO:813:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 460 base pairs
    - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA	•
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:813:	
GAATTCGGCC AAAGAGGCCT AAGCAAGCTC TGCTTTAGTT TCCAAGAAGA TTACAAAGAA TTAGAAAGAA TTAGAAAGAA TTAGAAAGAA TTAGAAAGAA	60 120 180 240 300 360 420 460
(2) INFORMATION FOR SEQ ID NO:814:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 225 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:814:	
SAATTCGGCC AAAGAGGCCT AAAGTGCTTT AAAACAATTT TTCACTGTGG ACAACCGAAG ACCACAAAAC ATTTGAGAAC TACCATGACA GACAGAGAAC AAAATTACAA AACAGAAAAA STTAAAAAAC AGGAGAACTG CACCACTGCA CTCCAGTCTG GATACCAGAG AGAGACTCCA CCTCAAACAA AACAAAACAA AACAAAAAAA CCCCCAAAAAC TCGAG  (2) INFORMATION FOR SEQ ID NO:815:	60 120 180 225
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 140 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:815:	
GARTTCGGCC AAAGAGGCCT ATTTATCGTT TAAAAAAGTC AGTAGAACTA AACATGAAAG TGATTCTTCT GATTTTTTGG GGGGTGGTTA TTTGCACATG GAAACAACAA CAAAAATGCT TCAGATACAA TTTGCTCGAG	60 120 140
(2) INFORMATION FOR SEQ ID NO:816:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 540 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
·	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:816:

```
GAATTCGGCC AAAGAGTCCT AAAACCAACA AGCCAGGCTG ATTTCTAGA GGGATCAGTG 60
ATGTGGGGTA CAATGACACC TTCCCTGTGG CTTGTTATGC CTCCGGTTTT GTTTTTGAAT 120
CTTGGTTGCT GGTGGGGTAT TGCCCCCTCG GCTCCTCTAT GCTTTCGCGT GTGTGAAAAT 180
GCAGGAGTGG ACCACTGTGC ACAGCAGGAC CATGGCTGTG AGCAGCTGTG TCTGAACACCG 240
GAGGATTCCT TCGTCTGCCA GTGCTCAGAA GGCTTCCTCA TCAACGAGGA CCTCAAGACC 300
TGCTCCCGGG TGGATTACTG CCTGCTGAGT GACCATGGTT GTGAATACTC CTGTGTCAAC 360
ATGGACAGAT CCTTTGCCTG TCAGTGTCCT GAGGGACACG TGCTCCGCAG CGATGGGAAG 420
ACGTGTGCAA AATTGGACTC TTGTGCTCTG GGGGACCACG GTTGTGAACA TTCGTGTGTA 480
AGCAGTGAAG ATTCGTTTGT GTGCCAGTGC TTTGAAGGTT ATATACTCCG TGATCTCGAG 540
```

- (2) INFORMATION FOR SEQ ID NO:817:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 597 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: CDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:817:

```
GAATTCGGCC ANANAGGCCT ACTINNAGGC CTGTCGANAN GCGTTGGGTN CTGANGTGAC
AGCTTTCCCC NTCCATGGGA CNCNTTTCCA GACNNTCGNC ACNTCTNCTG AGGTGAATTN
                                                                     120
NCTGTGGGTN TTANGTCTGG GGTGGANNTT CTCTCTCCCC NNNTCTNACT TCNGTAGATG
TGGACCTNGN CCNNCNNTCC ATTGGTCCNC TGCCCTGTGT CTCCAGGGTG CTGCCTCTGC
CTCCTCATAT CACCAGCGTC CCCACTGCCA CTAGTCTGTA GGGGGATTCC GGGCTAGGTG
                                                                     300
CTCTTCCCAT TCGACTTCAA CCAACTTATA TAGCTCCATG GTGGCCTGGG CATCTTCCAC
                                                                     360
AGAGGATGTC CGCTCTTCCC NACCTGGATA TCCCGGTTTA GCAGCTTCTT GGTGAGATGC
                                                                     420
TTCAGAGACA TGGTGGCATT CTCCGGGCAG TCAGCCTTCC GGTTGAGGGG GGGGATATGG
                                                                     480
GAGGTGTCAC GGGTGAGGGA CTTGGGGTGA AAGTACTGAA GGGCTTTGAA GTCGTTGTGG
                                                                     540
ATGGCATGCC CCACCACTAT CTTNCCCTGT GAGTATCTTC AAGATCTGCC CCTCGAG
                                                                     597
```

- (2) INFORMATION FOR SEQ ID NO:818:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 517 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:818:

```
GAATTCGGCC AAAGAGGCCT AGGAAATGAA ACGAATGCAT AAAGCTCTCC AGAAAGATCT
GCCAAGACCA TCAGAAGTAA ATGAAACTAT TCTAAGACCC TTAAATGTAG AACCGCCTTT
                                                                     120
AACAGATTTA CAGAAAAGTG AAGAACTAAT CAAAAAAGAA ATGATCACAA TGCTTCATTA
                                                                     180
TGACCTTCTA CATCACCCTT ATGAACCATC TGGAAATAAA AAAGGCAAAA CTGTAGGGTT
                                                                     240
TGGTACCAAT AATTCAGAGC ACATTACCTA TCTGGAACAT AATCCTTATG AAAAGTTCTC
                                                                     300
CAAAGAAGAG CTGAAAAAGG CCCAGGATGT TTTGGTGCAG GAGATGGAAG TGGTTAAACA
AGGAATGAGC CATGGAGAGC TCTCAAGTGA AGCTTATAAC CAGGTGTGGG AAGAATGCTA
                                                                     420
CAGTCAAGTT TTATATCTTC CTGGGCAGAG CCGCTACACA CGGGCCAATC TGGCTAGTAA
                                                                     480
AAAGGACAGA ATTGAATCAC TTGAAAAGAG GCTCGAG
                                                                     517
```

(2) INFORMATION FOR SEQ ID NO:819:

```
(i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 332 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:819:
GAATTCGGCC AAAGAGGCCT ACTAAATTCT CATATATCTG TGTTTCTAGA ATACTTTGCC
                                                                      60
TTTTTGGGCT TAGTTAATGG TAAGATTCTC ATGTCTGTCT ACATAGGAAT ACTCCACCGT
                                                                      120
ACAGGACACT GCTTTCTGGG TTTAGTTCAT TGATAATTTG TCCGAATGCT CATAAACATG
                                                                      180
TCTATAGGAA TACTCCAATA TATCTAGGAC ACAGTTTTCT CCGCTCCTGA ATACAGGCAG
                                                                      240
ATTTTGTTTC TTTCTGCCTC CCTGTGTTAA TGAGAAGGTA GTCCAGCAGG TTCTCTCTAC
                                                                      300
CTCCTTGCTT TTTTTTCCCC TTAATGCTCG AG
                                                                      332
(2) INFORMATION FOR SEQ ID NO:820:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 340 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:820:
GAATTCGGCC AAAGAGGCCT AACCTGCTCC GTGGAGCGCC TGAAACACCA GTCTTTGGGG
CCAGTGCCTC AGTTTCAATC CAGGTAACCT TTAAATGAAA CTTGCCTAAA ATCTTAGGTC
ATACACAGAA GAGACTCCAÁ TCGACAAGAA GCTGGAAAAG AATGATGTTG TCCTTAAACA
                                                                      180
ACCTACAGAA TATCATCTAT AACCCGGTAA TCCCGTATGT TGGCACCATT CCCGATCAGC
                                                                      240
TGGATCCTGG AACTTTGATT GTGATATGTG GGCATGTTCC TAGTGACGCA GACAGATTCC
                                                                      300
AGGTGGATCT GCAGAATGGC AGCAGTATGA ATACCTCGAG
(2) INFORMATION FOR SEQ ID NO:821:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 518 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:821:
GAATTCGGCC AAAGAGGCCT AGGAGCTATA ATCTTGTAAC AGAGTCTACG TGATTGTAGG
ACAATAGGCA CCACACAAT ATGAGGAAGC AGGTCAGAGA GCGGGCTGAC TTAATGATTA
ATGCTGAATG TGCTACAAGC TTGTTTCATT TTCATTTCTC CTCCTCCTT TTTTCCTGAT
                                                                      180
TAATTTAATA AAGTTCATAG GGGAGGCTTC AAACACATGA GAAATTAAAA CCTTTATTAC
CAGAGTCAGA GCCTGACTAT ATTGATTGAG TGAAGCTTTC CTTTATAAAA TGCAAAGCAT
                                                                      300
GTAAACAATT CCAACACAGT AACATATTCA TGAGTTTTTA AATTCATGAG TTTTAGAGAA
                                                                      360
AATATTTTAC TTAAAACCAG CACTTGATGA TCTCTGACAA TGTTATGTAG CCTGAACCTG
                                                                       420
GAGTTTTGGC TGATGGGTTG TCTCAGCCTG TGACAGGTTT TAGCTGGCTT TGGTTCATCT
                                                                       480
TGTATCACAC CCCCACACTC ACATGCTCAC CACTCGAG
                                                                       518
```

(2) INFORMATION FOR SEQ ID NO:822:

(i) SEQUENCE CHARACTERISTICS:

```
(A) LENGTH: 139 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:822:
GAATTCGGCC AAAGAATTCT AGACCTGCCT CGTGCGTAAG GCAATTGAAT CGAGGGTTAA
GGGTTCATCT TGCTAATGTC AAAAGTGACA CTAACAAGAT TCTTAGCCTC ATCCGCCAGA
                                                                      120
TGACGGGCCT CCGCTCGAG
                                                                      139
(2) INFORMATION FOR SEQ ID NO:823:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 302 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:823:
GAATTCGGCC AAAGAGGCCT AAGATGAGAA AATCAAGGTT CTTAGATGTT CTGGAATTTG
                                                                       60
TTCATTTTCA CATGATTGGA ACATTGTGGT CTTGTCTTTC AAGTCCATGT CTACCATACT
                                                                      120
CCACAGACCC TTTTCTGTCC ACTTTGTCAC CTATAATTCT GAACTCCAAT ATAAAGACTT
                                                                      180
CACCGTATTT GAAAGAGAAT AGTGGGAAGT CTGATGCTCA ATTTTGTGTA CAGAACAGTT
                                                                      240
GCCTCTGTGA CATTGTAACT GCTGAAATAA GAAAATCCCC TTTTGATTCA GGAGCTCTCG
                                                                      300
(2) INFORMATION FOR SEQ ID NO:824:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 291 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (11) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:824:
GAATTCGGCC AAAGAGGCCT AAATCAGCAG TGAACTCAGA ATCAATTGAG TGACATNGAG
                                                                       60
TCAGTAAATC TCTGACTGCC TCAGTTACCC CATATGATAG TTTTGAGGAT GGGAACATTG
                                                                      120
AGAGAGTTGA TTTGGAAGCA TATCAAGAGT AAAAATTCCA ACATTTTTAG TTCCTTTAAG
                                                                      180
TTAAATCCAG GCACTGTCTT TTCCTGCAAG TCTCCTGTTC CTTTCAGATT GCACAGGTGA
GAGTGCTCAG ATTAGGGCTG GAGGTTGTAA ACCATTGCTC CCGTCCTCGA G
                                                                      291
(2) INFORMATION FOR SEQ ID NO: 825:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 545 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
```

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:825:

GAATTCGGCC	AAAGAGGCCT	AAGCTTTTTT	TTTTTTTACA	GACTTCACAG	AGAATGCAGT	60
TGTNTTGACT	TCAGGTCTGT	CTGTTCTGTN	GGCAAGTAAA	TGCAGTACTG	TTCTGATCCC	120
GCTGCTATTA	GAATGCATTG	TGAAACGACT	GGAGTATGAT	TAAAAGTTGT	GTTCCCCAAT	180
				TGATAAAGGC		240
				AGCTGAGTAC		300
TGTATTTTTA	GGTAAAATGC	TTTTTGTTCA	TTTCTGGTGG	TGGGAGGGGA	CTGAAGCCTT	360
TAGICTTTTC	CAGATGCAAC	CTTAAAATCA	GTGACAAGAA	ACATTCCAAA	CAAGCAACAG	420
TCTTCAAGAA	ATTAAACTGG	CAAGTGGAAA	TGTTTAAACA	GTTCAGTGAT	CTTTAGTGCA	480
TTGTTTATGT	GTGGGTTTCT	CTCTCCCCTC	CCTTGGTCTT	AATTCTTACA	TGCAGGGAAC	540
TCGAG						545

- (2) INFORMATION FOR SEQ ID NO:826:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 91 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:826:

GAATTCGGCC	AAAGAGGCCT	AGGTGGTGGA	ATCAAGGCCA	TGAAGGACCT	GTTTATGCGG	60
TGCATGCTGT	TTACCAGAGG	AGGGCCTCGA	G			91

- (2) INFORMATION FOR SEQ ID NO:827:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 420 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:827:

GAATTCGGCC	AAAGAGGCCT	ACTAAGAAAT	GCTATTGGAT	CTTTAGTTTG	TTCAGCTTTA	60
TTTTTCTTAT	AAGGATGAAA	GTGTTGACTT	ACAAGCTCTT	TATATATCAG	ACCAGAAACT	120
ACTITITAAA	AAATATAAAA	TGTAATCACC	ATCTAAAGCA	CTTNGCACAA	TGCATGGCAT	180
GTAGTGAGCA	CATATTTTTA	GCTCTTACTG	TTATTTATTA	TTATTCCATT	GAGAAAAACA	240
TTTCCTAATA	ATAATGAAAT	GACAACATGA	TATGGTAGCA	TCACAAAAAT	CAATACATCT	300
TTCTAAACAT	ATTAGAAATT	ATTTCTGTAT	GAAATAACAG	GTTTAAGGAA	AAAATTTAAT	360
GTGGTCAGAA	GTGTGCAATC	AAAATAATGA	GATGACATTG	GCATGAAGAA	CAAACTCGAG	420

- (2) INFORMATION FOR SEQ ID NO:828:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 368 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:828:

GAATTCGGCC	AAAGAGGCCT	AGAATTCTAG	ACCTGCCTCG	AGCTTAGGGT	GACAGAGTGA	60
GACTCCGTCT	CAAGAACTAG	AAGAGTCCTG	AAGTTCTTTC	TGGAGTATTG	GTGTGATAGA	120
AGCATTAGTA	GTTTCTTTTA	TGTTCTGGAG	AACTTCTGTG	CACATAAATG	TTTATAGATA	180
TATACCCCGT	TTGTATACCA	AAGGAATCTT	CATTATTTTT	CACTGAACAA	AACACCTTAG	240
AGAACATTTC	GTTTGTTTTG	CCAATCAATC	TAATTCTTTT	AAATGACCAC	ATAGTATCCC	300
					TGTCCTATTG	360
CTCTCGAG						368

- (2) INFORMATION FOR SEQ ID NO:829:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 344 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:829:

GAATTCGGCC	AAAGAGGCCT	AATGTTTTTC	AATACCTCAG	TATATTGTAG	GGACTTGTTG	60
AGAACTTGTT	GAATGAATAT	ATTGTTCAGA	GTTTACCATT	ACTCAGTATT	TTAGTTGTCA	120
CATCTTAAAA	TAGATAATCA	TTTTTACCAT	CACACTCCCT	TCATAAGATA	TAGAAATAAA	180
GCCCTTCTTG	TTTGGAAATG	GTGGTATTTT	GGTTTTACTT	TTTTTTAAGT	TACTGTTGTA	240
AGGTACTACT	TTAATATTTT	TATTTAACTT	TATTTGTTTG	TCTTTAGTAG	GACTAAGCTA	300
ATGAGAGCTT	TGACTTGCTT	AAACGTTGGG	CAGGAAAACT	CGAG		344

- (2) INFORMATION FOR SEQ ID NO:830:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 351 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:830:

GAATTCGGCC	AAAGAGGTCT	AGAAGACTTT	TGTATTTTTG	ACTTTGCTAG	TTTGTGGCAG	60
AGTGGAGAGG	ACGGGTGGAT	ATTTCAAATT	TTTTTAGTAT	AGCGTATCGC	AAGGGTTTGA	120
CACGGCTGCC	AGCGACTCTA	GGCTTCCAGT	CTGTGTTTGG	TTTTTATTCT	TATCATTATT	180
ATGATTGTTA	TTATATTATT	ATTTTATTTT	AGTTGTTGTG	CTAAACTCAA	TAATGCTGTT	240
CTAACTACAG	TGCTCAATAA	AATGATTAAT	GACAGGATGG	GGTTCCCCTG	TGCTTTTACC	300
AGTAGCATGA	CCCTTCCTGA	AGCCATCCGT	AGAAAGTACC	TTGTCCTCGA	G	351

- (2) INFORMATION FOR SEQ ID NO:831:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 338 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:831:

GAATTCGGCC AAAGAGGCCT AAAACAAGAT CCACTGGAGG GTCATGTCTG AGTTGTTCTC TTGATGATTT TGGCTGATTA TCTTAATGCC CTTTTCCATT TCTGATGCTC TTGTTCTACA TTTTGGGTGA AAATACCAAT ATTTCTAATT CTGTATCACA TCATCTCACT GTGTAGCAAG GCAGGTCTCC ACAAATTACC CCGTTCCACC TGGAGAGCTC CTTATTGACT TAACGTGATA TTCAGCCAGG TTTTTCTTCC TGTAATAGTT GCTTTGCCTT TAGCAAATTG CCTGGATCAT TGACCTTTCT TAGCCCATGC ATAAAATGCC AACTCGAG	60 120 180 240 300 338
(2) INFORMATION FOR SEQ ID NO:832:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 412 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:832:	
GAATTCGGCC AAAGAGGCCT AATATTATAG AACCACCATA TGTACATTTT TCATAGAGTT TGGGAATGAA ATAGTAAAAG GTATATAGAA AACTAAGAAA AGGGAAAATT CTGGGGGGCT GGGATGAGGA AGTGATTAGC ACCAGGGAAA ACCAAAGTTT ATACCAGAAA GGAACTCTAA TATTAGGCTG CCATATTAAG CCATGTGGCT GGGCTACATT GTGTTAAGTC ACTGATGAAT GATCTAAACA AGAGTCTGGA TATAACCAAA TCAGGAAGGC TTGAAGAATG TGTGTGTTAT TGGGGGGAAC GGTGTCTACA GTAGGAGGTA GATGGTTATG TAAAACTAGA GAAAAGGAAC TAATATAAAG TGTTAGTTGG AATATATTAA TAATTGTCAG TGAAAACTCG AG	60 120 180 240 300 360 412
(2) INFORMATION FOR SEQ ID NO:833:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 151 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:833:	
GAATTCGGCC AAAGAGGCCT ACTGTGGGTT TATATTGATG TGTAACAAGT TGATTTGGAA CACTGGACTC TCATTCTGTT ATTCTGGTTT TGTTTTTTTT GTTTTGTTTT	60 120 151
(2) INFORMATION FOR SEQ ID NO:834:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 233 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(x1) SEQUENCE DESCRIPTION: SEQ ID NO:834:	
GAATTCAGCC TTCATGGCCT ACTCTCGTTG AAGATGTGAA TATCTGTCTG CAGGCATGCA GCAGTCTACA CGCTCTGTCC TCTTCCTTGC CAGATGATCT TTTACAGAGA TGTGTTGATG TTTGCCGTGT TCAACTAGTG CACCGTGGAA CTCGTATTCG ACAAGCATTT GGAAAACTGT	60 120 180

233

TGAAATCAAT TCCTTTAGAT GTTGTCGCGA TTGAATTCTA GACCCGCCTC GAG

(2) INFORMATION FOR SEQ ID NO:835:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 228 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:835:	
GAATTCGGCC TTCATGGCCT AGAACTGGGA GGTAGAAACA AAAATGACTG AACATCTTTT TATCCCCCAA TCGTTACAAA GCCTAAATAA CTCTAAACGG GATGGGAGGG CAAATTTTAG GTCAGTTGAC ATCCTGGAGA AGATATCCTA GGTCCTGTCT CATTCCCTAG ACCGCATAAC ACTCCAACCG TGTAGGCCAT GAAGATTGAA TTCTAGACCT GCCTCGAG	60 120 180 223
(2) INFORMATION FOR SEQ ID NO:836:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 224 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:836:	
GAATTCGGCT TCATGGCCTA GGCTGGTGAT CCATGATGCA AATAATAATA ATAATGATGA TTTTTTTTAA TGTACAGCTC TCACACAAAT TTCATTTTGT GAACACACTG GTAAGTACAC GATGCTGGGG CTTCCAAAAT GTGGCGTATC CCACTGATGG CTCCAACTTG CGAGTGGGCT CAGTTATGAA AAACTCGGGA GAGGACGGGT TGTCGCTGCT CGAG	60 120 180 224
(2) INFORMATION FOR SEQ ID NO:837:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 267 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:837:	
GAATTCGGCC TTCATGGCCT AGGAGCTGTT GCACTTTGGG CCTTGGCAGG ACAAACACTA AAACAACAAA AATATATGGC AGAACAAATT GGATACAGCT TTATAATAAA TATGCTTTTG TCACCATCAG CTAAAATGCA GTATGTTGGT AAGTTATTTT CCTTATTTTA TTTTATTTT TTAGAGACAG GATCTTGCTC TGTTGCCCAG CCTGGTGTGC AGTGGCACAA TTATAGCTCA CTGCAGCCTC AAACCCCTGG GCTCGAG  (2) INFORMATION FOR SEQ ID NO:838:	60 120 180 240 267
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 514 base pairs  (B) TYPE: nucleic acid	

(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:838:	
CANTECCCC TECHTOCCCT AND CANADA A	
GAATTCGGCC TTCATGGCCT AATCAAACTC AAACTACGCC CTGATCGGCG CACTGCGAGC AGTAGCCCAA ACAATCTCAT ATGAAGTCAC CCTAGCCATC ATTCTACTAT CAACATTACT	120
AATAAGTGGC TCCTTTAACC TCTCCACCCT TATCACAACA CAAGAACACC TCTGATTACT	180
CCTGCCATCA TGACCCTTGG CCATAATATG ATTTATCTCC ACACTAGCAG AGACCAACCG	240
AACCCCCTTC GACCTTGCCG AAGGGGAGTC AGAACTAGTC TCAGGCTTCA ACATCGAATA	300
CGCCGCAGGC CCCTTCGCCC TATTCTTCAT AGCCGAATAC ACAAACATTA TTATAATAAA	360
CACCCTCACC ACTACAATCT TCCTAGGAAC AACATATGAC GCACTCTCCC CTGAACTCTA CACAACATAT TTTGTCACCA AGACCCTACT TCTAACCTCC CTGTTCTTAT GAATTCGAAC	420
AGCATACCCC CGATTCCGCT ACGACCATCT CGAG	480 514
(2) INFORMATION FOR SEQ ID NO:839:	J.,
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 291 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:839:	
GAATTCGGCC TTCATGGCCT ACTACATAGA CGTGGATTTT AGGGGGACAA AATTCAACCA	
CTACCGTCTC TTTGCTTGAA ATCACACACA ATTTCCAGAG GCCTAGAGAT GCCACTTTGT	60 120
CCGCAGATCT CTTCCTGGCC CCGCCTCTGT CTGGGCAGCC TGGGTCTGAT TGTCCTTCTG	180
TCTGCCACCC TCACAGTCCT CAGCCGTGGC CTGGTTCCTG TCCTGGGGGC TGACCAGCCT	240
TCTGGGGCCT GGGACCTGGG GCATCGCTGC TGCCTGCCGG CTGACCTCGA G	291
(2) INFORMATION FOR SEQ ID NO:840:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 221 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:840:	
GAATTCGGCC TTCATAGCCT ACCTAAATTA ATAATAATGT ATAGTTCAGA ATTGCTAAGA	60
GTACTTTTT TTTTTTTTT TTGAGACAGG TTCTCGCTCT GCCCTCCAGC CTGGTGACAG	120
AGCAAGATTC CATCTCAAAA AAGAAAAAAA ACACACAGCT AATAGAATTG CCATTGTTTT	180
TCATAATAGA ATCTAGCTGC TTACTCCAAC CTCACCTCGA G	221
(2) INFORMATION FOR SEQ ID NO:841:	
(i) SEQUENCE CHARACTERISTICS:	

(A) LENGTH: 445 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:841:

GAATTCGGCC	TTCATGGCCT	AGTAAAGTTT	CTCTCACCCC	ACTTTAATTT	CATGTGCCAC	60
ATTTTTTCCT	TTCTGAAACT	ATATTGCTTC	CCACATTCGG	ATTTTAGAAT	TTTTCTTTTT	120
AAAGAGATTG	TATTTTTAAT	TATATTTGGC	CTACTTCCCC	ATTGTCAATG	CTTGTACCGT	180
GTGAGAAGTC	CCTAGGATGA	TAGTCATGGT	TTTTTCCCAT	CTTATTAGCT	TATTATTCTC	240
CTTGCCCACC	CCCCACCCCT	GGCAGCTTCC	CACCCTCTCT	AATGCTTCTG	GAAGCTACTA	300
				ATTTTAGCAT		360
			GAGAGGGTTG	TGAGGTGGCT	TATGATGATA	420
AAGAAAAAA	CCCACATATC	TCGAG				445

- (2) INFORMATION FOR SEQ ID NO:842:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 286 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:842:

GAATTCGGCC	TTCATGGCCT	AAATTTATAA	GGTACTCTTT	AACAATTTAT	ATCAGAGTTA	60
GTTGCTATCT	TTAGCACCAT	TGTCCTGATG	GCCTCCACTT	CTAGCTATAC	ATTGCCTCTT	120
TGAAATGAGC	CATTTGGGAG	<b>GCAAATATAT</b>	CAATTAGAAT	GCCTTTAAGA	ATAAAAAACT	180
TAAAAAGCAA	<b>AGAAAAACAG</b>	<b>AATGCCTTTA</b>	GGAAAAAATT	TAATAAAACC	AACTCAAAAT	240
TGTGCAAACA	AGGAAATTTT	AGTGTTTCCC	ATAATAAAAC	CTCGAG		286

- (2) INFORMATION FOR SEQ ID NO:843:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 354 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPÓLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:843:

GGTTCCCAAG	TAATTATATT	CCAAGGAACA	TAGGAGGGGC	AAAAATAATT	CTAAAGACAT	60
AAAGAAAGAA	ACAGGATATT	TTCTAAATAT	TTTTATCTTG	AGACAGAACT	TGGTTTTTTT	.120
TTTGGCTTTA	GCTTGGAAAA	TCTCGTGTCA	TAGATAAATC	TTTCTCCTAT	CTTGAAATTG	180
GTCTTATCAA	GGAACTACCC	GCATTGAGAT	ATGAAGCTCT	GGGCCTCTCT	GGTAGCCTTG	240
CACACCCTTC	ATTCATCACC	TGGTCCCCCA	GATAAGACAG	CCCTGACCTC	AGAATACACC	300
TTGGATTTAA	CATTCTATGG	GACATTTATT	TCTAGTCTAC	CCCCATCCCT	CGAG	354

- (2) INFORMATION FOR SEQ ID NO:844:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 335 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:844:

					ACAAGGCCTG	60
AATAAATGTG	TGGCAGTCTC	AAATTCTATT	CTATATCTCA	GGTGTAATCC	TTACATACTA	120
	GATCATCCTT					180
TTTGGGGTAT	GACAGTATAA	AAAAAGGTTT	AATTTGAGAA	AAAGGATTAA	GTTAAATAGT	240
AAACTTAGTG	TGAGATTTTA	ATCACAAGTA	CAAAAGAGTG	AAGAGCAGCC	TTCATGACAA	300
GGAATCATGT	GACCAGCCCC	CACCCCAAAC	TCGAG			335

- (2) INFORMATION FOR SEQ ID NO:845:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 365 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:845:

GAATTCGGCC	TTCATGGCCT	AAGAAAGGGT	GGGAACTAAC	ATTGATCACA	TTTATGGAAA	60
CCTGCCTTCT	CGTGCTGGGC	ACTTTATATA	TGTTATCTCC	CTTTGTGGTG	CAATCTCATG	120
ACATGCAGTC	ATTGTCCATG	TTTGTGGGTG	AGGAAACAGG	CTTAGGGGTG	GGAGGCTCGC	180
CTGAGGCCCC	ACACTGTTGG	CTGGAGACAG	CGTGGGGCCT	GAGTCTTGCT	CACAGCCTGA	240
ACGCTGCACT	CTGCTGCTCC	GCGTCCCAGG	AAGGAAAAGC	TGCTGCAGTG	GGTTTGTTTT	300
GCCAAATACA	TGGAGGCTTT	TTTCTGGGTG	AGTGCCCAGC	AGTTGATTGT	TCTGTATGCC	360
TCGAG						365

- (2) INFORMATION FOR SEQ ID NO:846:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 229 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:846:

GAATTCGGCC T	TCATGGCCT	AATCCATGTT	GTACAACTGA	AATATAAATA	ATTTTGTCAA	60
TTATACCTAA A	TAAAACTGG	TTTAAAAAAA	CTGGAAGTTT	ATATCTAAAA	ATGTTAATAG	120
TGCGTACCTC 1	TAGGAAGTGG	GCCTGGAAGC	CATTCTTACT	TTTCAGTCTC	TCCCATTCTG	180
TACTGTTTTT 1	TGTTTTACTT	TCGTGCGCTG	CAGGTCTAGA	ATTCAATCG		229

- (2) INFORMATION FOR SEQ ID NO:847:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 575 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:847:

GAATTCGGCC	TTCATGGCCT	AGGGGAGAGT	ATCATCTCAC	CAAAGGTGAA	AATGGCATTA	60
CGGACATCAG	GACATCTCTT	ACTGGGAGTA	GTTCGAATCT	<b>ATCACAGGAA</b>	AGCCAAATAC	120
CTTCTTGCAG	ACTGTAATGA	AGCATTCATT	AAGATAAAGA	TGGCTTTTCG	GCCAGGTGTG	180
GTTGACCTGC	CTGAGGAAAA	TCGGGAAGCA	GCTTATAATG	CCATTACTTT	ACCTGAAGAA	240
TTTCATGACT	TTGATCAGCC	ACTGCCTGAC	TTAGATGACA	TCGATGTGGC	CCAGCAGTTC	300
AGCTTGAATC	AGAGTAGAGT	GGAAGAGATA	ACCATGAGAG	AAGAAGTTGG	GAACATCAGT	360
ATTTTACAAG	AAAATGATTT	TGGTGATTTT	GGAATGGATG	ATCGTGAGAT	AATGAGAGAA	420
GGCAGTGCTT	TTGAGGATGA	CGACATGTTA	GTAAGCACTA	CTACTTCTAA	CCTCCTATTA	480
GAGTCTGAAC	AGAGCACCAG	CAATCTGAAT	GAGAAAATTA	ACCATTTAGA	ATATGAAGAT	540
CAATATAAGG	ATGATAATTT	TGGAGAAGGC	TCGAG			575

- (2) INFORMATION FOR SEQ ID NO:848:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 539 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:848:

ATCCTGGAGT	GCAAAAATAA	AATCCACTCA	AGAGTCACAA	GGCCCGCTGT	GCATAATCGG	60
TTTCACTTTT	ACCTTTTTTT	TTTTTTTTT	TTTTNGAGAC	AGGTCTCACT	CTGTCACCCA	120
GGCTGGAGTG	CAGTGGCACA	TTCTCGGCTC	ACTGCAATTC	CGCTTCCTGG	GTTCAAGTGA	180
TTCTCCCACC	TCAGCCTCCC	AAGTAGGTGG	GATTACAGGT	ACTCACCACC	AGGTCCAGCT	240
AACTTTTGTA	TTTTTAGTAG	AGACAGGGTT	TCACCATGTT	GGCCAGGCTG	GTCTCGAACT	300
CCTGACCTCA	GATGGTCTGC	CCACCTCCGC	CTCCCAAAGT	GCTGGGATTA	CAGGCGTGAG	360
CCACTGCGCC	CGGCCACTTT	CACACTTTTT	ACAGTGAGTG	GTGAATTAGC	AACAGTAACA	420
CTGATTATCC	AACATATATT	TTGGAATATC	TACTATGTGC	AAGGAATTTT	TCTTAAACTC	480
TAAGGTTATG	AATCACTGGG	CAAATCCATA	TAATTAGAGA	ATTTTAAGTG	CGTCTCGAG	539

- (2) INFORMATION FOR SEQ ID NO:849:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 193 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:849:

GAATTCGGCC	TTCATGGCCT	AGGGGGAAGA	CGGGAAGCAT	ATAAATAAAC	AAATAATTTC	60
TAAAAGCAAC	TTTTTTAAAG	CAAGTGGGAG	GGGCATGCTA	GTTTTAAGAA	CTGTAATAAA	120
AAACACCACC	CATTGTTTTT	TTTTTGGTTT	TTCTTTTTGG	AGACAGAGTC	TTGCTCTGTC	180
ACCCAGTCTC	GAG					193

- (2) INFORMATION FOR SEQ ID NO:850:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 286 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:850:

GAATTCTAGA	CCTGCCATGG	CTGTGGGCGC	GCTCCCCTCT	GACTGCGTCC	CCTTCTCTCC	60
CTGCATCCCC	TTCTCTCCCT	GCATCCTTCT	GTCTTCCTGT	GTGCCCTTAT	CTGCCTGGGC	120
CTTCCTGTCT	TCCTGTATCT	TCTCACCTGC	CTGTGTTGTT	TCTAGCTGTG	TCTCTGCCCT	180
TCCCTGTGTC	ATCATGCCCT	TCTGTGCACT	CCTGTCTGAC	TGTGGCCTCT	TGCTTTCTTG	240
TGTCCCAGCA	TCCACCTGCG	TCTTCCTATC	TGCACGTCCC	CTCGAG		286

- (2) INFORMATION FOR SEQ ID NO:851:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 501 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:851:

GAATTCGGCC	TTCATGGCCT	AATCTCGTTC	TCCATGTCTT	CCGTGTGCTG	GATACACTGG	60
CAGAGCTCAC	AGATGAGAAA	CGCCCCAGG	GTGGCCTCCT	CGTGGTTGTC	CTGGATGTCC	120
ACATTGACCA	CGTGCACAGG	CTGGCAGGTC	TCCTGTTCTC	TGGAATTCAG	ATCTTCCACC	180
ACCTGGTCAT	ACACTCTCTC	TTCGCAAGTG	AGGATCAGAT	CAAACAGGTC	TTTGCAGTTC	240
TGGAATCTTT	CTGGCCGGGG	CTTGATTCTC	TTATTTCTGT	CCAGCATATG	TAAAATCCCA	300
TTCTGTGTAT	AGAGTTCTTT	GTCTTTCCTA	AGAAGATCAT	TGTACATCTG	GTCATATGTG	360
GTTTTGAAAT	CATAAACATT	GGGCTTGTCG	GGAGCTGGTC	CTGGAAGCTT	CACGTGAGTC	420
CCTGTTCCAA	AGGATCGGAC	GCTGAATCCC	CGTTTGCTGA	GGATGTTGTG	CGCCTCCATG	480
CTCCGGTTCT	GGTTGCTCGA	G				501

- (2) INFORMATION FOR SEQ ID NO:852:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 485 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:852:

GAATTCGGCC	TTCATGGCCT	AAGTTGTGCT	GACACCAAAC	ACATCCAGTT	TATAATCAGT	60
ATATTGGAAA	GCTGGTATTG	ATGTAGAACC	AGTGCATAAC	TTTTTATGGG	GTTTTGTTAT	120
TGGTTTTTTT	TTGTAAAGTG	TGAATAAAAG	GTATGTTTAC	TCATTTTTCC	TGAACACTGT	180
GTTGGTAATG	TGCATCATGA	CAATTTCCAG	TGAAGGTGAG	CTGGAGCTGG	TTGGACTAAT	240
GAGACTGAGG	AAGCAGCTTT	TCCTACGATC	TGCATTATGT	AATCACAGGT	CCAGAGAGCT	300
TTATGGAAGC	GGGAGAGGAG	GAGCACTTAC	TCATGTTGTA	TTTGTTAATG	GAGGATGTCA	360
TCTTTTCATA	GATGCTGGAA	CTAGAGTGCA	CTTGTTAGAT	GCTAAAGGTT	TGAGCTTTAC	420
ACAAAATGTC	TTCATCTGTA	TTTGTTATTG	TCTACAATAT	ATTTGAATTT	GGGGCAAGTC	480
TCGAG						485

- (2) INFORMATION FOR SEQ ID NO:853:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 746 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:853:

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GAATTCGGCC TTCATGGCCT AGGTGGCTGC ACCATCGGGA TGTCCTGATC CAACATCGAG
GTCGTAAACC CTATTGTTGA TATGGACTCT AGAATAGGAT TGCGCTGTTA TCCCTAGGGT
                                                                120
AACTTGTTCC GTTGGTCAAG TTATTGGATC AATTGAGTAT AGTAGTTCGC TTTGACTGGT
GAAGTCTTAG CATGTACTGC TCGGAGGTTG GGTTCTGCTC CGAGGTCGCC CCAACCGAAA
                                                                240
TTTTTAATGC AGGTTTGGTA GTTTAGGACC TGTGGGTTTG TTAGGTACTG TTTGCATTAA
TAAATTAAAG CTCCATAGGG TCTTCTCGTC TTGCTGTGTT ATGCCCCGCC TCTTCACGGG
                                                                360
420
CGGTTGCCAC TCTCCTCCCC TCCCTCAGAG ACACCAAACT GCCAAAAACA AGACGCGTAG
                                                                480
CAGCACACA TTCACAAAGC CAAGCCTAGG CCGCCCTGAG CATCCTGGTT CAAACGGGTG
                                                                540
CCTGGTCAGA AGGCCAGCCG CCCACTTCCC GTTTCCTCTT TAACTGAGGA GAAGCTGATC
CAGTTTCCGG AAACAAAATC CTTTTCTCAT TTGGGGAGGG GGGTAATAGT GACATGCAGG
                                                                660
CACCTCTTTT AAACAGGCAA AACAGGAAGG GGGAAAAGGT GGGATTCATG TCGAGGCTAG
                                                                720
AGGCATTTGG AACAACAAAT CTCGAG
```

- (2) INFORMATION FOR SEQ ID NO:854:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 398 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:854:

GCAATTCTAG	TGGTAAGGTG	TTAATAATTT	CACTCTTTTT	ATGTAGACGA	GAGGTTGAGC	60
CTTGAAGGAT	GAGAGGTGTT	TACCGTCTTA	GGATGGGGTA	TAGTAGATAG	AACCATATGA	120
ACCGAAGAGC						180
TCATATGGGA	GCAGTATTTT	TTTTTCTATT	TTGTTCACTG	ATTTTTCTCC	ACTGGTACTT	240
AATAGGCACT	CAATAAATAT	TITGCTAAAT	AAATGAACTG	GTGATGTTGA	AATCCAGTTA	300
GTTTACATTT	TGGTTGGTTT	TGGTATTGTC	TTTTAAAGGT	AGCAAAGACC	AAGTAATTAA	360
ATTTGTTAGA	TGAATATGAG	ATAAAATGGG	CTCTCGAG			398

- (2) INFORMATION FOR SEQ ID NO:855:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 375 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:855:

GCCCTTTGCT	CCATTTCCAA	GGAAAGAAAT	TAAACCAAGA	TGGTGGCTGG	GATTACAGGC	60
ATGAGCCACT	GTGACCAGCT	CGCAAGATAG	AATTTTGAAA	AATGTATCTT	GAGCCTCTCT	120
TTCTCTTTCT	AGTTCTTTAA	GATTCAAGAA	ATCAAATAAG	GTGATAGCCC	TGAAGCCCTT	180
ACAGGCAGAG	GTGCCCTCGA	CTGTGGGTGA	GGAGGTATTC	ATCCCCAACC	AGTGAGATAT	240
TCTGAGTGGG	GAGAAGTGTT	TTCTATCGAT	GACACAGGGT	GGGCCCTATG	GGAGCAGCAG	300
CATGGCCCCA	CCTTCGACCC	AATGCTGAGA	GGAAAGGGGC	CTCAGGAAGG	GGAGACTGAA	360
GCCAGCACAC	TCGAG					375

(2) INFORMATION FOR SEQ ID NO:856:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 309 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:856:

GAATTCGGCC TCATGGC	CTA TGAATTTATT	TTATTTTACT	TATTTATTTA	TTTGGTAGAG	60
ACAGGGTCTC ACTATAT	TAC CCAGGCTGGT	CTCTTACCCC	TGGCCTCAAG	TGATCCTCCT	120
GTCTCTGCAT CCCAGGC	CTC CCAAAGTGGT	GGGATTACAG	GCATGAGCCA	CGATGCCTGT	180
CAGCCTTATT GCACTTC	ACA CACACACACA	CACACACACA	CACACACACA	CACACACACA	240
CACACACTGA TTCAGGC	CTT GAGAGTCAAG	CCCAAGAGCT	CCCTTGGCCC	TGTTCCCCAC	300
TCTCTCGAG					309

- (2) INFORMATION FOR SEQ ID NO:857:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 564 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:857:

GGAGAAATAT G	GCTTCAGTT	TTTCATTACT	TCCTGTTAGT	TCTGGTCTTT	CTGGATACAC	60
ACGCAGCTCA G	CCTTTCTGT	CTGCCAGGAT	GCACTTGCTC	AGAGGGAGTT	TTNGCAGGAC	120
TCTGCAGTGC A	CATCTGTCT	CCTTGGGAAA	GATCCCTGGG	AACCTTTCTG	AAGAGTTCAA	180
GCAAGTGAGA A	TTNGAAAAT	TCNACCNTTA	TTTGAGATGC	CCCAAGGNTC	TTTCATCAAC	240
ATGAGCACCT T	GGAATACCT	CTGGCTCAAT	TTTAACAATA	TCAGTGTGAT	CCACCTAGGA	300
GCCCTGGAAC A	CCTGCCAGA	ACTGAGGGAG	CTGAGACTGG	AGGGGAACAA	GCTCTGCTCA	360
GTACCATGGA C	AGCGTTCCG	TGCCACCCCT	CTCCTGAGGG	TCTTGGATCT	CAAACGCAAC	420
AAGATTGATG C	ACTCCCTGA	GCTGGCTCTT	CAATTCTTGG	TCAGCCTGAC	CTACCTTGAC	480
CTATCCTCCA A	TAGGCTTAC	AGTTGTATCC	AAGAGTGTCT	TCCTGAACTG	GCCAGCCTAC	540
CAGAAATGCC G	GCAGCCACT	CGAG				564

- (2) INFORMATION FOR SEQ ID NO:858:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 680 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:858:

GAATTCGGCC	TTCATGGCCT	AGGTGGTTTG	GAGTCATAAC	ACAGAAGTGG	TGAGAAGTGA	60
TCAGAGGCGG	ATTTCCTGGT	<b>GCATTGAATA</b>	TGGGATGTGA	GATAAGCAGA	GGAGTCAGGA	120
TGGCTTCCCG	GACTATGGTC	CAAACAGTGG	AAAGGATGCA	GTGGCTGTAA	CCTGAAGCAG	180
GAAGTCTGCA	GGTGGGACAG	AAATGTTTGT	TAAGGGAAGT	GTTTTCAGAG	TTTGGTTTTG	240
GATATGTTAA	GTTTGCCAGT	GTAAATGGAC	ATACTGTGTA	GACATTTGGA	AATATGAATC	300
TTGGAAATAT	GAGGTTCTGG	GTATGAGCAG	AGTCCAAGGA	TGAGCCTAGG	GATTGGAGAG	360
CTGAAACCAG	AAAAAGAAGC	TAGAAGGAGA	GGCCAGTTAA	GACAGTGAAA	AGAAGCGAGG	420

CATGAGGATC ACTTGAGGCC AGTAGCTCAA CAGCCTGGGC ATCATAGCGA GACCCTGTCT CAGCAACAAC AACAAAACGG ACAGTGAAGA GAGTATTTGA AGGAGAGGGG AACAGGCAGC GTATTGCTTA TTGCTGAGGG GCAAAGTGAA GACCAAGGAT AGACTGCTGG GCTTGACAGC ATGAGAGGTG CTGGGGGGCCT AGGCAAGTGC AATATTCATG TGGTGTCATT GGGCCAAAGG TGTCATTGGA GGTACTCGAG	480 540 600 660 680
(2) INFORMATION FOR SEQ ID NO:859:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 380 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:859:	
GCAAAAGCAA GTCACGTGGT CATGCAGGGC CTCAGTAAGC AAGAAATATT TACCCGCCCG GGGATGGACA GGTAGGAAAG GGTCTGTTAA GGAAGGGCAG CAAATATTTG GATAACAGTA CTATGTGTTT GTATGGAGCG ATATTTAAGA AGGTTTCCTA GGTTTTTTGA AGCTGAGAGG TTGGGGGCAG GCAGGAAGCT CTGCAGCCTG TAGCCTATGG TATCAAGCTT CATGAGAACG AGAATTAACT AGTTACATCT TTATTACCAT TTTTGGCATC TCTGCAGACA GTGGATCTAA TGCATGATAG CTGATTAATA AATGTTTGTT GAATTAATGA ACAAAATAGC AAGAAACACG TGTTCTCGAG	60 120 180 240 300 360 380
(2) INFORMATION FOR SEQ ID NO:860:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 305 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:860:	
GATTTTGAAT ACACNACNAA GTTAGAAGAA TCTTATTACT TAGATTCCAT TAATATCTTA CTATGTTTTA TTACAAATCT ATGTATCTCT CTAGCCATCC TTTAATCCAT GTTATGTTTT TGATGCTTTG CAAAGTAAGT TGCGAATATT GGTTCATTTT CCCTGAAATA CTTAAGCATG CAAATCATGA ACCAAGTTCC AATATTTGTG TGAAATGCAC AAATAAGTGT AAATTTGCAG AGTTTGGGCA TATGCGTATA CCTATCAAGA CACGGAGCAT TAATATCACC CTGGAAGTCC TCGAG	60 120 180 240 300 305
(2) INFORMATION FOR SEQ ID NO:861:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 312 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:861:	
GAATTCGGCC TTCATGGCCT AGTGAACAAG TAAAGACTGA ATGGGGCTGA GATGAAGGCA ATGTTTCCAA GGAAAGGAAA TGTTATGAGC AAGAGTGTGA GGCAAGAGAA GCTGGAACCA	60 120

GGGAGAAGAC TGGAAAGGTA AGTTGAAGGT AAGGAATGT TGGTGGGCCT CAGATCCCAG	180 240
GCTCATTCCT CAAATCACTT CTTACTTCCC TCACTTATCT TIGTTTAAAT AAGGTTAGCA	300
CACTCACTCG AG	312
(2) INFORMATION FOR SEQ ID NO:862:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 282 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:862:	,
CANTERCORD TECHNOLOGY ACTOROGOUS AND THE TOTAL ACTOROGOUS ACTOROGO	
GAATTCGGCC TTCATGGCCT AGTGGCGGCC ATCTTGTGTT TATCTTCTGG AGTGAAATAT GCTTTTCCAG TTGTCTTCGA AGTTTCACCT CTGCTCCATA TTTTCCAGTG GTCCCGTTGT	60
CAGCCAGAAT GAAGTGGGAA TGCATGCTGT TGAGAACAGT GAGCTTGCTC ATGGGATTGG	120 180
ACATGGTCTG GTATGGCCGG ACAACATCTC TTCCAATGAG GTCCTCCTGG TTTTCCACAA	240
TTCCCCAGGG GGCAATACCT ATGGTGCATA TCTTTCCTCG AG	282
(2) INFORMATION FOR SEQ ID NO:863:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 388 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:863:	
GAAATTCGGC CAAAGAGGCC TAGGGTGCCT GTGGTTCCGG CTACTCGGGA GTCTGAGGCA	60
GCACAATTGC TTGAACCTGG GAGGTGGAGG TTGCGGTGAG CCAANATGGT GCCACTGCAC	120
TCCAGCCTGG GTGACAGAGT GAGACTCTGT CTCAAAAAAA AAAAGACCTT CCTTAATAAG	180
TGGAGTTGGA TAGACATTTT GCTTTGGAAA ACAGAAGCTA TTTACTGTCA ATATTAGGTC	240
TACTTCATTC ATTTCACAGA ATAGGCAAAG ATGTCTGGGG CTTTGCTCAC TAGGGAATTC	300
TGGCCATGGC CTTTTGCTTC TCTTCTAACC AGGCCTTTTG CTTCTCTTCT	360
	388
(2) INFORMATION FOR SEQ ID NO:864:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 115 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:864:	
CARTTCCCC ARRONGE ARRONNETS ARRONNES ANDRESSAGE ASSESSAGE	
GAATTCGGCC AAAGAGGCCT AAAGTTTCTA AAGATTGTAA ATTTAAAAGG AAATGCCAAA TGAATTATTT GTAAAAATTGT TTAAAAAAAT TAATAAATA	60 115

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 137 base pairs

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(B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:865:
GAATTCGGCC AAAGAGGCCT AGATTGAGAA TGCTGACTCG CCTAAAAGCT TTATGCTTAT
CATGTCTGTG GTGCTTGGAG CCTGTGGCCC AGGTGATTTG GGGTTTGGGG ACGCCTCATG
                                                                      120
GGCAGAGACG GCTCGAG
(2) INFORMATION FOR SEO ID NO:866:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 622 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: CDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:866:
GAATTCGGCC AAAGTAGGCC TAAAATCCGT CCGGNAACTA TGAACAATGG CAGCTACAGC
GTANTCAGCT TCAAGGAGCA ATGCAGCAGT TTAACCAGAG ATTCATTTAT GGGGAATCAA
GATTTATTTG CTACATCACA AAGTAAAGAA TTTGATCCTC TTGGTCCATT GCCACCTGGA
                                                                      180
TGGGTCAATT AAATGAAAAG CCCTTACCTG AAGGTTGGNT TTTNAGATTC ACAGTGGATG
                                                                      240
GAATTCCATA TTTTGTGGAC CACAATAGAA GAACTACCAC CTATATNGAT CCCCGCACAG
                                                                      300
GAAAATCTGC CCTGTAAGTT TTCTAAACAT TGTAGATTAA GAGTAAAATA CTAGTCCTTC
AGATTTTGAT ATAAAGATTT GTATTAGCAA GGAGTGGAAG TCTTAGTATT TCTTGAGTTA
                                                                      420
GCTTGACAAT AGGTTTCTGT TCATTAAGTA TTTTGCATTT CCATCTCCCT CTTGGATATT
TTATCCTAGA GATTTTCATA TTTGTTACCA TTTGTTCACA CAGCACTAAA TGAAACTATT
                                                                      540
TAGAATTTAT AGGTATTGTA CTGCTTACCA ATTAGTCTCT GATTTCTGAT TTTCAGCTTC
TTTCATTCCC TNAACACTCG AG
                                                                      622
(2) INFORMATION FOR SEQ ID NO:867:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 453 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:867:
GAATTCGGCC AAAGAGGCCT GGCAGGCGTG TTTATTGACT CTTCCAATTA ATTTTAAAGA
ACCTGAAGAA ATGGACAAAG ACAGAGAAAA GNCNACCAGA TGTGATTCCG CCCTTCCAGN
AAGCAAAGAG CTTATTTCAT CCCATATGAT CGATGCCAGT CATGGGGANG AGTGGCTGTG
TGGAATTAAT GGATTTTCAA CATCCATCAC AGAGGACACA CATGTATATT AGCNAGTCTN
                                                                      240
AAACCTCTTA AATAAACTGC ATTGCTTTTC ATTTTCACTT CCAGTTATAA AACCAGTGGA
                                                                      300
TGATGNAAAG GCCATGTGAC NATACAGCAT GTACTCTCAG GNATGTTTGT GTGACAGGGA
                                                                      360
TATTATATCT GAAGGGACAG GGCAACTGGG AGGGTGAACT GCTCATAACT CTCAATTGTC
                                                                      420
CAGGTAATGA AGCATTGGGA AAGCGACCTC GAG
                                                                      453
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- (2) INFORMATION FOR SEQ ID NO:868:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 642 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:868:

ACGAGCACCT	CCGCCGCGCG	CCTCCTCCGC	CGCCGCGGAC	60
AGTCCCTGAN	CTCTCGCTTT	CTTTTTTAATC	CCCTGCATCG	120
ATGTCAGACG	CAGCCGTAGA	CACCAGCTCC	GAANTCACCA	180
AAGGAAGTNG	TGGAAGAGGC	AGAAAATGGA	AGAGACGCCC	240
AGGAAANTGG	GGAGCAGGAG	GCTGACAATG	AGGTAGACGA	300
AGGAAGAGGA	GGAGGAAGAA	GAAGGTGATG	GTGAGGAAGA	360
AGCTGAGTCA	GCTACGGGCA	AGCGGNCAGC	TGAAGATGAT	420
CANGAGCAGA	AGACCGACGA	GGATGACTAG	ACNGCCAAAA	480
AAAAAGGCCG	CCGTGACCTA	TTCACCTCCA	CTTCCCGTCT	540
CTTCGAGTAG	AGAGGCCCGC	CCGCCCACCG	TGGGCAGTGC	600
TCTCCACCAC	CCAACTCTCG	AG		642
	AGTCCCTGAN ATGTCAGACG AAGGAAGTNG AGGAAANTGG AGGAGAGAGA AGCTGAGTCA CANGAGCAGA AAAAAGGCCG CTTCGAGTAG	AGTCCCTGAN CTCTCGCTTT ATGTCAGACG CAGCCGTAGA AAGGAAGTNG TGGAAGAGGC AGGAAANTGG GGAGCAGGAG AGGAGAGGA GGAGGAAGAA AGCTGAGTCA GCTACGGGCA CANGAGCAGA AGACCGACGA AAAAAGGCCG CCGTGACCTA CTTCGAGTAG AGAGGCCCGC	AGTCCCTGAN CTCTCGCTTT CTTTTTAATC ATGTCAGACG CAGCCGTAGA CACCAGCTCC AAGGAAGTNG TGGAAGAGGC AGAAAATGGA AGGAAANTGG GGAGCAGGAG GCTGACAATG AGGAAGAGGA GGAGGAAGAA GAAGGTGATG AGCTGAGTCA GCTACCGGCA ACCGGNCAGC CANGAGCAGA AGACCGACGA GGATGACTAG AAAAAGGCCG CCGTGACCTA TTCACCTCCA	ACGAGCACCT CCGCCGCGC CCTCCTCCGC CGCCGCGGAC AGTCCCTGAN CTCTCGCTTT CTTTTTAATC CCCTGCATCG ATGTCAGACG CAGCCGTAGA CACCAGCTCC GAANTCACCA AAGGAAGTNG TGGAAGAGGC AGAAAATGGA AGGAACGCCC AGGAAANTGG GGAGCAGGAG GCTGACAATG AGGTAGACGA AGGAAGAGGA GAGGAAGAA GAAGGTGATG GTGAGGAAGA AGCTGAGTCA GCTACCGGCCA AGCGGNCAGC TGAAGATGAT CANGAGCAGA AGACCGACGA GGATGACTAG ACNGCCAAAA AAAAAGGCCG CCGTGACCTA TTCACCTCCA CTTCCCGTCT CTTCGAGTAG AGAGGCCCGC CCGCCCACCG TGGGCAGTGC TCTCCACCAC CCAACTCTCG AG

- (2) INFORMATION FOR SEQ ID NO:869:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 347 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:869:

CCCTATCAAA	60
CTGGCCTCTT	120
TTGTCCTAAA	180
CTAAGCTGTC	240
AAGGGCAGCT	300
	347
	CCCTATCAAA CTGGCCTCTT TTGTCCTAAA CTAAGCTGTC AAGGGCAGCT

- (2) INFORMATION FOR SEQ ID NO:870:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 353 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:870:

GAATTCGGCC	AAAGAGGCCT	ACAGAGAAGC	GGGGCGAACT	GAGGCGAGTG	AAGTGGACTC	60
TGAGGGCTAC	CGCTACCGCC	ACTGCTGCGG	CAGGGGCGTG	GAGGGCAGAG	GGCCGCGGAG	120
GCCGCAGTTG	CAAACATGGC	TCAGAGCAGA	GACGGCGGAA	ACCCGTTCGC	CGAGCCCAGC	180
GAGCTTGACA	ACCCCTTTCA	GGACCCAGCT	GTGATCCAGC	ACCGACCCAG	CCGGCAGTAT	240

GCCACGCTTG ACGTCTACAA CCCTTTTGAG ACCCGGGAGC CACCACCAGC CTATGAGCCT CCAGCCCCTC TCCAGCCCTCA GCTCCCTCCT TGCAGCCCTC GAG	300 353
(2) INFORMATION FOR SEQ ID NO:871:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 426 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:871:	
GAATTCTTAG TTTGTTTCA ACTGGAAAAT ATATAGAGAA AGATGAAGGG GCATTTTTGC CTCTACTCAT CAATTT.TGG TACCAAATTT CTTAAAAACC AGATGGTTCA AAGAAAATTT TTCCAAAAAT TATGTTAACA TTCTGCTCAG ACATGGCTGC TAAAAAAAATA GCATATACAC ATATAAATACT GAACAGCTTC TGCAGTGCCT GTAAACTCTC AGCTCATTTT CTCTTTTCTAA ANAAAATATA TATTATAACT GATCCCAGAA CTCAATCTCT ATTGTGCAGC AGTATCAAAG GTCCTTAAAT TCTCAACAAT GAAGGAAAAA CAAAAACCCA TTCCCCGGAC CGCTTGAGCA GGACTAGGGA AGGAGGAGTC CGTGGATGCA AAGGTTCGCT GCCCCGACGC CCTCAGANTC CTCGAG	60 120 180 240 300 360 420
(2) INFORMATION FOR SEQ ID NO:872:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 430 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:872:	
GAATTCGGCC AAAGAGGCCT AGGGAGGGCT GAGAGGAGG GAGGGAGGAA GGAAGGAAAA AGGAACAAA TGCCGCCTGA CCGTTCTTTG TGGAATGACT ACACCTATGA TGAGTACCTC CATGGACCAT GCACCTGCCT TGAAACAAGG AGGCACAGCA CACAGGGCCC TCAGCTAGAG TGACAGGGAA AGGCCCGAAA TCTGAACCAC TCTTGGGCCC ATCCTTCTC CTCCCACATT CACACCTTCG CCTGCGCTCC CATAATTGCA AATTAATTCA TCCACACATT CACACATTCT CTCCCTCC	60 120 180 240 300 360 420 430
(2) INFORMATION FOR SEQ ID NO:873:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 606 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:873:	
GAATTCGGCC AAAGAGGCCT ACGGGCATGG TGGTAGCTCA GGAGTTCAAG GCTACAGTGA ACTATGATTG TGCCACTGCA CCCCAGCTTG GGTGACAGAC AGTGAGACCC TGTCTCTAAG	60 120

AAATAAATAA AAATAAAAAA TAAGAGGAGC TTTTGGAATT CAGCTATTAG GAAGTTACTG GTGCCCATGG AGGGAAGTGT TCCAGGCAAG TGGTGGTGTT AAAGGTNGAG AGAAGAGACA TTAGCTCAGT GCTTCCCAAA TAGGATANCC CAGCTGGAAC CCCACCCCCT CAGCTGGAAC CCCAGACCAG CCTCCTCCTT CTATCCCGGT GTACCTTCCA TATCTCAGTT CCACCACGGG GAACCTCAAA CCCATTCAA AGCCTGGCT ATGGAAAGAA GAGGAAAGGG AAGTGTACTG AGCTGCACA CCCAGACCAG CCACCCGGG GAACCTCAAA AGCCTGGCA AGTTTGGGAG AAAGTGAATG GAGAGAAGAG CCGAGCTTGA AGATGAATGG GAAAGAAGAT GAGNGGAAGA GGAGGTGAGA CTGAGAGCAT CTGAG	180 240 300 360 420 480 540 600
(2) INFORMATION FOR SEQ ID NO:874:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 99 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:874:	
GAATTCGGCC TTCATGGCCT ACTGGGGGTG AAACTATAAA GAAAAGCAAG AAGTGATTAT CATAAAAGAA AGGTAATGAT GTTTTTTCCC TTTCTCGAG	60 99
(2) INFORMATION FOR SEQ ID NO:875:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 73 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:875:	
GATGAACAGA TACGATTGTG GGATTTTTAT CATCTGTGTA GCAGGTGGTG TATGCATCGG GGTACTCCTC GAG	60 73
(2) INFORMATION FOR SEQ ID NO:876:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 471 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:876:	
GAATTCGGCC TTCATGGCCT ACCAGAAGAT GCCTGCCTTC AATAGATTGT TTCCCCTGGC TTCTCTCGTG CTTATCTACT GGGTCAGTGT CTGCTTCCCT GTGTGTGTGG AAGTGCCCTC GGAGAGGGGG CCGTGCANGG CAACCCCATG AAGCTGCGCT GCATCTCCTG CATGAAGAGA GAGGGAGGTGG AGGCCACCAC GGTGGTGGAA TGGTTCTACA GGCCCGAGGG CGGTAAAGAT TTCCTTATTT ACGAGTATCG GAATGGCCAC CAGGAGGTGG AGAGCCCCTT TCAGGGGCGC CTGCAGTGGA ATGGCAGAA GGACCTGCAG GACGTGTCCA TCACTGTGCT CAACGTCACT CTGAACGACT CTGGCCTCTA CACCTGCAAT GTGTCCCGGG AGTTTGAGTT TGAGGCGCAT	60 120 180 240 300 360 420

CGGCCCTTTG TGAAGACGAC GCGGCTGATC CCCCTAAGAG TCGGACTCGA G 471 (2) INFORMATION FOR SEQ ID NO:877: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 457 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:877: GAATTCGGCC TTCATGGCCT ACGGAAAAAT AGTTATATTC CAGTCTAAGC CAGAAATCCA GTACGCACCA CATTTGGAGC AGGAGCCTAC AAATTTGAGA GAATCATCTC TAAGCAAAAT 120 GTCCTATCTG CAAATGAGAA ATTCACAAGC GCACAGGAAT TTTCTTGAAG ATGGAGAAAG TGATGGCTTT TTAAGATGCC TCTCTCTTAA CTCTGGGTGG ATTTTAACTA CAACTCTTGT 240 CCTCTCGGTG ATGGTATTGC TTTGGATTTG TTGTGCAACT GTTGCTACAG CTGTGGAGCA 300 GTATGTTCCC TCTGAGAAGC TGAGTATCTA TGGTGACTTG GAGTTTATGA ATGAACAAAA 360 GCTAAACAGA TATCCAGCTT CTTCTCTTGT GGTTGTTAGA TCTAAAACTG AAGATCATGA AGAAGCAGGG CCTCTACCTA CAAAAGTGAA TCTCGAG 457 (2) INFORMATION FOR SEQ ID NO:878: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 553 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:878: GAATTCGGCC TTCANGGCCT AATAACATCT CCCCAGACCC AGAAAAACAG AAAGCTCCAC AGAAATTAAA TGTTGAAGAG AAACTCTCAA AGGAAGTTAC AGAAGAAAAC TATCTCTTTC CCAGTAAGTT CAGTGGAAAG TGCACTAGAA CATGAATATG ACTNGGTGAA TTAGATGAAA 180 GTTTTTATGG ACCAGAAAAG GCCACAACAT ATTATCTCAT CCAGAGACCC AAAGCCAAAA 240 CTCAGCTGAC AGGAATGTTT CAAAGGACAC AAAGAGAGAT GTGGACTCAA AGTCACCGGG 300 GATGCCTTTA TTTGAAGCAG AGGAAGGAGT TCTATCACGA ACCCAGATAT TTCCTACCAC 360 TATTAAAGTC ATTGATCCAG AATTTCTGGA GGAGCCACCT GCACTTGCAT TTTTATATAA 420 GGATCTGTAT GAAGAAGCAG TTGGAGAGAA AAAGAAGGAA GAGGAGACAG CTTCTGAAGG 480 TGACAGTGTG AATTCTGAGG CATCATTTCC CAGCAGAAAT TCTGACACTG ATGATGGAAC 540 AGGAATGCTC GAG 553 (2) INFORMATION FOR SEQ ID NO:879: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 176 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:879: GAATTCGGCC TTCATGGCCT AGGTTCTTAG GCTCTGAGAT ACTTCCTGCT TCCCTCACAA 60

ACATGCTTAT GTTTGGTGTG CATGCACATT TGCCTATCAG CACATATAAA GAGACAGTGG AAAAGTCAGA AGTGTTTTCA GGTTATTTTC CGATTGAATT CTAGACCTGC CTCGAG	120 176
(2) INFORMATION FOR SEQ ID NO:880:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 320 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:880:	
GAATTCGGNC TTCATGGCCT ACTTCCTCTT CCTCCTCTTC CTCTTCCCCT TCCTGGTGCA GGTACATGAC ATTCCGCACG TTCCGGACGG CCCGGGCAGT CGGAGACAGG ATCACTGTGT CACAACTGTC ATCACTGTCC CCCTCACTGT CCAAAATGTA GTCCCGGGGA ACATGATTCC ACAGCCCATG ATGTCCCCTT TGTAACAGCG TGGCCCAAAG GGTCCCCCAC ACCACCTTCC TGCCCTCATG CTCCGGCTCT ATCTCTTCCC CATCCTCTT CCTCTCTCTT CCTCTTCCCC TTCACTCGAG	60 120 180 240 300 320
(2) INFORMATION FOR SEQ ID NO:881:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 324 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:881:	
GAATTCGGCC TTCATGGCNT AATCTGTAAC ATGAGGGAAT AAACTAGTAT TATCTAAGCA TTCTCTAGAC TTAAAATATG ATTCCTAGAC CACTGAGGAG ATTAAAAATG AGGTGAGAGG GATTTCAAAA TGAAGCGACC TGCCAGACAT GGTGGCTCAC AGCTGTCATC CCAACATTTT GAGAGACTGA GGCAGGGGGA TCGATTGAGC CCAGGAGTTC AAGACCAGCC TGGACAACAT CGCAAGACCC TGTCTCTACA AAATAAAAAA AATGTAAAAA TAGCTAGGTG TGGTGGCACA CACCTATAGT CCCAGCTACT CGAG	60 120 180 240 300 324
(2) INFORMATION FOR SEQ ID NO:882:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 293 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:882:	
GAATTCGGCC TTCATGGCCT ACAGAAATTG AGAGTAAACA GAAACATTTA TAGGTCATTT GCTATTGATT ACGAACGTCT AAGTGCATTT CAGTGTTTTA TATTTTACAA ATGTGTTGGA ATTTTACTTT ACTTATTCTT TTGAGACAGG TTCTCGCACT CCAGCCTAGG CAACAGAGTG AGACTCCGTC CCAATCAGTC AATCAATCAA TCAATCAATA CCACAGCGGA GAAAATCTTT ACAACCTTTTG GTTAGGTAAT GATTTCTTAG GTAGGACACA CAAAACACTC GAG	60 120 180 240 293

	(2) INFORMATION FOR SEQ ID NO:883:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 351 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:883:	
	CAATTCCCCC CTTCATCCCC TA COTACCCA COTACCCA	
	GAATTCCGGC CTTCATGGCC TACCTACGGA GTGCTTCTTT CTCACCCTGC ATGCTCACCA CCTCTCTATT CTGCCTAGTT GCCGTCGCTA TATCCGCAGA CTCCGGGGCTA TCCGGGAGCT	60
	CAATAGGTAT GTGCCATGAT ACCGTGTCCT GGGATTGCCT GAGTTACCAC TTTTTCTCAG	120
	GGGCAGGCAA TTCCATTGTG AACAGTAGTT TTGAATGTTG GGGGAGGTAT GTACGTTATA	180 240
	TAGTGTTTCT GTCTGCCTCC ACCGCCACAT CCATGTTGCT CAGTTGTCCA GAGTTCTTTA	300
	CCTGGTGAAG TGATCCAAAC CTTGATTTCT GAGAGTTCTG AACCCCTCGA G	351
	(2) INFORMATION FOR SEQ ID NO:884:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 454 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:884:	
	GAATTCGGCC TTCATGGCCT ACCTGGTGTT TTTTGTTTTT GTTTTTACCC CTTGTCTTAT	60
	GCCAGTGAGT TCCTTCGGGG TTACTCCTGC AGTAGGTGGA CTATCATCTG GGACAGTTGG	60 120
	GGAAGCTTCG ACAGCCCTGA GTTCAGCAGC CCAGGTAGCT TTGCAGTCTC TCTCTCATGC	180
	AATGGCTTCA GCCGAGCAAC AGCTACAGGT GCTGCAAGAG AAACAGCAGC AGCTTTTGAA	240
	GCTTCAGCAA CAGAAAGCAA AGCTGGAAGC CAAGTTACAT CAGACAACAG CTGCAGCAGC	300
	TGCAGCAGCA TCAGCAGTAG GTCCTGTTCA CAACTCTGTG CCTTCCAACC CAGTGGCTGC	360
	CCCTGGATTC TTCATTCATC CATCTGATGT TATTCCACCC ACTCCAAAAA CAACACCTCT	420
	TTTTATGACT CCACCACTCA CCCCAGCCCT CGAG	454
	(2) INFORMATION FOR SEQ ID NO:885:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 325 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
•	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:885:	
	GAATTCGGCC TTCATGGCCT AGACGAATTT CAAGTATTTA TTACCTCTGT TGAATATAAT	60

120

180

240

300

325

TTATTGAACT GTAAGCTTAT ATATAATTCA ACTTTAAAAA ATGGCCTGAG TTGAACAACC

AGCTCACCAC AATTCTATAA TCTAGGAGTT GGCTCTCGTG GGTCGGCACA GGTCAGCTAG

GGTGCCTGGT CCTGGTGGAG GGCAGGAGGC CCCCTTCCCC TGGCCTCCCT AGCCAGTCCC

CACACACAGC CCCAGTGGCC TCCACAGCTC CACCCTCCTT TCATGGCCGT TCTTTTTCTT

AGATGCCAAA AGCAGAAAGC TCGAG

(2) INFORMATION FOR SEQ ID NO:886:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 231 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:886:	
GAATTCGGCC TTCATGGCCT AGGGAGAATT ATTTGATATT TGTTGATACT TGACAGCAGA	60
TAATTTTTTA ACTGCAAGAC CACTAGAGGT CACCAGCGTA AAACTTTCAA CTTTGATTCT GCTGGTAGTG AACTGAAAAG TTCAACTACT ATTCTGCAAT GTTTCCTTTG TTTCTTTTTT	120
TTTCTTTTTT TTGTTTTGAG ATGGAGTGTT GCTCTGTCAC CCAGGCTCGA G	180 231
The state of the s	231
(2) INFORMATION FOR SEQ ID NO:887:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 355 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:887:	
GAATTCGGCC TTCATGGCCT AGTTGCAGAA GAAAAAAAA AAAATCCATC CCTGCCACTC	60
ACAAGCTGCT ACCTACAGCA GATTACTATC CTAAGCCTCA ATTTTGCCAT CTGAAAAAAA	120
CAGAAAAAC AGTTAATAAT ACCTCACCAG GTTCTTGCTA ATTCTTTAGT AACACAGAGG	180
AATCTTTTAG CCCTTCTTTT TTTGTCTTAT AGCTTAAACC ATGCTGCAGG AAATGTATCA	240
ATCCAAGATA AAAGAGCTGA AATCCAAGAA CCTCCCCCTC ACATTTTGTT TGTTTGTTTG	
TTTTGTTTTG TTTTGTTTAG ACACAGGATC TTGCTCTGTC ACCCAGGCTC TCGAG	355
(2) INFORMATION FOR SEQ ID NO:888:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 359 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:888:	
GAATTCGGCC TTCATGGCCT AGCCACCACG CCCAGCCTCA ATTGCATTC TACACACAAG	60
GANTANTCCA AAAAGGAAAT TAAGGAAACA ATTCCATTTA CAGTAGCATC AATATGAATA	120
AAATATTTAG AAATAAACTT AACCAGTGAT GTACAGTGAC AGTATGTACA CTGAAAGCTA	180
CAAAACATCA CTAACATAAA TGAAGACAAA TTAGACATCC TGTGTTAATA CATTGGAAGG	240
CTCTTAAGCT GTCAATACTA AAGGTGATCT ACAAATTCAG TGCAATCCCT GTCAAAATCC CAATGATGTT TTTTGAAGAA ATAGAAAAAC TCATCTGGGA ATTCATACGG AATCTCGAG	300 359
CANIGATOTT TITTOANGAN NIMONANANC TCATCTOGGA NITCATACGG NATCTCGAG	333
(2) INFORMATION FOR SEQ ID NO:889:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 203 base pairs	

(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:889:	
GAATTCGGCC TTCATGGCCT ACTAAATTGG AATAAAAGTT TTAATAATAC TAACTTGTCT TTTTTTTTTT TCTAAAATTG ATTCCATTGC TACTGTTAAT AGTATAAATC TTAAAAGGGT GAATTTTTTG GATGAAATTA ATGCTTATTC TTTTCTTTTT AAACAGGGCA ATAAATGTGT TCGTAAGTGC CAACCAACTC GAG	60 120 180 203
(2) INFORMATION FOR SEQ ID NO:890:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 376 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:890:	
GAATTCGGCC TTCATGGCCT ATAGGCCATG AAGGCCGGCC TTCATGGCCT AGTTGATTGG TTTTCTTAGG TCAGCAATGA GTCTTAAAGA TAAAATTTCT ACTGTGTAAT CTTTAGTGTT TTCTTTTTT TTTCAACTAT CTTTTAATCA GTTTCAAACA TTTCAGTGAT TAAAAGAGAG ATTTGTTTGT TACGGTGGT CTCTCTAGTG GAAAAAAAAT TTCCCCATCC CTTTGGAAAT ATTTTCTTTA AAGGAAATCA TGTTTTTAAA ACAAATTATC GAAATCAGCT TTCTAATCAA TTTGAATCAT CTCGAG	60 120 180 240 300 360 376
(2) INFORMATION FOR SEQ ID NO:891:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 335 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:891:	
GAATTCGGCC TTCATGGCCT ACGCTTGTCC GTGGCTTCTC TGAGAAGAAA AGTTGAAAAA GGGTAAAAGT TTTCAGGAAT ATTCGGGCTC TCTATTGCTA AGCATAGCGA GTGTCGGTTT TCTCTCTCCA ACAGACATCG CTATTGCGGT TCCCAGGCAG TGGGAAGAGA TGCGGCCCCT GGACATCGTC GAGCTGGCGG AACCGGAGGA AGTGGAGGTG CTGGAGCCCG AGGAGGATTT CTGCTCCCGG TCATCAACGA GATGCCGCGA GGACATCGCG TCGCTGACGC GCGAGCACGG GCGGGCGTAC CCACGGACCC TCGAG	60 120 180 240 300 335

- (2) INFORMATION FOR SEQ ID NO:892:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 288 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:892:

GAATTCGGCC	TTCATGGCCT	AGTATCTTTA	AAGTTAATGT	CTAGCCAAGA	GTTTAGTAAA	60
CGAAGAATTA	AACTGCACTG	TTGATCGGTG	CTTTGTGTAA	ATACATCTTT	AACATTTGGG	120
TGGAGAGGGG	CCTTAAGAAG	GACAGTTCAT	TGTAGGAAAG	CAATTCTGTA	CATGAGTTTA	180
AGCATTCTTG	TTGCATTGTC	TCTGCAGATT	CTATTTTTGT	TTACAATATT	GAAATGTATG	240
TTAGCAAAAT	GGGTGGATTT	TCAAATAAAA	TGCAGCTTCC	CACTCGAG		288

- (2) INFORMATION FOR SEQ ID NO:893:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 493 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:893:

GAATTCGGCC	TTCATGGCCT	ACTCATCGCT	AGTCCATATT	TGGCCTCCTT	TTAAGCAGTT	60
AATTAACAGG	TATTTTTATA	GCATAATGGG	TTTCCTCAAA	CCACCACCCA	ACCAAAACCC	120
AGCCCTTGAT	GATGACCTGC	GCCCACCACG	CAGGGCGCCC	TTGATGCACA	CGCACCTGCC	180
GCCCCCGCCC	TGTGACCACC	GCCCTGAGTG	CCGGGCTCAT	CATCCCTTCC	ATGCCCTTTC	240
TACATTGCTA	CTAAGAATCT	GTGTGTATTC	ATTAAGACCA	TTACTTTTCT	TTCAGATTTT	300
AAATTTATTA	AAGGCTTTAG	TGCTGAATGT	GATTTTGAGG	ACTCTTTTAA	AAAAATACTT	360
TTGGTTGGAA	TGTGGACATT	TCCCACTTAG	CATTGTGTTG	CTCATGTTCC	TCCATATTGA	420
TGTGTGTTTA	GCTAGAGTAC	CCCCGTCTAA	CTCTGCGAAT	ATGCCACACT	GTGTGCACCT	480
GCATACACTC	GAG					493

- (2) INFORMATION FOR SEQ ID NO:894:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 318 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:894:

GAATTCGGCC	TTCATGGCCT	AAAAAAAGGA	AATAGAATCC	TATAATTTAC	CATGAAAATA	60
TTATGAAAGA	TACAGGTCAG	CATGTATTGT	AGGAGCAAAC	TTAGTGGTCC	TGCTGGTCTT	120
TTGGGTTCAT	TGGTTTGTGG	TTAAGTTTCA	AGTAAGTTCC	CTCTTGGTCT	GGTGTGTTCT	180
GCTGCTGGTG	AGCTCCAGCA	GCTCAAACCA	GCTCTCTCCC	ATTAGTAAGC	CATGCTAAGT	240
TTAGTTTAAC	ACCCATAGTA	GGCCTAAAAG	CAGCCACCAA	TTAAGAAAGC	GTTCAAGCTC	300
AACACCCACA	TACTCGAG					318

- (2) INFORMATION FOR SEQ ID NO:895:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 319 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:895:

GAATTCGGCC	TTCATGGCCT	ACATTGAGTC	AGTCACCAGG	TGTTTTTTT	TGGTTTTGTT	60
					CTGTCATGCC	120
					GCCAAGAGCC	180
				CTTTACTCAG		240
		TGTCTGCAGA	ACCCCTCAA	AACTCTTTCC	TTCACGGTGC	300
AGCTCCACCC	ATCCTCGAG					319

- (2) INFORMATION FOR SEQ ID NO:896:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 275 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:896:

GAATTCGGCC	TTCATGGCCT	AAGACAGGGA	GGCAGACACA	TTGAGAAATA	ATACAAATTA	60
TTATCATCTT	CATAAATAAT	ATAGACAGCT	CTGACGATAA	AGGTGTGTAC	CAGATATGAC	120
AGGAGCAGAG	CTGAGGCATC	CAGCACCTTC	AGGGATGAGG	GGTAATGGTG	TTAGGAAAGG	180
TTTTCTGTAC	TTCCTCTACG	TGGGTGCTTT	TCTCCATCTC	TACTTTCAAA	TCCCACCCAT	240
GCTAAGGCCT	TATCCAAATG	ACCACTGCCA	GAAAG			275
	TTATCATCTT AGGAGCAGAG TTTTCTGTAC	TTATCATCTT CATAAATAAT AGGAGCAGAG CTGAGGCATC TTTTCTGTAC TTCCTCTACG	TTATCATCTT CATAAATAAT ATAGACAGCT AGGAGCAGGG CTGAGGCATC CAGCACCTTC TTTTCTGTAC TTCCTCTACG TGGGTGCTTT	TTATCATCTT CATAAATAAT ATAGACAGCT CTGACGATAA AGGAGCAGGG CTGAGGCATC CAGCACCTTC AGGGATGAGG	TTATCATCTT CATAAATAAT ATAGACAGCT CTGACGATAA AGGTGTGTAC AGGAGCAGGG CTGAGGCATC CAGCACCTTC AGGGATGAGG GGTAATGGTG TTTTCTGTAC TTCCTCTACG TGGGTGCTTT TCTCCATCTC TACTTTCAAA	GAATTCGGCC TTCATGGCCT AAGACAGGGA GGCAGACACA TTGAGAAATA ATACAAATTA TTATCATCTT CATAAATAAT ATAGACAGCT CTGACGATAA AGGTGTGTAC CAGATATGAC AGGAGCAGG CTGAGGCATC CAGCACCTTC AGGGATGAGG GGTAATGGTG TTAGGAAAGG TTTTCTGTAC TTCCTCTACG TGGGTGCTTT TCTCCATCTC TACTTTCAAA TCCCACCCAT GCTAAGGCCT TATCCAAATG ACCACTGCCA GAAAG

- (2) INFORMATION FOR SEQ ID NO:897:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 317 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:897:

CTCGAGTTCC	CCCATCAGTC	TATGTGCCCC	ATGAGAGCAG	GCACACATAG	GAACAGGTCA	60
GTCAGTTCCT	GATGCCCAGC	ACAAGGCCAG	GCACAGAGTG	GCAGGGGAGT	TGTGGGGCCC	120
CACAGACCAG	AGGCCAGCGC	CAATTCTGCC	CCTGCTATTT	GCATGCCCTC	ACCTCTGTGG	180
GCCCCTGTCT	GTCTGCGAGG	ATTCAGGGAG	TAAGTCCTGG	AGCACAGCGC	GGGTTGGAGC	240
ATGCAGAACT	GCCAGGTGCT	ATCAGCACCA	TCATTCTTTC	CACTCCCTAC	TCCCTTTAGG	300
CCATGAAGGC	CGAATTC					317

- (2) INFORMATION FOR SEQ ID NO:898:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 364 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:898:

MMG3 MGGGGG	3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5				
TTCATGGCCT	ATGACCTGGA	AGAGTGGTGC	GAAAGAGAGG	AAGGGGCAGA	60
GTCATGCAAT	TGCTCTCCCT		mma mma a a a a		
	1001010001	CCTCACGGAA	TTATTGAGTG	TGTCCCCTGT	120
CATCACAGTT	GTCTCTTCCA	GTACTTCGTG	AGCTCCCTAA	GGGCAGGGAC	180
TOTO COCO	****			COCCAGGGAC	100
TC TGGGCCCCT	AAAATGAGTG	TGAATCCATG	TCAGGCACTC	TGTGCCAGTC	240
ATATATGATT	TTATCTTAAA	TACTTCTTCA	ATCTACCTAC	TATCACTORCO	300
		INGITCHTCA	AIGIAGGIAC	INICACTIGG	300
GAGATACAGG	CACTAAGGTT	TGTGGAGGTA	AATAACTTTC	CCAAGATCCT	360
					364
	GTCATGCAAT CATCACAGTT TCTGGGCGCT ATATATGATT	GTCATGCAAT TGCTGTGCCT CATCACAGTT GTCTCTTCCA TCTGGGCCCT AAAATGAGTG ATATATGATT TTATCTTAAA	GTCATGCAAT TGCTGTGCCT CCTCACGGAA CATCACAGTT GTCTCTTCCA GTACTTCGTG TCTGGGCCCT AAAATGAGTG TGAATCCATG ATATATGATT TTATCTTAAA TAGTTCTTCA	GTCATGCAAT TGCTGTGCCT CCTCACGGAA TTATTGAGTG CATCACAGTT GTCTCTTCCA GTACTTCGTG AGCTCCCTAA TCTGGGCCCT AAAATGAGTG TGAATCCATG TCAGGCACTC ATATATGATT TTATCTTAAA TAGTTCTTCA ATGTAGGTAC	TTCATGGCCT ATGACCTGGA AGAGTGGTGC GAAAGAGAGG AAGGGGCAGA GTCATGCAAT TGCTGTGCCT CCTCACGGAA TTATTGAGTG TGTCCCCTGT CATCACAGTT GTCTCTCCA GTACTTCGTG AGCTCCCTAA GGGCAGGGAC TCTGGGCCCT AAAATGAGTG TGAATCCATG TCAGGCACTC TGTGCCAGTC ATATATGATT TTATCTTAAA TAGTTCTTCA ATGTAGGTAC TATCACTTGC GAGATACAGG CACTAAGGTT TGTGGAGGTA AATAACTTTC CCAAGATCCT

- (2) INFORMATION FOR SEQ ID NO:899:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 307 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:899:

					TGGATATGAA	60
GATTATTATG	ATTATTATGG	TTATGATTAC	CATAACTATC	GTGGTGGATA	TGAAGATCCA	120
TACTATGGTT	ATGAAGATTT	TCAAGTTGGA	GCTAGAGGAA	GGGGTGGTAG	AGGAGCAAGG	180
GGTGCTGCTC	CATCCAGAGG	TCGTGGGGCT	GCTCCTCCCC	GCGGTAGAGC	CGGTTATTCA	240
					TGTCCAACAA	300
ACTCGAG						307

- (2) INFORMATION FOR SEQ ID NO:900:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 478 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:900:

GAATTCGGCC	TTCATGGCCT	AATTTCCATC	ANGAANTCNG	TGAGGTTCTC	AGATGTGGCA	60
ATGTCCACGC	AGTTTCGCAC	CANGGCATGG	CGGTTCTTGT	CTCCCATTTC	TGGCTGTCCC	120
AGGTAGCGCA	GATGCCAGGG	TGCCCCTGCC	CTGTCCATAG	AGCGTCGGGC	CCTGAGAACA	180
AATGGGCTGG	CTTGCTGGNC	CTTAAGGAGG	AATACCATCT	CATGGTCAAG	GAAAGTCTCA	. 240
GGTTCCATGT	TGTCACACAA	ACCACGAAGG	CGGTGGATGA	GGCTTTCCAA	ACTGTGATCT	300
AAAACACTTC	CCTGCAACAG	GTACTCCATC	ATGTTAATGG	TGCCCCCAGT	GACAGGGATC	360
ATGGTGACTG	GAGGTGCCTC	CATGGTGTCT	AAGTTGAAGA	CAACACAACT	GGACTCAGAG	420
CCCCCAGTCA	GGTAAGGCAC	GGGATATACC	TCCTTGAGGC	TGTAGTGTCT	TCCTCGAG	478

- (2) INFORMATION FOR SEQ ID NO:901:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 468 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:901:

NATCCTGAAG	AGACACTACT	ACNACCAAAT	GGAACCCCAG	AAGAAATAAA	60
CNAATAAAGA	AAATTGAAAC	NACTGGTTGC	NACCNAGAAA	TAACATCATT	120
CTCAACCAAA	*****			IMCAICALL	120
CIGNAGGAMA	AAAAGTACCA	GGAGGACTTT	AACCCGCTGG	TGAGAGGATG	180
TGCTGTAAGA	ATCACACTCG	GGCATACATC	CACCATCTGC	TGGTGACCAA	240
GCCGGAGTCC	TGCTTATCAT	CCACAACTUT	CAACACTACT	TTCCCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	
	TOCTINIGAT	GCACAACTTI	GAACACIACI	I I GGGTTTTTT	300
CGGGAAGCAC	TAAAAAGTGA	CAAACTGGCA	CAGTTGAAAG	AGCTCATCCA	360
TCTTCACATC	TTCCAAATAC	8 8 CTCTC8 CT	CDECS CS CEC	100000000	
	LIGCAMATAC	MAGICICACI	CITCACACIG	AGCCTGTACC	420
CATGGGAAGA	CGTGAAGAAG	AAATAATCTG	AGCTCGAG		468
	CNAATAAAGA CTGAAGGAAA TGCTGTAAGA GCCGGAGTCC CGGGAAGCAC TCTTGAGATC	CNAATAAAGA AAATTGAAAC CTGAAGGAAA AAAAGTACCA TGCTGTAAGA ATCACACTCG GCCGGAGTCC TGCTTATGAT CGGGAAGCAC TAAAAAGTGA TCTTGAGATC TTGCAAATAC	CNAATAAAGA AAATTGAAAC NACTGGTTGC CTGAAGGAAA AAAAGTACCA GGAGGACTTT TGCTGTAAGA ATCACACTCG GGCATACATC GCCGGAAGCCC TGCTTATGAT GCACAACTTT CGGGAAGCAC TAAAAAGTGA CAAACTGGCA TCTTGAGATC TTGCAAATAC AAGTCTCACT	CNAATAAAGA AAATTGAAAC NACTGGTTGC NACCNAGAAA CTGAAGGAAA AAAAGTACCA GGAGGACTTT AACCCGCTGG TGCTGTAAGA ATCACACTCG GGCATACATC CACCATCTGC GCCGGAAGCCC TGCTTATGAT GCACAACTTT GAACACTACT CGGGAAGCAC TAAAAAGTGA CAAACTGGCA CAGTTGAAAG	NATCCTGAAG AGACACTACT ACNACCAAAT GGAACCCCAG AAGAAATAAA CNAATAAAGA AAATTGAAAC NACTGGTTGC NACCNAGAAA TAACATCATT CTGAAGGAAA AAAAGTACCA GGAGGACTTT AACCCGCTGG TGAGAGGATG TGCTGTAAGA ATCACACTCG GGCATACATC CACCATCTGC TGGTGACCAA GCCGGAAGCAC TGCTTATGAT GCACAACTTT GAACACTACT TTGGGTTTTT CGGGAAGCAC TAAAAAGTGA CAAACTGGCA CAGTTGAAAG AGCTCATCCA TCTTGAGATC TTGCAAATAC AAGTCTCACT CTTCACACTG AGCCTGTACC CATGGGAAGA CGTGAAGAAG AAATAATCTG AGCTCGAG

- (2) INFORMATION FOR SEQ ID NO: 902:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 570 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:902:

GAATTCGGCC TTCATGGNCT	AGCCAGGGAT	AAAAATACAA	TCTTCAAAGC	GGTCAGAGAA	60
AAAATGCAAA TTATGAACAG	AGGCATCAAG	GTAACAATAA	CAGCCGAATT	CTGGTCAGAG	120
ACAATGCAAA CCACACATGA	GCAGAGCGGN	CCCTTTAAAG	AACTCAAAGG	AAAGAAAAAG	180
TGAATCGACC TGGAGCTCAG					240
GAGAAGAGGA GCTCATGAGG	GGAGAGGGAC	TAGTGTAAGG	AAAGGTGTGT	AGGTGGGAAA	300
AGGNCCAGTG TGTTCAGCAA	TAGATAAGAA	AAGNAGACCA	CGCNAAAAGG	TAGACGAACA	360
GGCAAGGTTG GTCATCAGGT	GAAAAGACAG	GTTAGTGGAC	GATCAAAGAG	GNTCTTGACT	420
GCCGTGCTAC AATAAACTAC	ATATTTTTTT	TTCAGGCAAA	GTAAGGATTT	CAGAGATGAT	480
TTTTAACATG GGATGATATA	ATGCACAGTA	TTTTAGAAAT	ATTGTTCTAA	ATCAAGAGTG	540
GAGAACCCAC TGCGGAGACA	AATTCTCGAG				570

- (2) INFORMATION FOR SEQ ID NO:903:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 322 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:903:

GAATTCGGCT	TCATGGCCTA	CTCCCATCAA	ACTCCAGAGA	AGAGAGTGAA	TACTGGAGAA	60
GAAAGGAGGA	AAATATCTGA	GGAAGCAGCA	AGAAAGAGAA	GGCTGGAATT	TATTGAAAAA	120
GAAAAGAAAC	AAAAGGATCA	GATTATTAGT	TTAATGAAGG	CTGAACAAAT	GAAAAGGCAA	180
GAAAAGGAAA	GGTTGGAAAG	AATAAATAGG	GCCAGGGAAC	AAGGATGGAG	AAATGTGCTA	240
AGTGCTGGTG	GAAGTGGTGA	AGTAAAGGCT	CCTTTTCTGG	GCAGTGGAGG	GACTATAGCT	300
CCATCATCTT	TTTCTTCTCG	AG				322

- (2) INFORMATION FOR SEQ ID NO:904:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 330 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:904:

GAATTCGGCC TTCATGGCCT	AAATGTATGT	AAGGTACAGA	GAGGATGTCT	GGAGGTGCGC	60
CCTGTGGATA TCTTAAGCCT	TTAAGGGTGA	GCAAAAAAACA	ATAGGTTCAC	AAAGGAAAAT	120
GAGAATGGGC TATGAGAAAG	GTAAGAGGAA	AACCAAGGAA	AGAGAACGTT	TTGAGACAGT	180
AGTAGTGGTC AGCAATGTCA	<b>AATTGCTGCA</b>	GAAATTTTCT	AAGAGTGAAA	TTGGGTTTAG	240
CAGCTGCAAG AGGAGTTCAT	TTAATTGGTG	TAGCAGAAGC	CCATTAGATT	GCAGTGTGAT	300
GAGAAATTAT TGGGAACAAG	GATACTCGAG				330

- (2) INFORMATION FOR SEQ ID NO:905:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 452 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:905:

GAATTCGGCC TTCATGO	SCCT AGATGCCGCC	ATCTACCAGG	CCTCTGCCCC	AGAACAGCAA	60
GGGCATTGTG TCCTGCT	rcag gggtcctgga	GGTGGGCACC	ATGACTGAGT	ACAAGATCCA	120
CCAGCGCTGG TTCGCCT	NAGT TGAAGCGCAA	GGCTGCGGCA	AAGCTGCGCG	AGATCGAGCA	180
GAGCTGGAAG CACGAGA					240
CGACCGCTTC CAGCGA	AAGC GGCGATTGAG	CGGGGCTCAA	GCGCCGGGCC	CCTCGGTCCC	300
TACCAGGGAG CCTGAGG	GTG GGACCCTGGC	GGCTTGGCAG	GAGGCAGAGA	CTGAGACTGC	360
TCAGCACTCA GGTTTGC	GCC TGATCAACAG	TTTTGCTTCT	GGAGAAGTGA	CCACCAACGG	420
GGAGGCTGCC CCCGAG					452

- (2) INFORMATION FOR SEQ ID NO:906:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 518 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 906:

GAATTCGGCC	TTCATGGCCT	AGCCATGGAT	TTAAAGAAAT	TGTGACTAAA	CCAATGTTTT	60
AGCATTGATA	AATGGGAAAT	TGCGGAAGGA	TGTAAACGTA	GAGTTTAACT	CTACAACTTG	120
GCTTAGGGAC	TCAGGTATGG	ACAGTGAGAA	TAACTTGGTT	TAGGGACTCA	GATATGGACA	180
GTGAGACTGG	CCACATGAGT	GCCTTTCTCA	CTGTCACACT	CTTACCCAGG	TTGGAGTGCA	240
GTGGCTGTCG	ACAGGTGTGA	TCATAGCTCC	CTGCAGCCTT	GAATTCCTGG	GCTCAAGCAG	300
TCCTGCCTCA	GCCTCCCAAG	GAGGTGGGAC	TAAAGATGGT	GTGCCACCAC	ACCTGGCTAA	360
TTTTTAAATT	TATTGTAGAG	AAGGGGTCTT	GCTATGTTGC	CCAGGTTGGT	CTTGAACCCC	420
TGACCTCCAG	GGATCTCTCC	TGCCTTGGCC	TCCTCAGGAG	CTGGAACTAC	AGATATATGC	480
TAATGTCTTC	AATTTATGGA	AATGCAGAAA	TGCTCGAG			518

- (2) INFORMATION FOR SEQ ID NO:907:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 385 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: CDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:907:

		TTCATGGCCT					60
CC	ACACCTAC	TTCTACACCA	GCTTTGCAGC	CTACATCTTC	GGCCTGGGCC	TTACCATCTT	120
CA	TCATGCAC	ATCTTCAAGC	ATGCTCAGCC	TGCCCTCCTA	TACCTGGTCC	CCGCCTGCAT	180
CG	GTTTTCCT	GTCCTGGTGG	CGCTGGCCAA	GGGAGAAGTG	ACAGAGATGT	TCAGCTACGA	240
GT	CCTCGGCG	GAAATCCTGC	CTCATACCCC	GAGGCTCACC	CACTTCCCCA	CAGTCTCGGG	300
		AGCCTGGCCG		GCAGAAGCTA	GCTGGCCCTC	GCCGCCGGCG	360
CC	CGCAGAAT	CCCAGCGGTC	TCGAG				385
CC	CGCAGAAT	CCCAGCGGTC	TCGAG				38

- (2) INFORMATION FOR SEQ ID NO:908:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 630 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:908:

GAATTCGGCC 1	TCATGGCCT	ACCCCTGTCC	ACTTTGGTCA	CTGTTGGCTG	GGGCCCGTGG	60
AGCTGTCCAG A	AGGGGACCGG	GGCCAGTAGA	GTAGAGGACA	GTATTTGTAG	AGCAGGCATT	120
TCTTCTGAGG 1	TTCCTTGGGA	TCCCCTGAGC	TATGAAAGCT	GGAAGCAGTT	GAAAGTTTTC	180
AGGGAGAGGG A	ATGCTGGAGT	CTCAGAACTT	TAGAGGTGCT	GCAGGAGTCA	GTTCTGGCAG	240
TGAGAGAACA C	CTTGGGCGGG	TTTCACACAC	ACACAGCACT	TGAGCCATTC	TTGGGCAGAA	300
GGGGCCTCAC 1	TTCCAAGCAC	AAGGAGTGTT	AACGAAAAAT	TATTAACATG	GTAAGGAAGA	360
CTTTATTCAG C	GCCATTGCA	GTAGGCATCC	CAATAGTGGG	GAGAGATGGG	GCTCAATTCC	420
AAGTACAAGA A	AGAACAAGTG	GGCACTTAGC	CAAGGAGCAG	GTGGGAGGG	GTCAGAGGAT	480
AGAAAATTAC 1	TAAGAGGAGA	CGTCAAGGTT	AGGGGGATTC	TTGCTGAAGT	CAGGCCAAGG	540
AGCAGGTGGG /	AGGGGGTCAG	AGGATGGAAA	ATTACTAAGA	GGAGACGTCA	AGGTTAGGGG	600
GATTCTTGCT C	GAAGTCAGGC	CTTGCTCGAG				630

- (2) INFORMATION FOR SEQ ID NO:909:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 678 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:909:

GAATTCGGCC	TTCATGGCCT	AGACGGTGAT	GTTTTTGGTA	AACAGGCGGG	GTAAGATTTG	60
CCGAGTTCCT	TTTACTTTTT	TTAACCTTTC	CTTATGAGCA	TGCCTGTGTT	GGGTTGACAG	120
TGAGGGTAAT	AATGACTTGT	TGGTTGATTG	TAGATATTGG	GCTGTTAATT	GTCAGTTCAG	180
TGTTTTAATC	TGACGCAGGC	TTATGCGGAG	GAGAATGTTT	TCATGTTACT	TATACTAACA	240
TTAGTTCTTC	TATAGGGTGA	TAGATTGGTC	CAATTGGGTG	TGAGGAGTTC	AGTTATATGT	300
TTGGGATTTT	TTCGAGGGTG	TAGGGATGCG	AGCTCTGGAG	GGGACCCTCC	TTTCAGGACA	360
GCGCCCTGGC	CCCCAGTGCC	CCACTCACCT	TCCTGGGCGG	GAACCTCAAG	TGCAGCCAGG	420
CTGGGGGACA	GAGTTCCCCC	CAAGCTGAGA	CAGGAGGGGT	CTCAGGCGGC	AAAATTCCTC	480

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CTCCAACTCC TGGTGGGGTG GGGGTCATGG ATGAGGGGGG CCCCTTCCTT CCCCAGCCCA
CTCAGGGCAC CCCTGGCCCG TCCCGCCCCA CCTCCAGCTG CTTCATGGTC TCCTCCAAGC
                                                                      500
TGAGCAGGTT CTCCTGGATT TCCTGGGTCC GTGCTGGGCT CAGGGGGCCG CCCCCTGGGA
                                                                      660
CCCCATCCCC ATCTCGAG
                                                                      678
(2) INFORMATION FOR SEQ ID NO:910:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 634 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:910:
GAATTCGGCC TTCATGGCCT AAGAAGAGGA GGAAGAAGAC GGGGCTGCAG TTGCTGAGAA
                                                                       60
ATCACATCGA AGAGCTGAAA TGTAGCGGCA CCCAATTTCT AGACAACGCT CAGCCAACGG
                                                                      120
ATTCTTTTCA AGCTGCTCAA ACATAAATCT GCCTACTGAA CTCTAGGATA TTTAATTACA
AAAATTAAGA ACTTAGACTT TTTTAAAACT TTTGTATTAG AAATGCGCAT ACATTTATAT
                                                                      240
GAATATATTT TGATAACGTA GGTCTAGAGC TTCTTTTATA TTCAAGCTTA ACATGANAAA
                                                                      300
GAAGAAAAAC AATAAAGTAA ACCTGAGCCC CCACGTCCCA ATTTTTTAAT AGATTATGTG
                                                                      360
ATGTTGGAAA GCTCATTGAT TTTGTATATG TTTCAGCGTG TTACCTTTCT GGCTTCCAGT
TCCCAGGTGT TCTTTGTTTG CCTTTGATAA AATACAGGAT TTAAGAACAG AGAGTACTGC
                                                                      480
AAAATGCCAT GCAGACTTTA AAGAGAATGG CCTGTTTACT AATTGCTGCC CTTCTGATGT
                                                                      540
CTTTATGTAT AGCTCTGATA GAATTTTCAC CAGTCTATGT ATCTCTGGAG TGAGATCCTA
                                                                      600
TGTACAAAGT GACATACAAT TGGAAATCCT CGAG
(2) INFORMATION FOR SEQ ID NO:911:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 452 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:911:
```

CTCGACCTTC	ATGGCCTAAT	GAGCTGTTTT	GTAAACGAGA	TTTGTTTTGT	GGGAAAGGGA	60
ATTTTGTTTC	AAGACTTCCC	TAAGAAACTG	ATAGCATCGG	GTAATTCTTA	AATTTGACTT	120
ATCATAATGG	TATATCTGGA	AGGAATTTGT	CAACTGATAT	GTTATAATTA	TTTTTTAATT	180
TTTTTTTAATT	TTTGAGATAG	GTCTTACTCT	CTTGCCCAGA	CTGGAGTGCA	GTGGTGTGAT	240
CATGGTTCAC	AGCAGCCTCA	AACTCCTGGG	CTCAAGAGAT	CCTCCCACCT	CAGTCTCCTG	300
AGTAGCTGGG	ACTAAAGGCA	TGTGCCACCA	TGCCTGGCTA	GTTAATTTTT	TTTTTTTTT	360
TTAAGTAGAG	ATGAAGTCTT	GCTGTGTTGT	CCAAGCTGGT	CTCACACTCC	TGAGCTTGAG	420
CAACCCTCCT	CTAGGCCATG	AAGGCCGAAT	TC			452

- (2) INFORMATION FOR SEQ ID NO:912:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 503 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:912:

GAATTCGGCC	TTCATGGCCT	AGCGGGCTAT	GTGGCTGATT	GAAGAGTATG	CAATGAGCGA	60
TTTTAGGTCT	GTTTGTCGTA	GGCAGATGGA	GCTTGTTATA	ATTATGCCTC	ATAGGGATAG	120
TACAAGGAAG	GGGTAGGCTA	TGTGTTTTGT	CAGGGGGTTG	AGTTTGATGA	GTTTAGGCAG	180
GGCCTGGATC	ACCTCTTTCT	TCTCCAGCCC	ATTGAGCACC	GGGATGAGGA	AGCGGACGTC	240
TGGCAGTCGC	TTGTGGTAGA	GATCCCGGAC	CCGCTTCACC	AGCTCTGGGG	AGGGTGGGAC	300
TTTGTCTGTG	AGGCTGTGCA	GACATCTCGT	GACCAGTGTC	TCTGCTCCCT	TGGGACAATT	360
TTCCACCAGC	AGGAGCAGCT	CCGGGGAGTT	CATGCCCATT	CCTCGGATCG	GCTGCTCAAT	420
GACCCTCAGC			GATGGCTTCA	GTGTACACGG	CCGCCAGTTC	480
GTGGATCAGC	TTGTGGGCTC	GAG				503

### (2) INFORMATION FOR SEQ ID NO:913:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 336 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:913:

GAATTCGGCC 7	TTCATGGCCT	AAAAGATATT	ATTTTAAATT	AATTTTGAAC	TATAGAAAAG	60
TAGTACAAAT A	AATTCAGAAA	ACTCCCATAT	TTACTTTACA	TGGATTCACC	AATTTTTAAC	120
ATTTTGCTAC A	ATTTGTTTGC	TTCTCTCGCT	GTCTCTACAC	ACACATACAC	ACACAAATTT	180
TTGGGAGGTC T	TAGTGCACGT	CCCGGCCGGC	CCAGGAGGAC	AGGAAAACAT	CACTCACGAA	240
GTCATCCTTG (	GCCCCGAGCC	GCTTTGTCCT	GTCCTTCTGC	AGGAGGCCCT	CCAGGAGGTG	300
TCTTGCGGAA 1	TTTGTAATAT	TTGGTTTCAT	CTCGAG			336

### (2) INFORMATION FOR SEQ ID NO:914:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 366 base pairs
  - (B) TYPE: nucleic acid (C) STRANDEDNESS: double

  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:914:

GAATTCGGCC	TTCATGGCCT	AGACAGTCAA	TGTGGATGAG	AACTAATCGC	TGATCGTCAG	60
ATCAAATAAA	GTTATAAAAT	TGCAAAAAA	AAAAAAAAA	AAGAAGTGAG	GATGACAGGA	120
GAAGGTAGAT	GGTGCAACAT	GAGGGTGCTT	TCTACCAACA	AGGTGTGCAG	CATTGGACAC	180
GCATGACCAC	GTGACCTGCA	GCTCTGATGG	TGCAACATGA	GGGTATGTCC	TACCAACAAG	240
GTGTGCAGCA	TTGGACATAC	TTGACCACGT	GACCTGCGGC	TCTGAAGGTC	CCACCTGTTC	300
TCGTTCTAAA	GTCACCATTT	CTGACCGCTG	TGCTGTGGAA	GGGGAGGCAA	TCAACCAGAA	360
CTCGAG						366

## (2) INFORMATION FOR SEQ ID NO:915:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 391 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:915:

GAATTCGGCC TTCATGGCCT AGGC	AACAAG AGCCCTGAAG	TGCTCCGGGC	ATTTGATGTA	60
CCAGACGCAG AGGCACGAGA GCAT	CCCACG GTGGTACCCA	GTCATAAATC	ACCTGTTTTG	120
GATACAAAGC CCAAGGAGAC AGGT	GGAATC CTGGGGGAAG	GCACACCGAA	AGAAAGCAGT	180
ACTGAAAGCA GCCAGTCGGC CAAC	CCTGTC TCTGGCCAAG	ACACATCAGG	GAATACAGAA	240
GGTTCACCCG CAGCGGAAAA GGCC	CAGCTC AAGTCTGAAG	CCGCAGGCAG	CCCAGACCAA	300
GGCAGCACAT ACAGCCCCGC AAGA		GTGGACAGGA	TCCGGTCAGC	360
AGCCCCTGTG GCTAGAGGAA CACC	CACTCGA G			391

- (2) INFORMATION FOR SEQ ID NO:916:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 381 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:916:

GAATTCGGCC	TTCATGGCCT	ACGGGTGTTT	GAGGAGTACA	TGCGGGTTAT	TAGCCAGCGG	60
TACCCAGACA	TCCGCATTGA	AGGAGAGAAT	TACCTCCCTC	AACCAATATA	TAGACACATA	120
GCATCTTTCC	TGTCAGTCTT	CAAACTAGTA	TTAATAGGCT	TAATAATTGT	TGGCAAGGAT	180
CCTTTTGCTT	TCTTTGGCAT	GCAAGCTCCT	AGCATCTGGC	AGTGGGGCCA	AGAAAATAAG	240
GTTTATGCAT	GTATGATGGT	TTTCTTCTTG	AGCAACATGA	TTGAGAACCA	GTGTATGTCA	300
ACAGGTGCAT	TTGAGATAAC	TTTAAATGAT	GTACCTGTGT	GGTCTAAGCT	GGAATCTGGT	360
CACCTTCCAT	CCACACTCGA	G				381

- (2) INFORMATION FOR SEQ ID NO:917:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 621 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:917:

AGATGGACTG GCTTCAGCTG	GTTTTGGAGG	TGCTTGTGTT	TGGAANAAAT	GCAGGGATGG	60
CAGANGCCTG GCTCTGCAGC	CAGGANCCAC	TGGTGCGCAG	CGCTGAGCTG	GGTTGCACGG	120
TCGACGAAGT TGAGAGCCTC	ATCAAGCGGC	ACGAGGCCTT	CCAGAAGTCA	GCAGTGGCCT	180
GGGAGGAGCG ATTCTGTGCG	CTGGAGAAGC	TTACTGCGCT	AGAGGAGCGG	GAGAAGGAGC	240
GAAAGAGAAA GAGGGAGGAG	GAGGAGCGGC	GGAAACAGCC	GCTTGCTCCC	GAACCCACAG	300
CCAGTGTGCC TCCAGGGGAC	TTGGTGGGCG	GCCAGACAGC	TTCTGACACC	ACCTGGGACG	360
GAACCCAGCC ACGGCCACCA	CCATCCACAC	AAGCACCCAG	TGTTAATGGA	GTCTGCACAG	420
ATGGAGAGCC CTCACAGCCC	CTGCTGGGAC	AACAGAGACT	TGAGCACAGC	AGCTTCCCCG	480
AAGGGCCGGG ACCTGGCTCA	GGGGACGAAG	CCAATGGGCC	CCGGGGAGAG	AGGCAGACCC	540
GGACTCGGGG CCCGGCCCCA	TCTGCAATGC	CCCAGAGCAG	GTCTACCGAG	TCAGCCCATG	600
CTGCCACCCT GCCGCCTCGA	G				621

- (2) INFORMATION FOR SEQ ID NO:918:
  - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 547 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:918:

GAATTCGGCC	TTCATGGCCT	AACATGGGTG	ACACGGATGT	CTATAGTGTC	CACCACATTG	60
TCTGGCATGT	GGAGGAAGGA	GGCCCAGCCC	AGGAGGCAGG	ACTCTGTGCT	GGGGACCTCA	120
TCACCCACGT	GAATGGGGAG	CCTGTGCATG	GCATGGTGCA	TCCTGAGGTC	GTGGAGCTGA	180
TCCTTAAGAG	TGGCAACAAG	GTAGCAGTGA	CCACAACGCC	CTTCGAAAAT	ACCTCTATCC	240
GCATTGGTCC	CGCAAGGCGC	AGCAGCTACA	AGGCTAAAAT	GGCTCGGAGG	AACAAGCGAC	300
CCTCCGCCAA	GGAGGGCCAG	GAGAGCAAGA	AGCGCAGCTC	CCTCTTCCGG	AAGATCACGA	360
AGCAGTCGAA	CCTGCTGCAT	ACTAGCCGCT	CGCTGTCGTC	GCTGAACCGC	TCGCTGTCAT	420
CCAGCGATAG	TCTCCCGGGC	TCGCCTACGC	ACGGGCTGCC	GGCGCGCTCG	CCCACGCACA	480
GCTACCGCTC	CACGCCTGAC	TCCGCCTACC	TAGGCGCCTC	ATCCCAGAGC	AGCTCCCCAG	540
CCTCGAG						547

- (2) INFORMATION FOR SEQ ID NO:919:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 610 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:919:

GAATTCGGCC	TTCATGGCCT	ANACACTCTT	CCTCTTCTCC	TTTTTCCTTT	AGAGATATGA	60
ATCAGGTTCT	TGATGCCTAT	GAAAATAAGA	AGCCATTTTA	TCTGTACACG	GGCCGGGGCC	120
CCTCTTCTGA	AGCAATGCAT	GTAGGTCACC	TCATTCCATT	TATTTTCACA	AAGTAAGTAT	180
NGGATCTTAT	GGCTTTTCTT	ACTCTCTTAG	TGAATTGAGA	ATGTTGCTTA	TAAACCATGT	240
TTAGAACTGA	CAAGATCATG	CTAGTTCATT	TGCTGAGCAA	CCAAGATGTC	AAGAGTTGGC	300
ACTTTTTTGG	CTTCCATTCA	CTTTGTTCCT	GGGCTCACTT	TAGAGGACCA	TGGAGTGATG	360
GGGAGAGCGC	AGCTTTGGAG	TCAGCCAGGC	CTGCTCCTCT	TCTCATCCTG	CTCCCTGTCT	420
GCATGGCCAT	GGGCCTGCTA	CTTCTCTGAG	CCTAAGTTTC	CACATCTGCA	AGATGAGAAT	480
GAAGATACCT	ACCTCATAGA	ACTACTGTAA	AGCTTCAAAA	CAAAGTGTGT	AGAGCAGCTA	540
ACACAGAGCA	CACAGGGCCA	CCTGGTCGAT	AAATGGTAGT	AGACCTTATC	ATTATCCATA	500
GTCCCTCGAG			-			610

- (2) INFORMATION FOR SEQ ID NO:920:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 308 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:920:

GAATTCGGCC	TTCATGGCCT	ACTAACTCTC	CTTCTCAAAA	CACCAAAAGI	AAATTTTAAT	60
ACCCAAAACG	AAATTCATTT	TGTTAATCAC	AGCTTAGAAG	GTTTCATATG	ATCTGGCCAA	120
ATCTGTATCT	TGCATCACTC	TTATCACTCC	CCCTCTCTGC	TCACTGTATC	TGCATGATAG	180

GAATCAGCTC ATCTTCCTAT ACATCAGTAC TAAAACAACC TCACTCCTAC CTGAGGCCCT GTGTGCTGTC TGTAGATGGT CCATCTTCTC ACTTCACTCA GGACTCAAAT GTCCCCTCTT CACTCGAG	240 300 308
(2) INFORMATION FOR SEQ ID NO:921:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 293 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:921:	
GCAACCGGGT TTTGCCAGGG CCTATTGCAC CAGAGAGCAG CAAGAAGCGG GCCCGTAGGA TGCGACCAGA CCTTTCTAAG ATGATGGCCC TCATGCAGGG TGGAAGCACT GGGTCTCTAT CTCTGCATAA CACGTTCCAA CACAGCAGTA GTGGCCTACA GTCTGTGTCA TCTTTGGGTC ACAGCAGTGC CACTTCTGCA TCTTTGCCTT TTATGCCATT TGTGATGGGT GGTGCACCAT CATCCCCTCA TGTAGACTCC AGCACCATGC TTCATCACCA CCACCACCTC GAG  (2) INFORMATION FOR SEQ ID NO:922:	60 120 180 240 293
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 492 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:922:	
GAATTCGGCC TTCATGGCCT AGTGGGGCCT GTTTATAGTT GACTGACAGT AAGTTCTATA TGGTATATAA CACTAATTCT CTAGTCTTCT GGGCATATCT ACGAACAAAT ACAATCCAAA TATTATGAGT AACTGGGTTG TGACCACTGC ATGCATTACA CTGAAAGAAA CACCAACTCG AAGCACAAAT ATATTATTAT TATATTTCGG CTCAGCTCTC AGTGGGGAGA GCAGCTACCT CGGACCACAA TGCCATTTAA ACCAGATTCT TTTCAAATAA AATTCTCAAT CTAAGTGGAA AGCCCCCTCA GAGAATGCCT TATTCCCCTA CTAAGCAATC CAGGCTTGTA TAAAACGTCT GATAAGGCCT GTAGTGCCCA TTGAGTATGA GTCTGCTGTT TACATTCTGC ACAGGCCAGG AGGGGAACAG AAGGTGTGAG CCACAGGTGC TCCTGGGTCT GACCAGCAAG TCTAACCCAT GAAGATCTCG AG	60 120 180 240 300 360 420 480 492
(2) INFORMATION FOR SEQ ID NO:923:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 650 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:923:	
AAATAACCAC AAATATNAAG AAATTATAAT CAGGGCAACA GATTAAAATG AAAAGGGGTA TAGAAAGATA TATTTTAGAT AATATAAACT CCTGACAAGC TATGCCCTAG AATTGCAGCC TCCAAACCTT GCCCANGATT TCCACCTTTC CATAGCCTCA CTTCAAGTTC AAATGGAAAT	60 120 180

GAAAACAAAA	TAAAGTGAAC	AGGTGGTTGA	GCCAGCCNAA	GCCTCCCAAG	TTATGTTAGG	240
TGGACAGTAA	GACCAGGTGG	ACAGCATTTG	AGAAACTGGC	TGGACACAGG	GGAGCTGCTA	300
CTGGTAGTTA	TATTTAATTT	GGAGGAATTT	CCAGCCCACT	GATAAAGAGA	GAAACCAAGG	360
AACCAAATGA	CTTTTCTAGT	AACATATAAT	ATATGAGATG	AAATATAATT	CTGTTAGAGA	420
GGACATGGTG	GTGAGATGGG	AAAGAAAAGA	GAAGAGAAAC	AGGCAGACTT	CGGGCACCAT	480
CTCCCTTTGT	TTTCTACAAT	GCATTGGTTT	CCTTCTGTTG	CGGAGCATTC	TTTAGGATTA	540
GCTACAGACC	CCAATGTCCT	CTGAGTAAAT	ATATGTCAGC	TCAGCTCCTG	ACATGATATC	600
CATGCTTATT	GGCCTCCTGG	AGGGCTGGGT	GGTTCTCAGG	GTCCCTCGAG		650

- (2) INFORMATION FOR SEQ ID NO:924:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 527 base pairs
    - (B) TYPE: nucleic acid
      - (C) STRANDEDNESS: double
      - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:924:

TGAGCTGCGC	TAAACTCCAC	CGTGACCTCA	AACTCTTTGG	ACTGTTTGAA	АААААААА	60
NTNGGAAGAA	ANTCCATCCT	CCAANANAAT	CGGCTTAGGA	GGAGATGGAA	CTTTNCCCCT	120
TTCTCTNGGT	TTNGTCCGTC	TGGTGGTCTC	GAACCTGGGA	TTCGGCGAAT	GCGGATTCGA	180
TCATTCACAT	CGGAGCAATT	TTTGATGAAT	CTGCCAAAAA	GGATGATGAG	GTATTTCGCA	240
CTGCGGTTGG	TGACCTTAAC	CAGAATGAGG	AGATCTTACA	GACTGAGAAA	ATCACATTTT	300
CAGTGACGTT	TGTTGATGGC	AACAACCCTT	TCCAAGCAGT	TCAAGAAGCC	TGTGAACTTA	360
TGAATCAAGG	CATCTTGGCC	CTGGTCAGCT	CCATTGGCTG	CACGTCAGCA	GGATCCCTCC	420
AGTCTTTGGC	AGACGCCATG	CATATCCCCC	ACCTCTTCAT	TCAGCGCTCA	ACAGCTGGGA	480
CCCCAAGGAG	TGGCTGTGGA	CTCACCCGGA	GCAACAGGAA	TCTCGAG		527

- (2) INFORMATION FOR SEQ ID NO:925:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 312 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:925:

GATTCGGCCT	TCATGGCCTA	GAACTTTCTA	CTTGGACAAC	TAACACCCAC	AGTCCTCCAG	60
ACAGAAAGAC	AACAGGTACA	AAGCCCTAAG	GATTATAAAG	GTATGCTGCT	TACCATCATC	120
TTAGTGACCA	AGGCAGCGAA	GCTGTTTCTG	TACCTTGGAA	CAGTCTTCCC	TGACAAGCCA	180
GAGAACAGTG	ATAAAGCCAC	CAGCCTTGGG	ATCAGGACTG	AAAAGGCAAG	AGTGATGGAG	240
ATTTCTCCTG	CGCTAAGCCA	AGAGAAGGTT	TCAGCACTTC	AGACAGCTCC	CACCGAAGTA	300
GCCGATCTCG	AG					312

- (2) INFORMATION FOR SEQ ID NO:926:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 322 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:926:

GAATTCGGCC	TTCATGGCCT	AAGATGTTTG	TCTTTATCCA	GTAAGGTGTT	TGTATGCTCC	60
TTAAGTGGCA	GCGGGGAGTG	AGCAGAGCAG	TGAAGATAAA	CATGAAAGCT	GGTGGTAACA	120
AATCCTGATA						180
TTGTGTTTGC	AAGCTGTTGA	CACAACCTGG	AAAGGTTAAA	AGTTTTCAAC	AGACTTGTCA	240
GAGTTTGTGT	TCAATGGAAA	CTGACAGAGC	CTACCGGCTG	AGGGGCTAAT	TTTAATAGAA	300
ATAACCTAGG	TGCGCGCTCG	AG				322

- (2) INFORMATION FOR SEQ ID NO:927:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 430 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:927:

GAATTCGGCC	TTCATGGCCT	AGTGGAACTA	GACTGCCAGC	TGTGAGCCTC	AGAGCTCCTG	60
GCTGCCTGTT	GCTGAGTCTA	TCAGCTGCTG	AGCCTTTCTC	ACCNNAAAAA	AAAAAAAAA	120
AAAAAAAAN	TGNGCTTAAT	AAAATAACCC	TGCACAGAAA	TTTTCTGAAA	TTAAGATAAC	180
ATTCAATGGA	AAACAGAATT	TAATCTACAG	AAATACACTT	CACAGATGTT	TTAGGAACAG	240
AACCTAGAGA	AAATGAAAGT	CAAAATTTAA	TAAAAGAATT	TGTCAGGAAC	TTCAAGGTAA	300
AGACTCCATG	TATTTTTTGG	CAACTATAAA	ACACTAAGAA	GGCTTTTTAA	ATATTAAAAA	360
GCCATTTAAA	CACTTCAAAT	TAAGATTCCT	CAATATACTT	CAGATTTCTG	TACTGAGTTA	420
CCCTCTCGAG						430

- (2) INFORMATION FOR SEQ ID NO:928:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 498 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:928:

GAATTCGGCC	TCATGGCCTA	CGTTAGTGTG	TGGATAGTAT	GTGTGTGTCC	GCACTCATGA	60
TAACTTGAAA	CCAGACATAG	GGTTCATTTT	TGAAAGGTTA	AACCACACTG	TTTCAGGAAC	120
TTGCTCCAAA	TACTACTTGG	TTATCCCTTC	CTTTACCAG1	TAGAACTAAA	GAGTGTGATG	180
TATGAACACA	CTGGGTTGGG	ATTTTCTGTT	GAGGATATGC	AGGGCATTTT	GGCATGAGGC	240
AAATACAGAA	GCAAGATTTC	ATTCTACTTG	GTGATTTGAA	TCATGACAGT	CCTCATTCCA	300
ATCTCTCTTT	AATTCTCTCT	GGCCCTGCCC	ACACTCTGTA	TTTGAAAATC	TTGTTTTTGC	360
TCTTTCCGGA	GCTTCACCCC	TCTACTTACA	TATTGTAAAG	TTGTATAAAT	CTATCATTGA	420
AAGGTCCTCT	CTGCCAGCAG	TGGTGCCACC	CTTTGGTTTG	CTGTGGTACT	TTGCTGTGTA	480
CTCCGTGGCA	TACTCGAG					498

- (2) INFORMATION FOR SEQ ID NO: 929:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 566 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:929:

GAATTCGGCC	TTCATGGCCT	AGTTAAGGGC	ATTTACTCAT	GTTGAACCTA	GTTTTATTTA	60
CAGTATATTT	GTATGCATAG	AAGATGGAGG	TCCACCAAAG	TGTTAATTAT	CCTTACTOR	
AGGTCAGGTA	TAGCTAACTT	TCCTTTTTT	ATATAMAMAMA	TTACATTTGT	GCTTAGTTGT	120
TAATTTATCC	CATACATEGG	CLCCITITIA	ATATATATAT	TTACATTTGT	GTTTCCTTTA	180
TAMMARAGE	CATAGATTGC	CACGATTTTC	TTAAGTATAC	TTTTATAATC	AGAAAAATGA	240
TATTAAGGAC	TCATTTTAAG	TACACTAAAT	CAAATATTAG	AAGGCTTCTT	TATTTTAAGC	300
TAATTGTGAG	GATTATTTGT	CATTTAAAAC	TTTTGCTTCT	ACTTATTACC	CTGAAGTATC	360
TTTGTGGTGC	TTATGTTTTT	CACAGACTGT	ATAAATTCAT	ATACTCTCCC	CCCCCAMOOR	
AATGTTGCTA	CACATAAGCT	CTAATAATTA	TO TONI	TGTTTTAAGA	GCCCCATGGT	420
ת מידיידיים ממידים	AAAMAAMGCI	CIARIARIIA	ICATTTTAA	TGTTTTAAGA	TTAATTCAAC	480
TOTAL TITLE	MANIANICCA	TIGGTTACAT	ACATAAGAAA	GTACTGTATA	CAGATTCCCC	540
TGACTTATAA	TGGTTCGACT	CTCGAG				566

- (2) INFORMATION FOR SEQ ID NO:930:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 506 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:930:

GTGATATGAC ACTGACAGAA GGGGTCGCCT TGTAGGCCTT GGCTCAGCCG TGGCATGAAA GTCTGTTGGG ATGGTATATG TCCCTCGGGT CAGTCAGTAC GTGCCAGCTT GTGGACCTCA ACCAACTCCT ACAGTTGAGA	GTGAACATCC GGACGTGTTC GTGAAAAGTG CGCCTTGCTG CTGTCACTGC CGATTTGCTC	TGCCTGCTGC TTGCCCTCTG GACTAGAAGA CCCACCTGGG TACTCCCTCC ATGGAACAGC	CTACTTTTGG TGGCCTCGTC AAAATCAGAC ATCAGCCCTG GCACAAGTTG AGGTCTGGTG	AGAAAGGGCT TGCTTCCAGG TCCCATGACA GTTCTTTATT CCTGAAACCC TTCCTTACGG	60 120 180 240 300 360 420
ACCACCTC GTGGACCTCA ACCAACTCCT ACAGTTGAGA CCCTCTCAGG GGCTTTTGTG	CGATTTGCTC	ATGGAACAGC	AGGTCTGGTG	TTCCTTACGG	420
AAATGGGAGA ATCCGGATCC	CTCGAG	7100100001	IGITIATAAC	TCCTTTCCCA	480 506

- (2) INFORMATION FOR SEQ ID NO:931:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 271 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:931:

GGGAAATTAG	AAAGGGAGGG	CCTGAGTTGG	TTGCTATTCC	TGAAAGTTTC	TTTGAATGGA	60
ATACTGGATC	ATCGTTTTTG	AAGAGGTCTG	TTGTTACTTC	ATTATTACCT	CCTTTAGCAG	120
CACCCTTGTT	TTCCTCCAAC	CTCTGCCAAG	ATTAGTGTCC	TETETETACA	TTTGCCCCTT	180
CTGTTTCTCA	TACTCCCAGA	TGGAAATATT	ATATTTCTTA	CCACTETTACA	CTCTATTTGA	
ATTACTATTT	TCTACTCGAA	303000000	amilicity.	GGACTITICG	CICIATTIGA	240
··· ···	TCTACTCGAA	ACACCCTCGA	G			271

- (2) INFORMATION FOR SEQ ID NO:932:
  - (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 305 base pairs

(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEO ID NO:932: GAATTCGGCC TTCATGGCCT ACATTTACTT TTGTTACACA GGGCACTACT TTGATTTCTA 60 TTAGTGCTGT TTGTGATTGT GTATGTCTTT CACTTGAAAT CCACCATGAA GGTGAAAATT 120 TGTTTGAACC GTGGCACTAT ATGGCAGTGC AGTGTAGTCA GTTGTGTTTG TAGTCCGGAT 180 TATCAGAGCT TGAATTCTGG TTCTGCTGCT CACTAGCTTC TTCTTGCACA CTGTTTCAGT 240 GTACTCAGCC TCACCTTTTA TTTTATTTCT ACAGAGTCCC ATTTGGTGTG TAAGCTGGTC 300 TCGAG 305 (2) INFORMATION FOR SEQ ID NO:933: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 463 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:933: GCGGTGGCAC GATCTCGGCT CACTGCAACC TCCACCTTCG TTCAAGCGTC CACCATGCCT AGCTAATTTT TTTGTATTTT TGGTAGAGTC AGGAGTTCGA GACCAGCCTG GGCAACATGG 120 CAAAACCCCA TCTCTACTAA AAATACAAAA TGTACTCAGG CGTGGTGGTG CCCGCCTGTG 180 ATGCCAGCTA CTCAAGAGGC TGAGGTGGGG ATCACCTGAG CCCAGTATGT CGAGGCTGCG 240 GTGAGCCATG ATTGCGCCAT TGCACTCCAT CCGGGTGAGA CTGAGACCCC GTCTCCAAAA 300 AAAAAAAAA AAAGAAAGTG AAATAATTTG TGGACAACAC AGAATTACAA ACTTTTTATT 360 TTGTCTTTTT AAAGTTACCA CAAATTGTCA CCACCATTCT CTGAAAGGAC ATTAACACCT 420 GAATATATTT AGTTTCATGA AAATTTCACT TTTAACACTC GAG (2) INFORMATION FOR SEQ ID NO:934: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 290 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:934: GAGCATCCTG GGGAGCACCC ATTTCCTGGG AACAAGCTGA CCCTTTTGCG TCCTTAAAAA AAGTCGGCCA AGATTCCATA GTGCTGCTGA TCTGCATTAC AGTGTTTCTC TCCTACCTAC 120 CGGAGGCAGG CCAATATTCC AGCTTTTTTT TATACCTCAG ACAGATAATG AAATTTTCAC CAGAAAGTGT TGCAGCGTTT ATAGCAGTCC TTGGCATTCT TTCCATTATT GCACAGACCA 180 240 TAGTCTTGAG TTTACTTATG AGGTCAATTG GAAATAAGAA CACACTCGAG 290 (2) INFORMATION FOR SEQ ID NO:935: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 297 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: CDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:935:

GAATTCGGCC	TTCATGGCCT	AGTTTTGCCC	GGCAGCCTCT	CAGGTTGGAC	TTCTCAGGAT	60
TTGCCATTTG	TTTTAATCCC	TGAGACCACA	CAGTTGATGT	TTAGAGCCTG	CCCTGCATGT	120
GATCGTTCCA	GTGGAGGATA	CAGCATGGGG	TCTGGCCTCC	AGCAGGGTCC	TCCCCAGGCC	180
ACCCCTGGGT	GCCGGGAGGG	CAGCCCCTTG	GCCTGAGGCC	CACTATGACC	TGCCCCCTGC	240
				GCTCTGGTGG		297

- (2) INFORMATION FOR SEQ ID NO:936:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 337 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:936:

GTTTAATGAA	GAGTAGTCAG	TCTTCTAGAT	TGTTCTTATA	CCACCTCTCA	ACCATTACTC	60
ACACTTCCAG	CGCCCAGGTC	CAAGTCTGAG	CCTGACCTCC	CCTTGGGGAC	CTAGCCTGGA	120
GTCAGGACAA	ATGGATCGGG	CTGCAGAGGG	TTAGAAGCGA	GGGCACCAGC	AGTTGTGGGT	180
GGGGAGCAAG	GGAAGAGAGA	AACTCTTCAG	CGAATCCTTC	TAGTACTAGT	TGAGAGTTTG	240
ACTGTGAATT	AATTTTATGC	CATAAAAGAC	CAACCCAGTT	CTGTTTGACT	ATGTAGCATC	300
TTGAAAAGAA	AAATTATAAT	AAAGCCCCAA	ACTCGAG			337

- (2) INFORMATION FOR SEQ ID NO:937:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 299 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:937:

GAATTCGGCC TTCATGGCCT	ACATAGTTAT	TCAGATTTAG	GACCAGTAAG	GATAGAACTT	60
TCTCTTATTT ATGAAAAAAA	ATGCTAATAA	TTTTGGGGCA	GTTTTTTCCN	TTAATTATTT	120
TTTTCAATTT CAAGTTTAAT	TTTATTTTAG	CTGATCTGAT	GTGGTTTCAA	CTAACCCAAG	180
GTCTCACCAT GTTAAAANGC	CGGCGGACTC	TACGGCGTTT	TGTAGATCCC	CCCCCCCAC	240
CCACTGTGAA GGGGTGCCAT	ACTACCTTAA	ATGCTAATGC	TAGATATGCA	ACCCTCGAG	299

- (2) INFORMATION FOR SEQ ID NO:938:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 403 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:938:

CTCGAGTGGT	GTGTCATTAT	AGCGGACAAA	GGTCACGATC	ACAAAGGTGG	TGGCGATGAT	60
TCCCAATATT	GCAACAAACA	CAGGCACCAC	AGCCCAGGGA	GAATGCCACT	CCAATTTGAT	120
GATGGGGATA	AGCTGGCAGC	CTGTGCGGTT	CATGTTGGGT	CTCTGATCCA	GAGGGCAAAG	180
TTCACAGGAC	AGCTCATCCA	CCTGGTAGTT	GTAACCTTCA	CAGCGTTCAC	AGTGCCAGCA	240
GCAAGGGACC	CCTTTCACCG	TTTTCTTCCT	CTCCCCTGGC	TTACACGGCA	GGCTGCAGAC	300
AGACGCCGGG	TGAGTATGTT	CTCTATGAGC	CCACTGCATG	TCTTCCACTT	TTAGATGAAG	360
CTGATTGGTC	CAGTGGCCGA	TGACTTTGTA	CTCTGTGCTT	TTC		403

- (2) INFORMATION FOR SEQ ID NO:939:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 373 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:939:

GAATTCGGCC	TTCATGGCCT	AATTCTTTTC	TGTCCTTCAC	ATGCATGTCA	CAGTTCATCT	60
CACATTTCTG	TGTAGAGGGC	TCCATTTCTC	TGCATATGGC	ATTACCATTC	TGCCTGATGT	120
ATTCCAATTC	AGATAAACAT	AAGCTCCTTT	CTCGTGCTTT	CCCTGAGACC	CCTGGTGTGG	180
ACTTCTCTAA	TGTTCTCATA	ATATCTATGC	ATCTCTCTAT	GATTATACCA	TGTTATACTC	240
TGTGTGGCCT	TAGGCTTTGT	GAGGAGAGGT	TCAGAGTAGG	TTTTGCTCTA	GAGTGTGGTC	300
CTTACTCCTA	AGGTGACCCC	TTTCNGGTGT	CTCTGCTGGT	GTATGGCATT	AATGTGATTG	360
CTTCACTCTC	GAG					373

- (2) INFORMATION FOR SEQ ID NO:940:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 298 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:940:

GCAAGCTCTA	ACCTAAATCA	CAGAGACATG	CATGTTTCAT	GCATTAACAC	TGATTTCGCT	60
CTGTGGCCCA	CCAGAGGGGT	GGGCTCATGT	CCCCTGACTC	CTCACATGAG	TGCCTCAGCT	120
CTAAGNCCCG	TGGAACGGGG	GGTAGGGAAG	GTTTGCGATC	TGGAGCTCAG	CAACTGGCTC	180
AGCAACGTTT	TCTCCATTTC	ATTAGCACTA	AACAAGTTTC	TTGCTCTCAG	GAATTTGTCA	240
GAAAAAAGAA	TAACATCACC	TGAGACTCCA	CATACCAGAT	TATAAACTCT	TTCTCGAG	298

- (2) INFORMATION FOR SEQ ID NO:941:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 219 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:941:

GAATTCGGCC	TTCATGGCCT	AGGTTTCCGG	ACACTTGGGA	CACGCGTTTC	CATCCTGGCT	60
					AAGAGGCCCA	120
AAGCCCTCCC	CCGCAAAAAA	AGCCAGAAAG	GAATGGAGGT	GCCTCCGCAG	AAATCCAGAG	180
CATCTGCAAG	ACATCCTCGA	ATTCTAGACC	TGCCTCGAG		*	219

- (2) INFORMATION FOR SEQ ID NO:942:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 572 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:942:

GAATTCGGCC	TTCATGGCCT	AAGCAAGATG	GGTCTGAGGA	TACCTGTGAG	AAGTAATTCA	60
ACACATCTTT	CACACATGGG	CCAATTTGCT	GGTCTAAGTT	AAATNGGAGT	GACAAGGACA	120
GCTGCTTAAA	GAGTGAGTTC	TAAAGCCCCA	GGAATTAGGT	GATGTCTTGA	GCTGGGGTGA	180
AGCAAGNCAA	GTGGGATGGG	GAAGAGATGG	CTGGNTTCTG	CNGGAGTGAG	TTTAAGGGAG	240
GAAGGCAGGG	TTGCCCGGCA	GCCCGCATGT	TCCAGAAGAG	CCCACGAGAG	ATGTCTGTCC	300
CACAGGGCTT	ATAGCACNTN	GCANTCCNTC	AAAGGCCGGT	GTCTCATGTC	CCNTCTGTTA	360
GGCTCTGGGT	GGGCTTTTGT	GACAGCTTTG	ATAATGTTCT	GGAAGAGATG	CTGCTGGGCT	420
TCTGGGCTCC	CGCGACCCCT	TAGAGAAAGT	GGTGCAGCTT	CTCATTGGCT	CTGTCTCTCT	480
CCGAACACGC	CCCTTTTGGA	GCCCTCTGGA	AAGGAAGACA	CTGAGCAACC	AAATAACATA	540
TTTTGACACT	<b>AATTTCCTGA</b>	GACCGTCTCG	AG .		*	572

- (2) INFORMATION FOR SEQ ID NO:943:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 412 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:943:

GAATTCGGCC	AAAGAGGCCT	AAGGAAATGT	GTGTCTCTAA	AACAGATTTG	GATTTTATTT	60
ATTTGGGACA	TATAAAAGAG	GAAGGAAGAG	TTGATAAAGA	TTCTTATTTG	ACTCTTCAAA	120
GTCACTGTTC	ACCAGAAATT	CAGAGAATCA	ACATACAAAT	TACAATGGTA	GTTTGTTTTC	180
TGGAAGGCCA	GTGAAATACA	GCTCCTTAAT	TTATAATGAA	ATTTACTTTC	TAACAAATTA	240
AGTCTTTCTA	ATGAGACCAA	CATTGAGAAT	TCAGCCCTTA	CCTCGGGATG	GTCTGAGAAA	300
ACCAAAAGGC	CAACTGTTTT	ATTGCTTTAG	ATCAGTTAGG	TGATGATAAC	TATGAGCATT	360
TATAATAATA	TTTTAAATTG	GCCCTGAGAG	GCTTGAAGAC	ATAGAACTCG	AG	412

- (2) INFORMATION FOR SEQ ID NO:944:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 521 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:944:

GAATTCGGCC	AAAGAGGCCT	ACAAAAAAA	ААААААААА	NNACTTGAAC	TGAGACCTGA	60
aanngtaaaa	CTANNGNAAC	AAAACTTAGG	GAGAAAGCTT	CTTGACATTG	GCCTGGGCAA	120
AGATTTTTT	GGATATGGCC	CCATAATGAC	ATAGGACAGG	CAACAAAAAA	AAAAATGGAT	180
			ATAGCAAAGA			240
			GCAAACCACA			300
			AATAGCAAGA			360
AAATGAGCAA	AGGTCAGTTG	AGAGAGGAAG	AGAAAAACAA	TATGAGTAAA	AGACTTTAAT	420
AGACCTTTCT	CAAAAGAAGG	TATGTGCATG	GCTGATCTGT	GCATGAAAAG	GTACTTAACA	480
TCATTAATCA	TCAGAGAAAT	GCAAATTAAC	ATCATCTCGA	G		521

- (2) INFORMATION FOR SEQ ID NO:945:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 327 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:945:

GAATTCGGCC	AAAGAGGCCT	AGGTACACAA	AAGCAAACAG	AAAAACTCTT	AAGTTTTTCT	60
GCAATACTAA	AGAAAGTGAG	ATAAGACTTT	AAAGTTAAAG	ATCTATAGAC	ACTTTAGGCA	120
AAACAGGCTC'	ATAAAGCAAT	TAAAAAATCA	ACAATTTAGT	AAAAACAGGC	TACATAGTAT	180
TTTGTTTTTA	CGTTTCATTT	GTCTATTGAT	CTTTAAATTA	AATTAGACAT	TTCTACTGTT	240
TTCCTGTACT	CTTATACACA	CCTGTTTTCT	CCAATGTTCT	CCTTTAGTAT	GGCTGGTAAT	300
TGTTTTGGTG	ATTGCCACCC	CCTCGAG				327

- (2) INFORMATION FOR SEQ ID NO:946:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 573 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:946:

GAATTCAAGG	GCTAGGCGAG	TTATTGCAGT	CACGTCCTTA	AGTCAGCCGG	GTCCTCTTCT	60
TTTCCCTCAA	GGTGCCTGTG	TTTTCTATTT	CCCCGTCCAG	TCGGTGGCCC	CACCCAGCCC	120
CAGGGTGCTC	CCTTCCCCCC	TTTCGGGTTT	CTGCCTGGAG	GGTGTGGTTT	TCTCTCCCAC	180
CTCGGTGCCT	GCCAGTAGAC	TGGAGTTCCC	CGCCACGCTG	TCGGTCCCAT	CTCATCACCT	240
TTCCGCTTTC	ACGCCCGTAG	CTAGTCTTGG	GACTGGCCCT	GTTATAGCCC	CAACTTATGC	300
GCTCTCTAAC	CTTTCCTGGC	TTACCCGGAG	TCACAGTTCA	GTTCTACTTC	TTTTCAATTC	360
TGTAGGGCAT	TGGTCTCAAT	TGGGACTCAG	TTTTCCTCCA	CACCCGCCGT	TCCTGTAGTC	420
TGGTTATATC	ACAGTTCATT	ATTTAATGTA	GGTTTTTGAG	CGCTTTGTAA	ACGGCAAAGC	480
TCTCTCTGTT	AATAATACAT	ACTCAAAATG	TTATTCTTTC	ATTGGTGCAT	TACAACTCAG	540
TTGTTTGCCT	CTGAATCACT	TTCCCGACTC	GAG			573

- (2) INFORMATION FOR SEQ ID NO:947:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 335 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: CDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:947:

GTTGAAGTCA	TTTATTATTT	TATAAATTGA	GAACAACCAC	ACCACCAAAT	GTCACACCTT	60
CTTATAAAGT	GTGAACAAGG	AAGGTCATGT	TTTTGTGGGT	ATTTTGTCAG	ACTTAGAGGT	120
TTCATTTCAG	GGCATAGTCA	AAGGCATCAT	CCTCCCAACT	ACCCACTTGA	TTATGTATTT	180
CAGATCCCTC	CGTGGGGGCC	TTCTTCTGAC	AGAGAATTCT	TTGAGGTACG	CAGTAGTGCT	240
TTTGTCAGCA	CAGACTGCTA	ATCTACATCT	TGCTGCGTTC	TGTTTGCTGA	GGTTGGGCTT	300
ATTCATTTAA	CACGTACCAA	CCATTATCAC	TCGAG			335

- (2) INFORMATION FOR SEQ ID NO:948:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 372 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: CDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:948:

GAATTCGGCC	AAAGAGGCCT	ACGGCCAAAG	AGGCCTAGTC	GGAGGAGGAA	ACATATGTAG	60
GGAACAGCCT'	GGGTCTTGTG	AATCCGTTTC	CCAGCTATGA	TGCCTATTTC	CTCAGCAGAA	120
	ATGTCTCCCA					180
ATCTCACAGC	TTACTGTTGG	AAATGCTATC	AGTTGTAAAG	ATAGGGAAAA	TCTCTCTTCC	240
ACTACGGTGG	TAGGAAATGA	ATACATATCA	TTTCCCAGCT	TCCAGGATGT	CCTGTCATCT	300
TAACTGTGCG	TCCCCAAGGA	CCTACAGATC	ACAGGGCAAC	AGGGGCTGTG	AAAGAGTAGC	360
CCGGGGCTCG	AG				•	372

- (2) INFORMATION FOR SEQ ID NO:949:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 450 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:949:

CTAGCATTAC	GAATCTCTTA	GGATTTTTAA	GATTGTATTT	GATAATACTT	ATATTTCACA	60
GGGCACACTT	TTGGCACACC	TCAGAGCACA	CTGCTGCTAT	TTTGGGTCAT	ATCACTGTAA	120
AATACATAAT	<b>AAGTACTACT</b>	TAACTGTGAC	ATGAAGAATT	GGAATCCCAG	AGGGCAACAT	180
TTGATTCGAC	TAAGATCAGG	CATAAGATAG	AATTTTTGTC	ATTTTTCCTT	GCAGTTTTAT	240
TGACTTAGTT	TATGAGCTTG	GATAAAATAA	TTTTTTGATG	AATCATGTCA	ATAAAAGGAA	300
AAATAATGTA	ACTACCTCAT	<b>AAGTCTGATA</b>	AAAGGAAGTT	GCTAGTGTTT	TATAGAATTT	360
CTGAAGGTGG	TTAAATCAAG	TATGATTTCA	AAATATCAAC	TAGTTCCACT	TTTGTGATTG	420
CAGGATGCTT	CTTATACTAA	AGTTCTCGAG				450

- (2) INFORMATION FOR SEQ ID NO:950:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 342 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:950:

GAATTCGGCC AAAGAGGCCT	ACGTAGGCAA	AGGTTGACCC	AATCAAAGAT	AAAAGAAAAT	60
CGACAGCAAA TCGTTCGTGC	TCGAAAATAT	TATGATGATT	ATAGAGTTCA	GTTGTGTGCA	120
AAAATGATGA GAATGAGGAC	CCGGGAAGAA	ATGATATTTA	AGAAACTGTT	TGAAGAAGGT	180
TTAAACATTC AAAAGCAAAG	ATTACGAGAC	CTAAGAAACT	ATGCCAAAGA	AAAGCGAGAT	240
GAACAAAGGA GACGCCACCA				TAAGGACCAG	300
TTTTCATTGC TGGCAGAAGC	CATATCACAG	GAACAACTCG	AG		342

- (2) INFORMATION FOR SEQ ID NO:951:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 494 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:951:

GAATTCGGCC AAAGAGGCC	T ACCCTGTTTT	AATCACATGA	CTACCTGTCC	CAGTACACGA	60
AAGGCCCTG GTTGGCATT	C TTCTTAATGT	ATTTAGTAAA	GATTATAAGA	CATCCTTTAA	120
GAGTTTAAAT GTCTCTGAA	A CAGGCATACA	GGCTCTAGTC	AAGAATGAAT	TAGAGTGAAG	180
GAAAGCTGTG TGACACCTG	G CATTCCTCTC	TGTTCATGGA	GCTTCTTTGA	GGCTTGAAGT	240
TTGATTTTAC TATCTAGAC	C TCTCTGGCTA	ATACCTATTC	TTCAACCACC	TCGGTTACTC	300
TGACATAGGA ATTTACTTC	T TTTCCTTGAG	TGGAAAACAC	TTTAGAAAAT	AATAACAAAC	360
ATTATTATAA ACTAATATA	T GTGAGAGTAC	TTAGTTGAAA	CAAAAAGGAA	TTTTAGTAGA	420
CAGTATTATA TTATCTTTC	A AAATCAAGGA	GAAGTTTATG	CAACTGAAAA	TGTTTACACA	480
CTGTGCTACT CGAG					494

- (2) INFORMATION FOR SEQ ID NO:952:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 522 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:952:

CAAAGAGGCC	TAGGGAGTGT	CGCTCTGTCA	CCCAGGCCGA	GATTGCACCC	CTGCACTCCA	60
	CAGTACGAGA					120
	TGCGCAATGT					180
	GAGAGTGTTT					240
	TTTTGTTTAC					300
	AAAAGCTGAA					360
	GAAAAGACTG					420
AATAGGATAA	TAGGCAATTT	TAAAACAGAC	TCCTTTAAAA	AAACAAACAA	acnaaaaaa	480
CATAGACTTC	TTTATATCTT	TTGAGCTCCC	CCCCNACTCG	AG		522

- (2) INFORMATION FOR SEQ ID NO:953:
  - (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 483 base pairs

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:953:

GAATTCGGCC	AAAGAGGCCT	AGTGTGTTAT	ACAGTTGTTG	CCACTGCTGT	TTTCCAAATG	60
TCCGATGTGT	GCTATGACTG	ACAACTACTT	TTCTCTGGGT	CTGATCAATT	TTGCAGTAGA	120
CCATTTTAGT	TCTTACGGCG	TCAATAACAA	ATGCTTCAAC	ATCATCAGCT	CCAATCTGAA	180
GTTCTTGCTG	CATTGTGTCA	AAAGAAATTT	CCTTATTTTC	TACTGCCATT	CCCATAAAAG	240
TAAGTAGTCT	CATTTTTGCC	ATATTCTGTT	CATGTAACAG	GCCAAGTGAA	TCAATGAAGT	300
CTTTATTATT	CTGATAAAAC	TTGACATATG	ATGCCAATTT	AGCACTCACA	AAAATGGTTA	360
AAAGATCATG	AATAAGCTCG	CCTTCCAAAA	ACTTGACTGG	TTTTAAAGTA	AGAAGGTGGT	420
CAAAAAGAAA	TGCATTTGGA	TCTTTCAATG	CTCGTACAAT	ACACCTGTGG	GCATCAACTC	480
GAG						483

- (2) INFORMATION FOR SEQ ID NO:954:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 372 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:954:

GAATTCGGCC	TTCATGGCCT	AGGTGCCCTC	TGTGAAGCCA	GTGTTCTCTG	CTCCCCGGGT	60
CAGAGGTCAC	AGGTCAAGTT	CAGTCAGTCC	GAAGAATCAT	GGGCGGGTGC	TCGCTGTCCT	120
CATCCAGGCG	CAGGGCGCTG	GCCTCGTCCT	CCAGGCAGGC	GCCACCCACA	GCACCCAGGT	180
CGTCTGTGTA	GGCTGCAAAG	AGACGACGAA	GTCACCCTTC	AAAGGCTGGG	GACACACCAC	240
AGACCCCATG	ACACACACTG	AGGACTGTGT	TTTGGAAACA	CTGGTGTATA	TTTATAAACT	300
GAAGCCTGTA	CTAAGACGTT	CTGAATTCTG	ATTGCTTTCT	AATGAACTCT	TTGCAGCCTT	360
AGGCAGCTCG	AG					372

- (2) INFORMATION FOR SEQ ID NO:955:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 436 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:955:

GAATTCGGCC	TTCATGGCCT	ACTATTACCA	TTATATATCA	CCCATCTGCA	ACAAGGTACT	60
GTACAGACAA	GTAAGAAGTA	TGTTATCTAG	TTCCCTTTCC	CCCAGAAGGT	TGAGGCTCAG	120
GTATAGGGGT	AATTCTCCTG	TGCAGTCTTT	ATTTATGCTG	ACTCAGTGAC	TTCAACAGGC	180
TTAATCATGT	GGTCAGGTTT	GTTGCCAGCT	GCATAATGCT	CCCACATCTG	TAGATAGAGC	240
CGCTCTAGTT	CCATTGTGTA	TTGTTTGGTG	TTGAACAGAG	GGCTAGATAT	TCTTTGCTTC	300
CAGACTTTGC	CACGAACTTT	CTTCAGGTAT	TCTAGATCAG	TTCCCAGCTT	CACAGCTATG	360
TCTTCATATT	CTTGTCTGTT	TTTAGCAATA	AGCTCAAGAC	AACCTAAGCA	AGTGAGCTGG	420
GATGCTGCAA	CTCGAG					436

## (2) INFORMATION FOR SEQ ID NO:956:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 331 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:956:

GAATTCGGCC	TTCATGGCCT	AAGGAGATGG	GAGAATGTCC	GGGGAGGGC	TGGCAGGAGG	60
GGCCAGCCAA	ACTGCACGGA	CTTTGCTGGT	TAGTGAAGGA	TTTTAAGTCC	TCTAGTGGAA	120
TTAAGTGATT	AGATTTTTGC	CTTACAAAGG	AAACTCTCCT	ATGGAGAACA	AACTACCATA	180
TGAAGCTAGC	GGCCTAAACC	AGGAGAATGT	GGGGAAAGAA	GAGAGGTGAG	GATAACTGGA	240
GGGGTATTAT	GTAACAACAG	AAAGCATCAC	AGTTCAATGA	ACAGGGCAAG	GTGGGCAAAT	300
GAAGAGGGCA	GAGGAGGACT	GGGCCCTCGA	G	•		331

- (2) INFORMATION FOR SEQ ID NO:957:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 424 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:957:

GAATTCGGCC TTCATGGCCT	AAGACTGTGA	GTTCTGGGGC	CAAGAAAAGT	TTTGAATTGC	60
TCTCAGAGAG CGATGGGGCC	TTGATGGAGC	ACCCAGAAGT	ATCTCAAGTG	AGGAGGAAAA	120
CTGTGGAGTT TAACCTGACG	GATATGCCAG	AGATCCCCGA	AAATCACCTC	AAAGAACCTT	180
TGGAACAATC ACCAACCAAC	ATACACACTA	CACTCAAAGA	TCACATGGAT	CCTTATTGGG	240
CCTTGGAAAA CAGGTCTGTC	CTCCACCTGA	ACCAGGGGCA	CTGCATTGCC	CTGTGCCCCA	300
CCCCAGCTTC CCTTGCTCTG	AGCCTACCCT	TCCTCCACAA	TTTCCTAGGG	TTCCATCACT	360
GCCAGAGCAC ACTGGACCTA	CGCCCAGCAC	TGGCTTGGGG	TATATACTTG	GCCACCTTCT	420
CGAG					424

- (2) INFORMATION FOR SEQ ID NO:958:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 597 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:958:

GAATTCGGCC	TTCATGGCCT	AGATATGGCC	AGGATGCTAT	AGCATTGTCA	GTGAGGAGAC	60
ATCACAGCTT	TCCCAGATCG	GGAGGAAAAA	TATGGAATGT	GTTTTACCGC	TGACTGAACA	120
CAACCAAATG	AACTGTCCTG	ACAGTAGTTT	GCAAACCAGC	AGCTAGCAGT	TTGTCCAGCC	180
TCTAACATTG	TCCAGCACTT	TCCAGAGCAA	ACTCACTGTT	TACAAGAACT	CTTGGCCTTA	240
CGAAGTTTAT	AACCTCAAGC	TTTGTTTATT	TAAAATATTC	CTGCAAAAGA	AAAGTACCCG	300
GCCCATGACC	ATTCGTGACA	GGCCCTTTGA	ACGGACGATT	ACCATGCATA	AGGATAGCAC	360
TGGACATGTT	GGTTTTATCT	TTAAAAATGG	AAAAATAACA	TCCATAGTGA	AAGATAGCTC	420

TGCAGCCAGA AATGGTCTTC TCACGGAACA TAACATCTGT GAAATCAATG GACAGAATGT CATTGGATTG AAGGACTCTC AAATTGCAGA CATACTGTCA ACATCTGGGA CTGTAGTTAC TATTACAATC ATGCCTGCTT TTATCTTTGA ACATATTATT AAGCGGTGGC ACTCGAG	480 540 597
(2) INFORMATION FOR SEQ ID NO:959:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 290 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:959:	
GAATTCGGCC TTCATGGCCT AGTGTTTTCT TGTCAACTTC ATTCTCTTCT CTTGTTTTCT ACGTCTGAGA TCTTTCTGAA CACATTTTTG TAGAGGCTGC TGTCTCCTGC TGTCTGAGA ATGATCTTTA GAGGGAACGG AAGCTTTCTT CCTGTGCGTG TGTGTCTTCC TGTGTCCTAG CACTTGGGGG TGGAGAGTCT CGGGGCGGGG	60 120 180 240 290
(2) INFORMATION FOR SEQ ID NO:960:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 300 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:960:	
GAATTCGGCC TTCATGGCCT AGTGAGTGAG TAAGACAGGT TGCTCTTTGG AAAACAAGGA AAATCCCTTT ATTAGAACAA GGCATGAAAT TCTGCCACTA GGTGGCGATG CCCTATAACT TTACAACTTA GTGTACATCA CACGAGCACT ATGGAAGATT TCTCCATTCT GCGCCCCACC AACTCCCTCC CCTCCTTCAT TTTTCAGGAT GACAACACCT TAGAGGTTTA TGGCCATCAG GAGAATTTAC TACTAAGCTA TATACTGATG TAATGAAATC TAATATATGT TGTGCTCGAG	60 120 180 240 300
(2) INFORMATION FOR SEQ ID NO:961:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 503 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:961:	
GAATTCGGCC TTCATGGCCT ATTTTCCCTT CAGGATTGTG TGTTGGGGTG GGGGCATACT GGGGATGACA GAGGGAGAAA GAAAGATTTT TATTTTTCCT TCTAATAAAT GTTCATTGAG AAAGTTATAG AATATGGAGA AAATGAAATT TATAACTCTC CTGCGCAGAA ATACTGTTAG CTGTGAGTTT CTTTTCTATA TATGCTTATA TAGTTGAGAT TATGCATGTA TACAGTTCTG	60 120 180 240
CATCTTAGCT TTAAAAATAA TGTCACATCT TGATAATTTC CCAGTCATTA AAATTATTTG	300

360

420

AAGATATCAT TGATGTATCA CCTTATTTTA TATTCTATTT GAATAATACA TCCAAGGTCA

CCAAAAGATG ACAGTGAAAT GTATTGTTTG TAATCTACAT TAGCATCAGT AAATATGGAC

CTACATTTGA TGGGACTCTC GAG

(2) INFORMATION FOR SEQ ID NO:962:

(i) SEQUENCE CHARACTERISTICS:

CATTTAAATT GTGTTAAGTC AACCTCTCTG ATCTTATTTT ATTAAAGTTT AGGATAGGCA

480

503

(A) LENGTH: 394 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:962:	
GAATTCGGCC TTCATGGCCT AAGCAGCTGC TGCCTGCCAG AGAGGCGCCT TCAGAGACCC	60
AGCGCTTACA CAATACCCAC CATGTCCCAG GCTGGTGCTC AGGAAGCCCC TATCAAGAAG	120
AAGCGCCCCC CTGTGAAGGA GGAGGACCTG AAGGGGGGCCC GAGGAAACCT GACCAAGAAC	180
CAGGAAATCA AGTCCAAGAC CTACCAGGTC ATGCGAGAGT GTGAGCAAGC TGGCTCGGCC GCCCCGTCGG TGTTCAGCCG CACCCGCACA GGTACCGAGA CTGTCTTTGA GAAGCCCAAA	240 300
GCCGGACCCA CCAAGAGTGT CTTCGGCTGA GAAGTGTGCG CCACTCCCCT TGCTGCCCGA	360
ATGCTCGGAA ACAGGAGCCT TACCCAGGCT CGAG	394
(2) INFORMATION FOR SEQ ID NO:963:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 497 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:963:	
GAATTCGGCC TTCATGGCCT ACCCTTCATG GCCTAGGAAA CTCACAAAAT GAAATATCCT	60
TCTCAACGTC ACTAGAGAGT GGCAGAGTTT AGAGACAAAG CCATCTGATT TTGGAGCCTG	120
TGCTCAGCTT TTAGCAGACA CACTGATTTC CAAGAATTGC TAGGATGTTT CTCAGTGCAG	180
TTGACCACAG GACTCTCTGG AAAGCCTTCA GGACTGAACT TCCTCCAGAC AGTTTGGGAA ACACTGCATG TGTCTATTAT GAAGCCATCA GCTGAGCTCA TCCCCCGTGC ACTCCACAAC	240 300
GCTGAGGCTC TGCACATGGC TCACCAGTGC CAGGTGCTGC CAGTCAGCAG TGCCGTGCTG	360
TTTCCACAGC AGCCTGCATA CGTCTATATT GCCCAGCCTG TTTCACCTGG CGGGGTCACA	420
CAAACCACCC CCTGGTATTG TTAGCACGTC CACATAATGG CATCTCCACA GCTGTGTCAT	480
CCAAAAGAAA CCTCGAG	497
(2) INFORMATION FOR SEQ ID NO:964:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 395 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:964:	
GAATTCGGCC TACATCTTTT GATGACTCTG ATACCTTCAT TCATTTTTCA AAGGAATTTA	
CTGATCATGA GGTTGGAAAA TCTGTATTTC TCTTGCTTAT TATGTATTAA TAATCATAAA	60 120
413	

TGTCTAGATT	CACCAGAAGT	CACCAGAAGG	TCTGTCTCAG	TGAAGAAAAC	TTATAAAGCC	180
ACTTTGTTGC	ATTTTGTGTT	TCAGTGTTAC	AGTTTGAGAT	CTGTATATTT	GTACACAGCT	240
ATGTGTTTTT	CATTGAAATA	ATGTACAAAG	ACTGATCTTG	ATGCTGTGTA	TTTTTATGAG	300
TTGTCTTAGG	CATTCCTGAG	CTCAGCTTCA	GTTGGATGGT	GGGTCAGCAC	CCTGCGTTTC	360
TGAACATACT	AGACTTCAGT	TTAAAACTGC	TCGAG		-	395

- (2) INFORMATION FOR SEQ ID NO:965:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 471 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:965:

(	SAATTCGGCC	TTCATGGCCT	ATAGTAAATG	CCCACTAGGC	ACCCTGGAGT	CATTTGTGTA	60
(	SAGTGGCATC	TCTATACAAC	TGTTCGACTA	ACTGTCGGAG	ACACCCTAAT	CACCCCAGCC	120
1	ACAAACAAAT	AGAACATTGT	ATGTGTGCTG	AATCCCACAA	AGGCCAGACA	TGATGCCATG	180
2	AGACCAAGAA	GGAAAAGAAA	TAATGTGGAA	AGGGTTTGGG	GTGGAAAGGT	GGGGAACCTG	240
(	BAGGCGGGCC	ACATGGGGCC	CCAGAAGCCA	TGTTGAGGGT	TTTGTCTTCA	CCAAAGGATC	300
ž	AGTGGGAGAT	TAGTGTAGAA	CATTAAACAG	AGGTGGGGTA	TGTGTCATAT	TTCCATTAAA	360
i	AAATTCATCC	TGGCCACAGT	GTAAAGAATA	GATTAGGGAG	GAAGCCAATC	AGGAAGCAAT	420
•	TGGAGTAGGC	AATGCAAAAG	GCAAAGTGAA	CTTGGACTAG	TGGTTCTCGA	G	471

- (2) INFORMATION FOR SEQ ID NO:966:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 611 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:966:

GAATTCGGCC	TTCATGGCCT	AAGCCAGCTC	AGNTGCNTCA	GAGATTTTGT	GTGTCCTTGC	60
ATACACAACT	TAATTTCTCT	AGGATTCAGT	CTCCTCGTNT	TATTTTTAAA	ATNATTTTAT	120
TTGTAAATAC	CTCATCGTGG	ACTCCAAAAG	CATGTCTCCT	CGTTTTAAAA	ACTGGCATAA	180
TACCTACCAC	AAAGGTGGAT	GTGAGAATTA	AATAGAGCTT	TATACAGAAT	TCCCTCAGGC	240
ATTTTTAAGT	TTATGTAATA	GGGATGTATC	TTACAGTTGA	TGGGTACATT	TAGTGTAGTC	300
CCCCTACCTC	CCAAGCTAAT	AATGGTGCGT	CGTACAATTG	ATGGTACCAA	ATTGAGGTGA	360
TAATAACATA	GAAAGAGTTT	AATGCAACGT	GAAGTACAAA	ATGCATTCAA	TAAGTAGCTG	420
CTATCATTTT	TTTAAAAATT	AAATATGGCT	GCTTGTTAAG	GCCATATCCC	AGGAGGAAAG	480
TGTGGTCTCT	GCTGGGAGGT	TGGTCTACAT	ACAGGAAGCC	AGATGTGTGA	GATGGCTCTA	540
GATAGGCAGA	AGGGGAGAGC	TCGTGCCCTC	TAGGAACCTA	TTAATAGATA	TCAAGGGAGG	600
GATAGCTCGA	G					611

- (2) INFORMATION FOR SEQ ID NO:967:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 343 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:967:

GAATTCGGCC	TTCATGGCCT	AATTTAAGTT	TTTCTAGCAG	ATCGCTCAGG	TTGCTCTTAA	60
CTGGAATGTA	GTGTTTCCAG	GGCTGCAGCT	CATTGTAAAA	ATGTTCATAG	TAGATGGAAT	120
CCTGCTTCAG	CACAACACTG	TCACCAACTA	GCAAATATGG	CAGGCGATAA	GCTGCTACAG	180
TGCCATCGAT	ATTTATTTGA	TACTTATGCT	TGAAGAAATC	AAAAAATGAA	ATATCTTTCA	240
CAATGGGACC	ATACAGGTTT	TCATCGTGTT	TAAACAACAA	AAACTTCCTC	ALAIGITICA	
CTATGAGTTC	TCCCTCTTT	CENCECTOIL	TANAGAAGAA	WWWGIIGGIG	AAAGCAGCGT	300
CIMIONGILC	1000101111	CINCIGAGII	TAACCAGCTC	GAG		242

- (2) INFORMATION FOR SEQ ID NO:968:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 593 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:968:

GAATTCGGCC	TTCATCGCCT	AGCCAGGANC	TTTCTCGGAC	GCCTTGCCCA	GCGGGCCGCC	60
CGACCCCCTG	CACCATGGAC	CCCGCTCGCC	CCCTGGGGCT	GTCGATTCTG	CTGCTTTCCT	120
GACGGAGGCT	GCACTGGGCG	ATGCTGCTCA	GGAGCCAACA	GGAAATAACG	CGGAGATCTG	180
				CTCCGTTACT		240
GTACACGCAG	AGCTGCCGCC	AGTTCCTGTA	CGGGGGCTGC	GAGGGCAACG	CCAACAATTT	300
CTACACCTGG	GAGGCTTGCG	ACGATGCTTG	CTGGAGGATA	GAAAAAGTTC	CCAAAGTTTG	360
				ACAGAAAAGT		420
				TGTCACCGGA		480
				GCACCAAAGA		540
				AATCCGACTC		593
		"" CANOCOMCI	aracretace	WHICE GWEIG	GAG	223

- (2) INFORMATION FOR SEQ ID NO:969:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 409 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:969:

GAATTCGGCC	TTCAAGGCCT	AGTTTGTTTG	TTTTCGTTTG	GTTAAAGCTT	ATTGCCATGC	60
TGGTGCGGCT	ATGGAGACTG	TCTGGAAGGC	TTGGAATGGT	TTATTGCTTA	TGGTAAAATT	120
TGCCTGATTT	CTTACAGGCA	GCGTTTGGAA	ACCTTTTATT	ATATAGTTGT	TTACATACTT	180
ATAAGTCTAT	CATTTAAAGA	CATGTACTGA	AACAAATGTA	TTTGTTTCAT	AAGCATCTTC	240
CTGTAATCTA	TTATAAAATT	GAAATTAAAT	ATAGAGAATG	TTTTAACAAT	TTTTTAACTC	300
AAAATTTGTC	AATCATTTTT	AATAGTTCTT	TTTTTTATAAA	AAGAAAAAGG	AATTTAAGGA	360
CAGGCAGTAG	TCTCTTTTAA	AATTTATTCA	CAAAACCCAT	TAACTCGAG		400

- (2) INFORMATION FOR SEQ ID NO:970:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 373 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:970:

GAATTCGGCC TT	TCATGGCCT	AAGATTATAT	AAGATTATGC	CAATAAAACT	CATGCCTGAG	60
GAAGTGGTTG CT	CCCTTTCT	ATGGGTCAGT	ATTGGTGCAA	GAACTGGAAA	CCAGCCCTTG	120
GAGAATAGTT AT	TACATTGGC	CATGATTTTC	CACAGCCCTG	GAAATGCACA	ATTCTATCCT	180
CCTACCAGGA TO	GATTGTTAA	GTTTTAGCTA	ACATTTGATT	ATAAAAGGCC	GTAAGTATGA	240
GTATCTCTGA GA						300
CCTAGGTGTG A	AGGAATTAC	AAGTCCAGAA	GGCTCAAAAT	CTATAGTGGA	AGGAATCATA	360
GAGGAAGCTC GA	AG					373

- (2) INFORMATION FOR SEQ ID NO:971:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 656 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:971:

GTGGAACTCC TGACCTCAGG	TGATCCGCCC	ACCTTGGCCT	CCCAAAGTGC	TGGGATTACA	60
GGCGTGAGCC ACCACGCCCG	GCCTATCTCT	TGTTTTTAAA	TCAGTCTAGG	GTGCCAAAGC	120
ATCAGGGTTC CCGGCCTGCA	AGAAAGGGAG	ATTCCTGTTC	ATGTTAAAGT	GTCATATTTA	180
TGAAACTGCC CTTTTTGGAA	TCTTTGAGGT	TGTCTGTACT	ATAGGACTGG	GGAAATGCAA	240
GTGAGTCTAA GAAGAAACCC	AGATGTGTCC	TACCCTGGCT	GGCAGTAGTG	AGAAGGGAGG	300
AAGTTCTTCC TTGGACACTA	GTACTATTGG	AAAGTTCCTT	ATGTCTGGTT	CACTGATGAA	360
GCTTGAGGAT AGAATTGGTG	AGGAGGGAGG	GGAGAACAGG	TCACAGCTGG	AGGGGAGCCT	420
GGGCCCTATA GGGTGTGAGG	CAGAGCAGAG	TGGCAGATAG	GACATGTGGA	CGGTGGGGAA	480
AATATTCCTC ATGGGACAGA	AGATACCTGG	CACATGTACC	CACAACCTGT	ACACAGATGA	540
TCTGTACTGG ACACACGTGG	AGATATGGCC	ATGCCACGCA	TGTGCAAACA	GAGGTGTACA	600
CACAGGAGTG CAGTGATACA	GGACACAGAT	AAACAGAATG	TACACAGCTT	CTCGAG	656

- (2) INFORMATION FOR SEQ ID NO:972:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 318 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:972:

GCAGGAATAG	AGTTGGAGCG	GTGCCAGCAG	CAGGCGAACG	AGGTGACGGA	AATTATGCGT	60
AACAACTTCG	GCAAGGTCCT	GGAGCGTGGT	GTGAAGCTGG	CCGAACTGCA	GCAGCGTTCA	120
GACCAACTCC	TGGATATGAG	CTCAACCTTC	AACAAGACTA	CACAGAACCT	GGCCCAGAAG	180
AAGTGCTGGG	AGAACATCCG	TTACCGGATC	TGCGTGGGGC	TGGTGGTGGT	TGGTGTCCTG	240
CTCATCATCC	TGATTGTGCT	GCTGGTCGTC	TTTCTCCCTC	AGAGCAGTGA	CAGCAGTAGT	300
GCCCCACGGG	TCCTCGAG					318

- (2) INFORMATION FOR SEQ ID NO:973:
  - (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 313 base pairs

- (B) TYPE: nucleic acid (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:973:

GGAAAAATAC	AAAAATTAGC	CGGGTGTGGC	GACGTGCGCC	TGTAGTCCCG	GCTATTCAGG	60
AGACTGAGGC	AGGAGAATCG	TTTGAACCTG	GGAGGTGGTG	GTTGCAGTGA	GCCAAGATTG	120
CGCCATTGCA	CTCCAGCCTG	GGCAACAGGG	TGAGANTCTG	TCTCCAAAAA	АААААААА	180
AAAAGCTGGA	TTACAGGCGT	GAACCACCGC	ACCCAGCCAA	TTCATAGGTG	TTTTAAGTGT	240
GACACTTGGA	TGGTTTAAGT	CTGATAGAAC	TTTTACATTT	ATTATACATT	TAAATATATA	300
CCAGGGGCTC	GAG					313

- (2) INFORMATION FOR SEQ ID NO:974:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 372 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:974:

GAATTCGGCC	TTCATGGCNT	ATTCTTCGCA	GATTATGAAG	ACTACATTAA	ATGCCAGGAG	60
AAAGTCAGCG	CCTTGTACAA	GAACCCAAGA	GAGTGGACGC	GGATGGTGAT	CCGGAACATA	120
GCCACCTCTG	GCAAGTTCTC	CAGTGACCGC	ACCATTGCCC	AGTATGCCCG	GGAGATNTGG	180
GGTGTGGAGC	CTTCCCGCCA	GCGCCTGCCA	GCCCCGGATG	AGGCCATCTG	AGCCTCCAGA	240
CCAGACCCCA	AACCAGCCCT	TGAGTCTGTC	ACACTCTCTT	GGGCCAGCCC	CAGCACCTCA	300
TGCAGAGGGT	GGGGTACTGG	AGTTAGATCT	CTAAGCCCCT	CCTGGAACCC	TCATTTTCCC	360
CACGTGCTCG	AG					372

- (2) INFORMATION FOR SEQ ID NO:975:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 449 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:975:

GAATTCGGCC	TTCATGGCCT	AAAGGATTTG	ATTCAGAGTG	ACATAGCTGC	TCTCCATCAC	60
TTTTACTCCA	AGCATCTCGA	ATTCCCTGAC	AATGATAGCC	TCGTAGTACT	CTTTGCACAG	120
GTTAACTGTA	ATGGCTTCAC	AATTGAAGAT	GAAGAACTTT	CTCATTTGGG	ATCAGCGATA	180
TTTCCTGATG	TTGCATTGAT	GAATCATAGC	TGTTGCCCCA	ATGTCATTGT	GACCTACAAA	240
GGGACCCTGG	CAGAAGTCAG	AGCTGTACAG	GAAATCAAGC	CGGGAGAGGA	GGTTTTTACC	300
AGCTATATTG	ATCTCCTGTA	CCCAACGGAA	GATAGAAATG	ACCGGTTAAG	AGATTCTTAT	360
TTCTTTACCT	GTGAGTGCCA	GGAGTGTACC	ACCAAGGACA	AGGATAAGGC	CAAGGTGGAA	420
ATCCGGAAGC	TCAGCGATCC	CCGCTCGAG				449

- (2) INFORMATION FOR SEQ ID NO:976:
  - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:976:	
GAATTCGGCC TTCATGGCCT ATAGTGTCTT CCTNGGCGCT GCGACAGCCA ATGTAATGGC CTTTCTGTTT CTCATAAGCA GTTTTGTACA GATAATCACT GGCAATATCC CTGGAAGCCT TGGCATGCTG GATCCCAATG GCATCAAACT CGAG	60 120 154
(2) INFORMATION FOR SEQ ID NO:977:	•
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 485 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:977:	
GAATTCGGCC TTCATGGCCT AGAAGAAATC TCTCTTCCAT TCCTGAAAAC AATTTTAGTC CATTCCTCTT CATTAACCTA AGTATAAAAC TACTAATATC TTTCAAGTGC CAGAAGTTCC TCAAGAAGCC GCAGAAAAAG AAATTCCCGT GGCTCCACCC AAAAAACCAG AAGCTCCGAT TGTCCCAGGT ACACTTTAGC CCTGACTTCA TTCTGCAGAA GAGATATCTC CTCTCCTACT GTAAACAATT TTAGCCCAT TCTCTTCATT AACTTAAGTC TAAAACTACT AATATCTTTC AAGTGCCTGA AGCTCAAGAA GTTGTCCCAG AAAAGAAAGT TCCTAAGGCT CCTCCCACAA AACCAGAAGC CCCACCTGCC ACAGGTATTT TTTACCCCTG TCCTTTTTCT GCAGAAGAAA TATCTCTTCT GATCTTAGAA ATATTTTACT CCATTTGTCT CATTAACCTA AGTGAAAAACC	60 120 180 240 300 360 420 480 485
(2) INFORMATION FOR SEQ ID NO:978:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 322 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA	
(x1) SEQUENCE DESCRIPTION: SEQ ID NO:978:	
GAATTCGGCC TTCATGGCCT AGAAAGATTC CTACGTGGGC GACGAGGCTC AGAGCAAGAG AGGTATCCTG ACCCTGAAGT ACCCTATCGA GCACGGCATC ATCACCAACT GGGATGACAT GGAGAAGATC TGGCACCACA CCTTCTACAA CGAGCTTCGC GTGGCTCCCG AGGAGCACCC CACCCTGCTC ACCGAGGCCC CCCTCAATCC CAAGGCCAAC CGCGAGAAGA TGACCCACCA ATCACCTAGG CCATGAAGGC CGAATTCGGC CTTCATGGCC TAGCGCGCACC GGCGAGGAGG GAAGAAGCTCG AG	60 120 180 240 300 322
(2) INFORMATION FOR SEQ ID NO:979:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 499 base pairs  (B) TYPE: pucleic acid	

(C) STRANDEDNESS: double (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:979:	
GAATTCGGCC TTCATGGCCT AGCCGCATCT TCTTTTGCGT CGCCAGCCGA GCCACATCGC TCAGACACCA TGGGGAAGGT GAAGGTCGGA GTCAACGGAT TTGGTCGTAT TGGGCGCCTG GTCACCAGGG CTGCTTTTAA CTCTGGTAAA GTGGATATTG TTGCCATCAA TGACCCCTTC ATTGACCTCA ACTACATGGT TTACATGTTC CAATATGATT CCACCCATGG CAAATTCCAT GGCACCGTCA AGGCTGAGAA CGGGAAGCTT GTCATCAATG GAAATCCCAT CACCATCTTC CAGGAGCGAG ATCCCTCCAA AATCAAGTGG GGCGATGCTG GCCCTGAGTA CGTCGTGGAG TCCACTGGCG TCTTCACCAC CATGGAGAAG GCTGGGGCTC ATTTGCAGGG GGGAGCCAAA AGGGTCATCA TCTCTGCCCC CTCTGCTGAT GCCCCCATGT TCGTCATGGG TGTGAACCAT GAGAAGTATG ACAACAGCG  (2) INFORMATION FOR SEQ ID NO:980:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 333 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	66 126 186 306 366 426 486 499
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:980:	
GAATTCGGCC TTCATGGCCT ATAGGCCATG AAGGCCGGCC TTCATGGCCT ACTTGCCTCC TTTGCTGTCT TAGGAACAAT TCCATGGGAG GGTCTATTCT GGATTAGGAA TTCTTTCTTG AGTAATTTTT ATTACCTTTT AATTGTGTCC ATTTCTTTGG GAAATAGCAA GCTCTCCCTG CTCCCGCCAA TCTCTCCTCT TACTTTTTGG ACCAGTTCTT GTACCTCTTA GCTCACCTCA TTCAGTGAAA ATTGACAAAA GAGACGTGAG TTTCTGTACC TGTGAGACAG CTTATTTTTG TGTCTTTATG GTTTCTAAGC CAAAAATCTC GAG	60 120 180 240 300 331
(2) INFORMATION FOR SEQ ID NO:981:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 91 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:981:	
(XI) SEQUENCE DESCRIPTION: SEQ ID NO. FOI:	
GAATTCGGCC TTCATGGCCT ATCGAGTAAT CCTGATGTTT TCACTTTCTC TAATCACTTC TTCCTATTTT TGTCCAGTGG CTTTTCTCGA G  (2) INFORMATION FOR SEQ ID NO:982:	6 9
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 351 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
419	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:982:

GGCCGCTCGT	GGCTGCGTTC	CCGCTGATGC	TTGTGCCTGC	AGAGCCTCTC	CAGGCTGCTG	60
GTGGGGGAGC	ACTCCCTTCC	CCGAGGTCTG	GACGCTGATC	TCCTTTTCTT	CTTCTTCCTA	120
CTCTCATAGT	GCTCATAGGA	AGAGCTGCCA	GGGCTCCCCG	ACCGCGACCG	GGACGTCCTC	180
CGGCTGTGGC	CCCAGGGGCC	CCGCCTGTGC	TCCCTGCTCT	TGTCCTTGGC	TTTCTTCCTC	240
TTAGCTCGCT	CTCGGCTGCT	GGAGCGGTCA	CTGGAGGACC	GCCGGCTCTT	GGCCTTGGAC	300
CGCTGCCTCC	TGGGGCGCTC	CTCACCCACT	GATGGTGACG	CCGACCTCGA	G	351

- (2) INFORMATION FOR SEQ ID NO:983:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 488 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:983:

GAATTCGGCC I	TCATGGCCT	ACACAAATAT	TGCTGTTCCA	TGTTCTCCAC	TTTCATTTTC	60
CACTACAAAT G	BAAAAGCAAT	TTTTGAGACT	GAATCTGTTG	CTATTTTAAA	GGTTATTGTG	120
GGAAACTGAG C	TAAAGGAGT	TAGCATCTTT	ATTTTTGTAT	CAAAAATAAA	GGTTATTTTG	180
AAATTATTAG G	ATTTTTACA	CAATTCTGAA	ATCTGTTGCT	TTTGTAAACA	AATTGTTTGA	240
TCTTAGTGAT C	CCCCTACTA	CTACCACCAA	TTCACTTCAC	AAAGTCAGTT	ATGAGTCTAC	300
CAGACTTTGT T	CTGAAAAAT	AGAAACAAAA	CACCTGATTA	AGCTCTTGAG	TATGGCATAG	360
GAATTTTTTA G	BAAGAATGCA	TTCAAGGATT	CTTTTCCTTT	CCTTCAGTGT	CATTAATGTT	420
AAAAGAGCAG C	CACTGTTTT	GTTGAAACAA	ACAGCTTAAC	TTCAGAAATA	AGAACTAGCA	480
CACTCGAG						488

- (2) INFORMATION FOR SEQ ID NO:984:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 338 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:984:

GAATTCGGCC	TTCATGGCCT	ACCTCCTGGC	TCAGCAGGCT	CCCTCCTTTT	ACCAAGACTG	60
CTGGGACGTT	GAACTCCGGT	GTCTGATCAT	CTCACCTACT	CTCCTCCTAA	CTCCCAACTG	120
AAATCCATCT	CCTCTCTTCC	TCCCCAACAT	CCATCTCTTT	CCCAACATGC	CTTTGCACCT	180
AGAGCAGGTG	AAGAAAGCCC	ATGACTAAAA	CTAAAGACTC	AGAATGAAAC	AAAAGGTGTG	240
ACAAGTTATT	TGTGGGGAAG	GTTTTCAGAT	ATGTTCCAAG	AGAAAATAAG	GTAAAACAAC	300
CTTGTTCATC	AGACCAACAG	TGCTGGAAAG	GGCTCGAG			338

- (2) INFORMATION FOR SEQ ID NO:985:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 505 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:985:

${\tt GAATTCGGCC}$	TTCATGGCCT	ACCTGAATTG	GGTGGCGAGT	TCCCTGTGCA	GGACCTGAAG	60
ACTGGTGAGG	GTGGNTTGCT	GACAGTGACC	CTGGAAGGGA	TCAACCTCAA	ATTCATGCAC	120
AATCAGTGTT	ACCTTTTATC	TCTCAGTGGA	CATTCCTTAA	GCTAATTCCT	TTCTGAGGCC	180
AGCGCATCAT	CCCAGGAGCG	GAAGGTTTTC	ATAGAGCTGA	ATCACATTAA	AAAGTGCAAT	240
ACAGTTCGAG	GCGTCTTTNG	TCCTGGAGGA	ATTTGGTAAT	TACACTATTT	TGCTCTTAGG	300
TCTGGACTCA	CATGGCAGTA	ACTCAAACCT	CGGAGCTCCA	GAGGAGGGTC	TAGGGGCAGG	360
GAGAAGAAGA	ACCTCTGTAG	AGAAGTCTGG	AGGAGCAGGA	GTGACAAGGA	AGAAAAGGGA	420
CCCCTGAGAT	GAGAGCCGGG	ATGTGGAAGG	GAAAGATAGA	TAATGGATCG	CAGAAGAGCA	480
AATGGGGCCT	CNGGTGGTAC	TCGAG				505

- (2) INFORMATION FOR SEQ ID NO:986:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 292 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:986:

GAATTCGGCC	TTCATGGCCT	ACACCTTCAC	ACCTGTCCTT	ACCTCCATTC	TCACTTCCAC	60
TGTCTTCACT	AACTCCACCA	TCATCACTTC	AATCTTCCCT	TCCATTCTCA	CTCTCTTCTC	120
ACTCACTGTC	CCTCTTTCAC	CTCCATCCTC	ATCTCTGTCC	TCCCGTCTAT	TCTCCTCTCC	180
AACCTCACTT	CTGTCCTCCC	CTTCCTCCTG	CTCTCCATCC	TCACCTCCAT	CCTCACCTTC	240
AACCTCACCT	TTATCCTCAC	CTTCAACCTC	ACCTTTATCC	TCACCACTCG	AG	292

- (2) INFORMATION FOR SEQ ID NO:987:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 239 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:987:

CTCGAGTATC	CACTTGCCTC	GGCCTCCCAA	GGTGCTGGGA	TTACAAGCAT	GAGCCACCAT	60
GCACGGCTGT	AGATGTAAAT	TTTGGAAAGA	GGAAGGCATC	AAATTAGGGG	TGGGGGGATG	.120
GAGGTACATC	CAGCTTAGCC	TTCAGACCTT	AATGGAAATG	CTTTCTAAAC	TAGCGATCCC	180
AGAGCAGTTG	ACTOTOCTGA	AATAAAACAG	GATCTGAGTA	GGCCATGAAG	GCCGAATTC	239

- (2) INFORMATION FOR SEQ ID NO:988:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 394 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:988:

GGCAGACTGC	AATACCTGCG	TGGAAATAGA	AGACAGAAAG	GTTTCAAGAC	AACAGATGAA	60
TTGTGAAAGA	GAGCAGCTAA	GGGGTAATCA	GGAAGCAGCC	GCTGCCCCTG	ACACAATGGC	120
TCAGCCTTAC	GCTTCGGCCC	AGTTTGCTCC.	CCCGCAGAAC	GGTATCCCCG	CGGAATACAC	180
GGCCCCTCAT	CCCCACCCCG	CGCCAGAGTA	CACAGGCCAG	ACCACGGTTC	CCGAGCACAC	240
ATTAAACCTG	TACCCTCCCG	CCCAGACGCA	CTCCGAGCAG	AGCCCGGCGG	ACACGAGCGC	300
				GCACCGACGG	ATGGCCAGCC	360
CCAGACACAA	CCTTCTGAAA	ACACGGGGCT	CGAG			394

- (2) INFORMATION FOR SEQ ID NO:989:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 366 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:989:

GAATTCGGCC	TTCATGGCCT	ACTTCCGGGC	TTTGACTCAA	TTCATGGGAA	ACAGGAAAAG	60
CAAAACTAGT	TGATCTTGCT	ACTAAGGCGG	ACTGAAGTTT	CTTGTCTTCA	TTGCTAAACA	120
ACTTCCAAAT	CACTTTGACT	CTTTGACCAT	ATTCATGTCT	ATTTCCCATT	AAAGCATCAC	180
AAAATAATGA	AGGAATTCTT	AGGAAGAGCC	TCAAGATGCC	CATGTGGCGT	CTGTGTGGGC	240
TGCCTCGTCT	GGTAGTTCAG	GGACCCACTG	GGCCATTTGA	AGGGCAAAGA	GAAAGCCCCA	300
GGTCTCATGG	CAGGAGACAA	GACTTCCACA	GTGGTGAGCC	AGTAAGGAAC	AGGGCACGTA	360
CTCGAG						366

- (2) INFORMATION FOR SEQ ID NO:990:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 364 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:990:

GAATTCGGCC	TTCATGGCCT	ACATGTTCAT	TATGAAGTTA	TTAGTAATAC	TTTTGTTTTC	60
TGGACTTATA	ACTGGTTTTA	GAAGTGACTC	TTCCTCTAGT	TTGCCACCTA	AGTTACTACT	120
AGTATCCTTT	GATGGCTTCA	GAGCTGATTA	TCTGAAGAAC	TATGAATTTC	CTCATCTCCA	180
GAATTTTATC	AAAGAAGGTG	TTTTGGTAGA	GCATGTTAAA	AATGTTTTTA	TCACAAAAAC	240
ATTTCCAAAC	CACTACAGTA	TTGTGACAGG	CTTGTATGAA	GAAAGCCATG	GCATTGTGGC	300
TAATTCCATG	TATGATGCAG	TCACAAAGAA	ACACTTTTCT	GACTCTAATG	ACAAGGAGCT	360
CGAG						364

- (2) INFORMATION FOR SEQ ID NO:991:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 302 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:991:

GAATTCGGCC TTCATC	GCGG GGAAGAAGAC	AAGAAAATTA	ATGAAGAACT	GGAGTCTCAA	60
TATCAGCAAA GTATGO	SACAG TAAATTATCA	GGAAGATATC	GGCGACATTG	TGGACŤTGGC	120
TTCAGTGAGG TAGAAT	TACCA TGATGGAGAA	GGTGATGTGG	CTGGAGATGA	TGATGATGAC	180
GATGATGATT CACCTO	SATCC TGAAAGTCCA	GATGATTCTG	AAAGCGATTC	AGAGTCAGAG	240
AAAGAAGAAT CTGCTC	GAAGA ACTCCAAGCT	GCTGAGCACC	CTGATGAAGT	GGAGGTCTCG	300
AG					302

- (2) INFORMATION FOR SEQ ID NO:992:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 484 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:992:

GAATTCGGCC TTCAT	IGGCCT AGGTGCAGCA	GGTCCTCTGG	GAAGTGTCGC	ACAAAGGAGT	60
CGCCCACTGG AAGGT	ITCTGG GCAGGCGAGA	TGCCCAGAGG	TGATCCCTGC	CCGCCCCTCC	120
CACCTCCCTT CCCAC	CACAGC CCATGGAGGT	GTTTGTGGAC	GACGAGACCA	AGCTCACGCT	180
GCACGGCCTG CAGCA	AGTACT ACGTCAAACT	CAAAGACAGT	GAGAAGAACC	GCAAGCTCTT	240
TGATCTCTTG GATGT	IGCTGG AGTTTAACCA	GGTGATAATC	TTCGTCAAGT	CAGTGCAGCG	300
CTGCATGGCC CTGGC	CCCAGC TCCTCGTGGA	GCAGAACTTC	CCGGCCATCG	CCATCCACCG	360
GGGCATGGCC CAGGA	AGGAGC GGTGAGTNCG	AACCGCCCGC	CAAGGCTGCA	GGGNGCACCA	420
CCAGGAGCCC AGTGT	ICTGAC GGCCTCCACT	TGTTTCTCCT	GCACCCCNNC	CCATCACGCT	480
CGAG					484

- (2) INFORMATION FOR SEQ ID NO:993:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 186 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:993:

GAATTCGGCC	TTCATGGCCT	AAAGGAATTT	ATCTATTTAA	TCATTGAATG	TATIGAACAT	60
TCATTTGTTT	ATAATTTTGT	TTTGTTATTG	AAAATGTCTG	TAAGATTTAT	AGTGATGTTC	120
CCTTTTCTAT	TCCTGACATT	GTTAATTTGT	GTTCTCTCTC	CCTCCATCCC	TCTCTCACAT	180
CTCGAG						186

- (2) INFORMATION FOR SEQ ID NO:994:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 343 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:994:

GAATTCGGCC TTCATGGCCT AGTGTTTTCA TAAAGGGGTT GAGGCCACCA GTACTGCAGC GAATTCCTT TTCTTCTCCC TCCTCCTTCC TTCTCTGAGC TTGCTTTTAG GGAAGGTTAA TCTTACAGGC TACCTATGTT TCTCTCCACC TTACTAAAAT CTAAATAATG ATAGAAATTT TAAGTTTTTA AATTGAGTAG TCTGAGGTAA TCCTAGAATA TTTTTCCAAA TTAAATAATC CTTTATTATT TGCAAGTTGG GCCAAATTTT TTTTTTTTTG GAGACGGACT CTTAACAATC TAAGATTGTT TCAACAGGAC TTTCTTATTC CCATTCCCTC GAG	60 120 180 240 300 343
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 265 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:995:	
ATCTTTAACA GAATTATTAT TATTTAATAT AGAAGCACAA GCAGGGGAAA AATACGTCAT CAAAAATTTTC AAGTAGTCAA CTCATTATTG GAGCCATTTT ATTTTATAAT TTTATTATC AGCTGGTTCA GAATTCAAAA GGGCATGTAA TGAAGTCGCT ATCCTGCTTC TGTTTCCCAG CTATCCAGCT TCCCTCCCTG GAGGCAAACA GTGTCATTGG TTTTCAATAT ATCCTTCCAG ATGTATGTTA TCCGTAACTC TCGAG	60 120 180 240 265
(2) INFORMATION FOR SEQ ID NO:996:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 77 base pairs  (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:996:	
GATTCGGCTT CATGGCCTAC AGCAGACACC CTCCTGCCCA CACCTACTTG TCCGCGCGGT CTGAGGTTTG CTTCGAG	60 77
(2) INFORMATION FOR SEQ ID NO:997:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 270 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:997:	
GAATTCGGCT TCATGTCGCT CTTCCTGCAG GTCAACATGT ACAGCAGCGT CTTCTTCCTC ACCTGGATGA GCTTCGACCG CTACATCGCC CTGGCCAGGG CCATGCGCTG CAGCCTGTTC CGCACCAAGC ACCACGCCCG GCTGAGCTGT GGCCTCATCT GGATGGCATC CGTGTCAGCC ACGCTGGTGC CCTTCACCGC CGTGCACCTG CAGCACACCG ACGAGGCCTG CTTCTGTTTC GCGGATGTCC GGGAGGTGCA GTGGCTCGAG	60 120 180 240 270

(2) INFORMATION FOR SEQ ID NO:998:

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 264 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:998:	
TCTGCAAGAC CATGTCTACA CAGACAACAC CATCTTCTGA ATGACAGAGG ATCAGAAGAG 1 CCACCTGGCA GCAAAGGTTC TGTCACTCTA AGTGATCTTC CAGGGTTTTT AGGTGATCTG 1 GCCTCTGAAG AAGATAGTAT TGAAAAAAGAT AAAGAAGAAG CTGCAATATC TAGAGAACTT 2	60 20 80 40 64
(2) INFORMATION FOR SEQ ID NO:999:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 241 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:999:	
CCCAGTTCAA ATAACGCTAT GCTTGGGGTT CATGCATCAG CTTCAGCGAT CATCCAGTAT GGAAAAATCG CCCGGAAACA AGGACTGGTC AATGTAGCTC TGGATATATT AAGTCGGATT CATACTATTC CAACTGTTCC TATCGTGGAT TGCTTCCAGA AGATTCGACA GCGTACTCGA 2	60 .20 .80 .40
(2) INFORMATION FOR SEQ ID NO:1000:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 295 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1000:	
CTCTTTTGTC TATAGGCCCG AAATGTTTGA GACGGCGATT AAGGAGAGCA CCTCCTCTAA GAGCCCTCCC AGAAAAATAA ATTCATCACC CAATGTTAAT ACTACTGCAT CAGGTGTTGA	6( L2( L8( 24)
(2) INFORMATION FOR SEQ ID NO:1001:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 248 base pairs  (B) TYPE: nucleic acid	

- (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEO ID NO: 1001: GAATTCGGCC TTCATGGCCT AGATATTTAG AAATTTTGTG TATTATATGG AAAAAGAAAA 60 AAAGCTTAAG TCTGTAGTCT TTATGATCCT AAAAGGGAAA ATTGCCTTGG TAACTTTCAG 120 ATTCCTGTGG AATTGTGAAT TCATACTAAG CTTTCTGTGC AGTCTCACCA TTTGCATCAC 180 TGAGGATGAA ACTGACTTTT GTCTTTTGGA GAAAAAAAC TGTACTGCTT GTTCAAGAGG 240 AGCTCGAG 248 (2) INFORMATION FOR SEQ ID NO:1002: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 331 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1002: GAATTCGGCC TTCATGGAGT CAGCCTTCCA GTCCTCATCT CAGAAATTGA CTAGCCAGAA 60 GGAACAGAAA AACTTAGAGT CTTCAACAGG CTTTCAGATT CCATCTCAGG AGTTAGCTAG 120 CCAGATAGAT CCTCAGAAAG ACATAGAGCC TAGAACAACG TATCAGATTG AGAACTTTGC 180 ACAAGCGTTT GGTTCTCAGT TTAAGTCGGG CAGCAGGGTG CCAATGACCT TTATCACTAA 240 CTCTAATGGA GAAGTGGACC ATAGAGTAAG GACTTCAGTG TCAGATTTCT CAGGGTATAC 300 AAATATGATG TCTGATGTAA GTGAGCTCGA G 331 (2) INFORMATION FOR SEQ ID NO:1003: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 248 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: CDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1003: GAATTCGGCC TTCATGGCCT ACAGTATTGG ACTTTCAGAA GCTGAACAGA TGATGGGTGA 60 GCAAACTGGT TTAGCAGACC CAAGAGAGCT GAATCCTAAG CCAGCAAATA GAGAAATCCA 120 AGATTCAGCC CAAATTATGC TTTAGAATTC CTCAAAGGCT CAGAAACTGG CTGCACTAGT 180 TCCCCCGACA GGAAGCATGG ATTGAGGAGG TACCAAACCC ACTCCCCACC AAAAACCCAA 240 AACTCGAG 248
  - (2) INFORMATION FOR SEQ ID NO:1004:
    - (i) SEQUENCE CHARACTERISTICS:
      - (A) LENGTH: 281 base pairs
      - (B) TYPE: nucleic acid
      - (C) STRANDEDNESS: double
      - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1004:

GAATTCGGCC	TTCATGNCCT	GGNGAAGAGN	AACAAGAGAA	CAAAAAAAAN	ANAAGTCGAG	60
AGTCAGTAAT	TTTCTTACTT	AATATTGNGG	GGATNTTACT	TNATACATAA	AGTTANTGAA	120
				ATTAACCTAT		180
					TTTTTTTTTC	240
			GCGCACTCGA			281

- (2) INFORMATION FOR SEQ ID NO:1005:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 290 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: CDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1005:

GAATTCGGCC	TTCATGGCCT	ACATAAACCA	TCACATTTAA	TCTGGCAGCT	GCCCTGTTTT	60
TGAGGTTTTC	TTTGTATTTA	TCTTTCTTTG	GTAAATGAAA	GCTCTCATCT	TTGTTTACAG	120
GCCAGAAAAA	CTGAAAAAGA	CACAGGCTCT	TCCACTTACT	GGATGTTTGA	CAAAATGATA	180
TTTTGGGGCC	AAAACATTGG	CATTACTGGT	AAACTTGGTA	GAGATTCAGT	AACTCAGACT	240
TTATTTCAGA	TCTCCTGAAA	AAATAATCTG	CATTAACATG	ATGACTCGAG		290

- (2) INFORMATION FOR SEQ ID NO:1006:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 327 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1006:

GAATTCGGCC	TTCATGGCCT	AAATTTTCAC	ATATATGTAT	ACTTAATTTT	CAGCAATTAT	60
GACACAATAA	AAAGAATATG	CAAATTTATT	GTTGTTTCAG	AAGGTTTTGC	AGGACTGGGA	120
ACGCTTTAGT	GTCATCAACA	GTAAACCTCA	GATACTGTTC	TGCACAGTTC	AGAAGTACCA	180
TACCAGGTAT	TGTGAGTGGC	AAGAACGCCA	GGGGACAGAG	ATGCTTCTGG	TAGATGAGGG	240
CCAGAGAAAC	CAGCTCTCCT	CCATTTTGAC	AGCAATTTCT	CACTGTGGCC	ATTTGGCCTC	300
CATTATGTTT	TGAGAGGAAC	GCTCGAG				327

- (2) INFORMATION FOR SEQ ID NO:1007:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 248 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1007:

GAATTCGGCC TTCATGGCCT ACAAAAAAT ATAGTGTTTT ATGCCACAGA GAATCAAGTT

GCATTGTGTA TACTAAATGG TCAAGCATTT TCAAGAACAT GACAAAATAA AAACATACAA ATTTATATCT CAAAAGGAAA GTATCTTCTT TCATGTCAGA TCATCAGCAC AGAAGCCCTC GATGCATGCA AAGGCAAGCA CAGGCTCTGC AGATGAGATG	120 180 240 248
(2) INFORMATION FOR SEQ ID NO:1008:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 460 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1008:	
GAATTCGGCC TTCATGCCTA CATCAAACCC TTTTCTTGTA GCAGCACAGG ATTCTGAGAC AGATTATGTC ACAACAGATA ATTTAACAAA GGTGACTGAG GAAGTCGTGG CAAACATGCC TGAAGGCCTG ACTCCAGATT TAGTACAGGA AGCATGTGAA AGTGAATTGA ATGAAGTTAC TGGTACAAAG ATTGCTTATG AAACAAAAAT GGACTTGGTT CAAACATCAG AAGTTATGCA AGAGTCACTC TATCCTGCAG CACAGCTTTG CCCATCATTT GAAGAGTCAG AAGCTACTCC TTCACCAGTT TTGCCTGACA TTGTTATGGA AGCACCATTG AATTCTGCAG TTCCTAGTGC TGGTGCTTCC GTGATACAGC CCAGCTCATC ACCATTAGAA GCTTCTTCAG TTAATTATGA AAGCATAAAA CATGAGCCTG AAAACCCCCC AGAACTCGAG	60 120 180 240 300 360 420
(2) INFORMATION FOR SEQ ID NO:1009:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 241 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1009:	
GAATTCGGCC TTCATGGCCT ACGACAAGTT TTTAAATTTA CTCTTGAGTA TGGTTCCAGT GATTTACCAG AAAAACCAAG AAGACAGGCA CAAAAAAGCA AACGGCATTT GGCAAGATGG ATTATCAACT GCAGTACAGA CTTTTAGTAA TAGATCTGAG CAACACATGG AGTATCACAG TTTCTCAGAG CAGTCTTTC ATGCCAATAA TGGGCACGCA TCATCAAGCT GCAAACTCGA G	60 120 180 240 241
(2) INFORMATION FOR SEQ ID NO:1010:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 241 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1010:	
GCGATTGAAT TCGACCACCT TGTTCAAATT TGTTATTATT TTTCTACTTT TGTATTGATT CTGTTAATTC TTATCTATTG GTTCAGCTTA CTTTTTTATG TTGGTCACAT TTCTCTTCAT TGATTGTGTT AATTTTTCTA TGTTGATAGA CACATTTTAT GTTCATCACT TTTTTCTCTC	60 120 180

CTCCTTCAAT TATTATCCTT CTGATTTCTT TTTGTTTTCT CATAGTGTTG GCCATCTCGA	240 241
(2) INFORMATION FOR SEQ ID NO:1011:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 338 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1011:	
GAATTCGGCC TTCATGGCCT AGGCCACAC TCAAAAGCAT TATCTTTTT AGGGTTAGTA GAAATTGTTT TATGTTGAT GGAGGTTGT TTGATTGTCA AAATGTACAG CCACAGCCTT TTAATTTGGG AGCCCCTGTT GTCATTCAAA TGTGTACCTC TACAGTTGTA AAAAGTATTA GATTCTACTA TCTGTGGGTT GTGCTTGCCA GACAGGTCTT AAATTGTATA TTTTTTGGAA AAGTTTATAT ACTCTCTTAG GAATCATTGT GAAAAGATCA AGAAATCAGG ATGGCCATTT ATTTAATATC CATTCATTTC ATGTTAGCGG AACTCGAG	.60 120 180 240 300 338
(2) INFORMATION FOR SEQ ID NO:1012:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 97 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1012:	
TGAATTCTAG ACCTGCCTCG AGCTCCAGCT GCCAACACCC TTGGACACAA TATTCCAGTC TCCACTGCCC ATCTCATGTG GTTGCAGGNT CCTCGAG	60 97
(2) INFORMATION FOR SEQ ID NO:1013:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 412 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1013:	
GAATTCGGCC TTCATGGCCT ACACATTCTG GGGGAAAAAA ACTGGAATTG TTTGTATTTT GTTTTTTTGG GGGGGGATCT TTATGTGAAA AATCAGAGCT ACTTGTTACC ATAAGCCCTT ACTATCAACA AGATAATTAT TTGTAATCAC TTTTTTATCC CAGGTTGGAA TTGCTTTCCC CTTCTAAGTT ATCTTCCCTT AATAATATTT ATGATACCAG GACAGTGAGG GTATAAGAGC AAATGTAGTG AGGTATTCAA AAATCCTGCA TATATGGACT CAAAAGTTCT TTAGTTATTT GAATTATATA TAGCTATATT ATTTTATTAG CTTGGGTTGT CAGAAGATTG CCAATTTTAA	60 120 180 240 300 360
GAGTAAAGAG GAGAGAGATA AGTAATAAAA ATAGAGGAGG GGTACTCTCG AG	412

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 218 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1014:	
GAATTATGTC TCCCATCTGT GCTTTTCCTA AGTGGGGCTC CCGTGCCGTT CACCTCACAT TCCTGGTTG TTACTTGGCA GGCACTCCCA CCACTCCGAA AGGGAGGCCC TTCCTGGGAG GGAGGCAAGA AGGCTCCCCA GCCCTTTGC CCCCTTTCCT GGGCCTGCGT TCCCAGGGCC TCCCCAGCCC CTCTGGCTAC CCCGTGACCT GCCTCGAG	60 120 180 218
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 513 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1015:	
GAATTCGGCC TTCATGGCCT ACCTTATTAC CAGACAACCT TAACCAAACC ATTTACCCAA ATAAAGTATA GGCGATAGAA ATTGAAACCT GGCGCAATAG ATATAGTACC GCAAGGGAAA GATGAAAAAT TATAACCAAG CATAATATAG CAAGGACTAA CCCCTATACC TTCTGCATAA TGAATTAACT AGAAATAACT TTGCAAGGAG AGCCAAAGCT AAGACCCCCG AAACCAGACG AGCTTCGGGG GAAGTATGTA GGAGTTGAAG ATTAGTCCGC CGTAGTCGTT GACCTCGTCT GTTATGTAAA GGATGCGTAG GGATGGAGG GCGATGAGGA CTAGGATGAT GGCGGGCAGG ATAGTTCAGA CGGTTTCTAT TTCCTGAGCG TCTGAGATGT TAGTATTAGT TAGTTTTGTT GTGAGTGTTA GGAAAAGGGC ATACAGTCTC GAG	60 120 180 240 300 360 420 480 513
(2) INFORMATION FOR SEQ ID NO:1016:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 74 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1016:	
GAATTCGGCC AAAGAGGCCT ACCAAAATAA AAACAGAAAT TATGAGATTG CCTCAACTCC CACATATGCT CGAG	60 74
(2) INFORMATION FOR SEQ ID NO:1017:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 361 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
420	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1017:

GAATTCGGCC	AAAGAGGCCT	AAAGACCTGA	GGTCCAGGAT	GAGCTCTTTC	CCACAGAAAC	60
TTTGACAAAT	GTGTGGACAA	TAAAGNAGCA	CTGCTTCCCT	CATTCACCAT	AGCTCAGCTG	120
GATTTATAGA	TTTAAATCTT	TTAACGAAAA	AGTTCATGTT	GAGGTATTTA	GATACTTTTT	180
AGAGGGTTAA	ATACCAAGTT	ACAGTGACAT	TTAAACCGAG	TGTCTAGAAC	ATGAAGGCAA	240
AGAGTCTGCT	ATTCGGAGGT	AAATTTTATC	AGTGTTTGAA	AGGTGAAGCA	TTTGCTCATG	300
AAATGTTGAA	TGAATTTCTG	TGACATGGCA	CGAGGGTGGT	AAGAAAAAGT	GGGAACTCGA	360
G						361

- (2) INFORMATION FOR SEQ ID NO:1018:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 407 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1018:

GAATTCGGCC	AAAGAGCTAC	GAGAGTGTCA	TGAAATATCT	CCGAGAGTCC	TTCAGTGAGA	60
GGTTGTTTTT	TTTTCCTATG	GCTGGTGTCA	CTTCCTCTGG	AGCATCTTCA	TCGTTTCATC	120
ACAGTCACTT	TCTAACTGGA	GTCAGTAAGT	TCACCTTCTT	TAAGCTTCCC	AGGCTGCAGA	180
TACAGAGAGT	GTCCACATTC	CACAGTCAGC	TATTTCTACG	ATCACTCCAT	TTACGCTTGG	240
TTCAAATTTC	ACTCCCAGTG	TTACCACTTC	TCATTCTTTT	GCTGTGTTTC	ATCTGGGCCA	300
TTTGCTTCTT	ATGATTACCT	GTTTTTGTAA	ACTGTCATGT	GGGTTTATCC	CTGGGAGACA	360
AGGAGACAGC	ACAACCCCTT	GGTTTGCTGT	CTGTGAGCGA	ACTCGAG	•	407

- (2) INFORMATION FOR SEQ ID NO:1019:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 327 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1019:

GAATTCGGCC	AAAGAGGCCT	ACTAAGTTCT	GTGAAGTGTA	TGTAGCATCT	GGGCTATAGA	60
TTTGGAGCTT	TTACTGACTC	TNGAGAGTGG	TGAAGGAGTA	TCTGCAGCTC	TGATGACAGG	120
NACAGAGAGA	GAGAGAGA	GATGGGTATG	CCATCCGTGG	ACACCAGGAA	GAGTACCGAG	180
GACTGCTGTA	GGCTCCTTCA	GTTCTAGTTT	CCAACTCAAA	GCAATTTTTA	AGTTTTTGTT	240
TAATTATGNN	TCGGCTCTGC	TAAGANANNA	AGGTACCTTA	CATAAGTCCC	TCAAAAGACT	300
TGTGTGTTTG	AAGATGGCGC	CCTCGAG				327

- (2) INFORMATION FOR SEQ ID NO:1020:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 140 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1020:

GAATTCGGCC	AAAGAGGCCT	ATGAATGCTA	TATACCCTTT	TTATATCAAA	AGTCTCAAGC	60
ACTTATTTTT	ATTCTATGCA	TTGTTTGTCT	TTTACATAAA	TAAAATGTTT	ATTAGATTGA	120
	ATTACTCGAG					140

- (2) INFORMATION FOR SEQ ID NO:1021:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 354 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1021:

					TCACACCAGT	60
GTGGAACGTC	CCCGCCCNTC	CCCTTGGGTC	CCTTATCTTA	GGGGACCGGG	ACGTCCATCC	120
CTTCTGCAGT	GGCAGCNTCT	GAGCCAAAGC	GCCTCTCCCA	GAAGCCGGAC	TTTCCAGGAC	180
CCTCACTCCC	AGCCACACCC	TGACACGGCC	TGACTGGGGT	CTCCTGTGAG	TCCCATGCTC	240
					GGCTCTCCAC	300
			GCTCCACACA			354

- (2) INFORMATION FOR SEQ ID NO:1022:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 633 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1022:

GAAAGAGGCC	TAATCGTCAC	ATCCATCAGA	GGATTGCTGA	TCACTCTTAC	CAAGTTCTTT	60
TATGCCATCT	CTAGCAGTAA	GTCCTCCAAT	GTCATTGTCC	TGCTATTAGC	ACAGATAATG	120
GGCATGTACT	TTGTCTCCTC	TGTGCTGCTG	ATCCGAATGA	GTATGCCTTT	AGAATACCGC	180
ACCATAATCA	CTGAAGTCCT	TGGAGAACTG	CAGTTCAACT	TCTATCACCG	TTGGTTTGAT	240
GTGATCTTCC	TGGTCAGCGC	TCTCTCTAGC	ATACTCTTCC	TCTATTTGGC	TCACAAACAG	300
GCACCAGAGA	AGCAAATGGC	ACCTTGAACT	TAAGCCTACT	ACAGACTGTT	AGAGGCCAGT	360
<b>GGTTTCAAAA</b>	TTTAGATATA	AGAGGGGGGA	AAAATGGAAC	CAGGGCCTGA	CATTTTATAA	420
ACAAACAAAA	TGCTATGGTA	GCATTTTTCA	CCTTCATAGC	ATACTCCTTC	CCCCTCAGGT	480
GATACTATGA	CCATGAGTAG	CATCAGCCAG	AACATGAGAG	GGAGAACTAA	CTCAAGACAA	540
TACTCAGCAG	AGAGCATCCC	GTGTGGATAT	GAGGCTGGTG	TAGAGGCGGA	GAGGAGCCAA	600
GAAACTAAAG	GTGAAAAATA	CACGAAACTC	GAG			633

- (2) INFORMATION FOR SEQ ID NO:1023:
  - (1) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 665 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: CDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1023:

GAATTCGGCC	AAAGAGGCCT	ATCTTCCCAC	TOCACTOTO	GCTCTCCCC	CCCCTCCAAC	
						60
	CGGCCTTCAT					120
TATCTGAAAT	CTAAAGGAGC	TGAGATTTCA	GAAGAGAACT	CGGAAGGTGG	ACTTCATGTT	180
	AAATTATTGA					240
GAAAGTGTGA	TGAACAGTGT	GGTATCCCTA	CTCTTGATCC	TGGAACCAGA	CAAGCAAGAA	300
	AAAGCCTATG					360
	AGTTGTTAAG					420
	TATTGCAGCC					480
	CTGGATCAAG					540
	CTTTTAAGAC					600
	GTCATGGTGG	MALIGUTUGG	AAGTTACACA	GAGGACAATG	CTTCCCAGGC	660
TCGAG						665

- (2) INFORMATION FOR SEQ ID NO: 1024:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 549 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1024:

GAATTCGGCC AAAGA	AGGCCT ACTTGATTTG	GATTCACATT	GCTTTCATTT	CTTAAAATGC	60
TTCACTTCAG GTTCT	TTGGTC TTGGAAATAA	ATTTCAAGGT	GCATTGTATC	CATTTTAAGC	120
TGCTTTATTT TATTT	TTCACT TGTATGAGCA	AATTCTTGGG	GGAGCTTTGC	TTTTCTTCTG	180
CCAGAAAAAC AAAAG	GGGGA AATGAAAATC	TTTTTTGGAA	TGAGTTCTGT	GGGTTTTCTT	240
AACAGCCACC ATGTT	TTATTA GTTACATTGT	GTTTTGGCCA	ATCAGTGCAA	TGTAACAAAT	300
TTTACAGTTA ATTG	TTTCA ATTGAGTCAG	TAAACCTGTG	ATAGATAATT	TATTTAACTG	360
GAAAACCTAG GTACC	CATAA GAAAAAAGAT	TCATTCTCTG	TGAAAACTGT	AGGAATCTGT	420
TGTTGTTTTC ATTTC	SAATAT GCTCTACTTC	TGCTCTAGTA	TTTGGTTTGG	AATATATTTT	480
GTGGCTCTAA TTACT	GTATT TTTAAAAACC	CTACCTCCAT	TAACAGTTGG	TAAAGGCCCC	540
CTTCTCGAG					549

- (2) INFORMATION FOR SEQ ID NO:1025:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 92 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1025:

GAATTCGGCC AAAGAGGCCT AGTTAAGTCT GAACTAGTCT TTTCCTTTGT GATGTGGTTG 60
GAAAGTCTTC CCTGTTCCAA GGACTCCTCG AG 92

- (2) INFORMATION FOR SEQ ID NO:1026:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 383 base pairs

(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1026:	
GAATTCGGCC AAAGAGGCCT AGTTAAAAAC TAATATTTAT ATGACAGAAG AAAAAGATGT CATTCCGTAA AGTAAACATC ATCATCTTGG TCCTGGCTGT TGCTCTCTC TTACTGGTTT TGCACCATAA CTTCCTCAGC TTGAGCAGTT TGTTAAGGAA TGAGGTTACA GATTCAGGAA TTGTAGGGCC TCAACCTATA GACTTTGTCC CAAATGCTCT CCGACATGCA GTAGATGGGA GACAAGAGGA GATTCCTGTG GTCATCGTG CATCTGAAGA CAGGCTTTGGG GGGGCCATTG CAGCTATAAA CAGCATTCAG CACAACACTC GCTCCAATGT GATTTTCTAC ATTGTTACTC TCAACAATAC AGCAGATCTC GAG	180 240
(2) INFORMATION FOR SEQ ID NO:1027:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 403 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1027:	
GAATTCGGCC AAAGAGGCCT ACATGTGGAC TGCACTGTTT ACTTTTGGTT GGACTGGGAC AATTTGGGGA ATATCTACTA TGTTTATTCT TCAAGAACCC ATCATCCCAT TAGATGAGAC AACCTGGAGT TATCTCATTG CTATATGTGT CTGTTCTACT GCAGCATTCT TAGGAGTTTA TTATGCCTTG GACAAATTCC ATCCAGCTTT GGTTAGCACA GTACAACATT TGGAGATTGT GGAGGGGAT ATCATTATGA TTAGTGTTTT TGTCCTTGCT GGCTATAAAC TTTACTGGAG GAATTTAAGA AGGCAGGACT ACCAGGAAAT ACTACGACTC GAG	
(2) INFORMATION FOR SEQ ID NO:1028:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 71 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1028:	
GAATTCGGCC AAAGAGGCCT AAAACCGAAA CTTCGATGAA AATGAAATTC CTCAAGAGAA TGGCACTCGA G	60 71
(2) INFORMATION FOR SEQ ID NO:1029:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 349 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
42.4	

- (ii) MOLECULE TYPE: CDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1029:

GAATTCGGCC AAAGAGGC	CT AGAAACATGT	CTAAGGTNGC	ACACAGCTAG	TANGCGTTAG	60
AAACGTGTCT CAAACCCA	AG AGGTCTGGCT	CTGGCATCCG	TGATCATAAC	CACTNGCTTT	120
GCCTGATCTA ACAGTAAA	GA TGGATGAAAA	AATAAATCAA	GTGTGATGAG	TGTTATATAA	180
GAAAGGGGAA ATAGCAGG	GT TCAGTGTGGA	ACATAGGAGA	GTGGGCCTTC	ATTCCCTCCA	240
GTTGAGGGCC AAATAAGG	CA TCCCTGAGGA	AGAGACATTA	AGCTGAGATC	TGAAAGGTGA	300
GCCTGAATAA GTTAGGTG	AA GGAGCATGAG	TAAAGGGAAG	CCGCTCGAG		349

- (2) INFORMATION FOR SEQ ID NO:1030:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 236 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1030:

GAATTCGGCC	AAAGAGGCCT	ACTGATGATA	ATAAAACAGA	GCTTTACTTG	GGAGAAATTA	60
GCCTTGAAGG	TGTGACATCC	AAAACAATTT	TTTTAAAAAA	ATTTAGACAA	CTAAAAAGGG	120
AAATGTCAAA	AGGGAGAAAC	TTAAAAAACA	AAAGGAAAGT	AGTCAGAGAA	TCAGAGAGAA	180
AATATGAACA	GAACACAGTA	AAAAGGAATG	GCTACAAGAG	GGATCAGCAA	CTCGAG	236

- (2) INFORMATION FOR SEQ ID NO:1031:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 443 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear

    - (ii) MOLECULE TYPE: cDNA
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1031:

GAATTCGGCC	AAAGAGGCCT	ATTAGAAATA	AATATCTTCC	TTCAATAGAT	GAAAATGAAA	60
ATACAGAAAA	AAGAGAGCAG	TTGTCAAATT	TAAAAGTTTT	GAATCACTCC	CCAATGTCTG	120
ATGCCTCTGT	CAATTTNGAC	TACAAATCTC	CATCCCCATT	TGACTGCAGC	ACTGATCAAG	180
AAGAGAAAAT	TGAAGATGTT	GCTAGTCACT	GTCTGCCTCA	GAAGGACCTG	TATACTGCTG	240
AAGAGGAAGC	TGCTACCCTT	TTTCCTAGGA	AAATGACATC	CCATAATGGG	ATGGAGGACA	300
GTGGAGGAGG	AGGTACTGGA	GTGAAGAAGA	AACGGAAGAA	AAAGGAGCCA	GGAGACCAAG	360
AGGGTGCAGC	AAAGGGAAGC	AAGGACAGAG	AGCCCAAGCC	AAAGAGGAAA	CGAGAACCGA	420
AAGAGCCAAA	GGAAGAGCTC	GAG				443

- (2) INFORMATION FOR SEQ ID NO:1032:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 397 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1032:

GAATTCGGCC	AAAGAGGCCT	AATAAAGAGC	AAAAAAATGT	TAATGTCAAG	TCAAATTGCC	60
TGTAAATGAC	TTAAGGAATA	TGTTAATGAT	CTTGCTCCAA	ATGAATAATT	ATAAAGCAGG	120
TGCACTGGAG	ATATGATCAT	TTAACTGAAA	GAAAACAGCT	TCTAATGGCT	TCAATAACCA	180
AGATAATGGT	GATATTGGAG	<b>AAGCCTGTTA</b>	AACTCATTGT	TCATGCCATT	CATTTAATAC	240
ACAAGAGAAC	TTCAGATGGA	ATCTCCCTGT	GGACTCATTG	CCCTGCTTAT	TTAAATAGCA	300
GTTAATTTAA	ACACACACCC	AAGTCAAAAC	TGCATTATTT	CTAACACACC	TCTTTCTAAT	360
AAACTATGTT	CTCCAATAAC	AGAACCCCTG	TCTCGAG			397

- (2) INFORMATION FOR SEQ ID NO:1033:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 372 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1033:

GAATTCGGCC AAAGNGGCC	AAAAATTTTA	TCACTTTAAG	NATCCAATAG	AGAACAACAA	60
AGCCATATTG AGATGCAGG	TTTAGGAATT	TGGTAGTAAT	CCCTCACAAG	GTCAGACTTG	120
ATCTCCTGGA CAATCAGGG	ATGCTAGTCA	GCTTTCATGA	CTCAGCAAAG	CTACAAATTA	180
TGTATTTTGG CTTTTTGTGG	<b>AAATTGCCAA</b>	CCCTACAGAT	AGCAAACGTC	TCCTCGGTTG	240
TCAAAAAGTA AGAGTAGTT	TTAGAATTCT	GCCTTTGGGT	CTTGTAGAAT	GAAATATTTA	300
CAAGATTTGC TATTTGTTA	CATTTTAGCT	CCTTCCTTGT	TCCTTCAGTC	TTGCTGCTGT	360
GCACACCACC AG					372

- (2) INFORMATION FOR SEQ ID NO:1034:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 355 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1034:

GAATTCGGCC	AAAGAGGCCT	AAATATGTTT	TTTCCTGCTT	TTATAACTGT	AAAATGGAAT	60
GTTCTTCTTA	CCTTTAACCT	TATGATTGAG	CTGTCCATAT	CAGGTTTTTT	TTTCTACTGA	120
CTATTTATTG	GGACTAGCTC	ACTTTATTAA	TTATGCATCC	TGATATCTTA	TAGAATGGAT	180
AGTGTATTTC	AATATTATTA	ATTAAGTGGG	CCTTTGTTAG	<b>ATATAAAGCA</b>	AGATACCTCC	240
AGTAGGTCCT	GTTAGCAGTA	AGTTTTATAT	TGTGGAGGTG	AACAAGGTAT	TTTTGTGTAA	300
ATCAGTTTAC	TAAATTGTAT	TATTTTCAAG	CTAGATTGTG	ACGGTAAGGC	TCGAG	355

- (2) INFORMATION FOR SEQ ID NO:1035:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 111 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1035:

GAATTCGGCC TTCATGGCCT ACGTCTCAGC ATTATGCATT CCAGTTGGTT TTTCCCCATG 60 CTTTTCCTGA GCTGTATCCA AGTGAGTCGT ATTAATTTCA GAGGAGTATT T 111

- (2) INFORMATION FOR SEQ ID NO:1036:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 560 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1036:

GAAATTCGGC CTTCATGGC	C TANATGAACA	AAACTCCAGA	TACCATTGAT	AAGAAATTTT	60
GCATCAAGAA GGGCTTCTG	A AAAGACCCAC	GTGCTCCAGT	CCCAGCTCCA	AAAGCCACTG	120
ATGACAAGGG CCCCACTGT	GAACCTAAGT	CTGGGAGCCC	CCTGACTTCT	GGCTGGCCAG	180
AGCTGCGGTC CGTCAAGGG	C TTGCCTCGCT	TCAGAATCAG	TAACATAGAT	CTTAAGTGCA	240
ATTGATTAAT AAGCAGTGA	TTACTGTAGC	TTCCTTTAGC	TCTACCGAAC	TCTTTTTAAA	300
AACTCAAACT TGAGCAGCC	T TAGAAAAGGG	GTTGGGGGGT	GGAACCACAG	GCCATTTCTC	360
TAAGTGGGCT GCTGTGAAG	I TTTAAATGAA	AGCTCTAGCT	TTAGGAGCTT	GAGCCATTTC	420
CTGACTGCAC TGGCCTGGC	A GTCTGGCTGC	TGCAGAAGAG	TTTTTAAAGA	GGGGTCGGAG	480
CCCGCCCGTG AGAGCGGGT	C TTCTCACCAT	GTGGGGCTGT	ACTACGTGGT	GGTCTTGGTT	540
TCTCTTCACA GAAATGCTC	r				560

- (2) INFORMATION FOR SEQ ID NO:1037:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 322 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1037:

AAATTGGGCA	GTGGTAGCAC	CTGACCCAGG	GCTGCTGTGA	GGCCCCCCTG	GGCTGAAGCA	60
CATGTGGTGC	AGAGGCCAG	GTTGGGGTGT	GAGTGCCAGT	TCCCACTGGC	CTTAGGCCCC	120
ATCCACTGCT	GCTCCCAGGG	CCATGGGTGA	GCCTTTCCAC	TTCTTATAAA	GTAGAGAAAA	180
GTATTTATAG	TATCTTCTTT	GGTAATTCCT	TTTTCTTGGT	GATGTTCATC	TGCAGTTCTG	240
TACATTTTTT	CAGATCTTCT	GATGAACAAA	TTCCTTTAAT	TTGTCATGTC	AAACTTGTTA	300
ATATTTTCCT	TTGTGACTCG	AG				322

- (2) INFORMATION FOR SEQ ID NO:1038:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 517 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1038:

GAATTCGGCT	TCATGGCCTA	CACTGTAGCA	AATTGCGTTG	GAAAAGAACT	AGCTCCACAT	60
GTCAAGAAGC	ATGGAAGCAA	ATTTGTTCCA	GAATCTCTTA	AAAAAGACAA	AGATGGGAAA	120
TCTCCTCTGG	ATGGTGCTAA	TGGTTGTAGC	AGCAAGTAGT	GTTCAAGGAT	TTTCAACTGT	180
CTGGCAAGGA	TTGGAATGTG	CAGCTAAATG	CATCGTTAAC	AATGTTTCAG	CAGAAACTGT	240
ACAAACTGTC	AGATACAAAT	ACGGATATAA	TGCAGGAGAA	GCTACCCACC	ATGCGGTGGA	300
TTCTGCGGTC	AATGTTGGCG	TAACTGCCTA	CAATATTAAC	AACATTGGTA	TCAAAGCAAT	360
GGTGAAGAAA	ACTGCAACAC	AAACAGGACA	CACTCTCCTT	GAGGACTATC	AGATAGTTGA	420
TAATTCTCAG	AGGGAAAATC	AAGAAGGAGC	AGCAAATGTC	AACGTGAGAG	GGGAGAAGGA	480
	AAGGAAGTAA					517

- (2) INFORMATION FOR SEQ ID NO:1039:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 548 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1039:

GAATTCGGCC	TTCATGGCCT	ACAGAATGAA	GAAAGCAAGC	AGGAGTGTTG	GCTCAGTGCC	60
TAAAGTGTCT	GCAATAAGTA	AAACGCAAAC	AGCAGAAAAA	ATTAAACCTG	AAAACAGCTC	120
TTCAGCATCT	ACGGGAGGCA	AACTTGTGAA	ACCTGGAACA	GCAGCATCAT	TGTCAAAGAC	180
CAAGAGCAGT	GATGACCTTT	TAGCTGGAAT	GGCCGGAGGG	GTAACGGTGA	CTAATGGTGT	240
TAAAGGAAAG	AAAAGCACCT	GCCCATCTGC	AGCACCTTCA	GCATCTGCCC	CTGCCATGAC	300
CACCGTGGAG	AACAAATCCA	AGATTAGCAC	AGGCACAGCT	TCTTCAACCA	AGCGGAGCAC	360
TTCTACAGGT	AATAAAGAAT	CCAGTTCTAC	TAGAGAAAGA	TTACGTGAAC	GTACCCGATT	420
AAACCAGAGC	AAAAAACTAC	CTTCTGCAGG	TCAGGGAGCT	AATGACATGG	CATTGGCCAA	480
ACGTTCCCGC	AGTCGAACTG	CTACAGAATG	TGACGTTCGT	ATAAGCCTCC	CTATAGTGAG	540
TCGTATTA						548

- (2) INFORMATION FOR SEQ ID NO:1040:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 336 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1040:

GAGGAAATGG	CCAAACAGAA	AGCAGCTCCT	GAAGCCAAGA	AACAGAAAGT	GGAAGGCACA	60
GAACCGACTA	CGGCTTTCAA	TCTCTTTGTT	GGAAACCTAA	ACTTTAACAA	ATCTGCTCCT	120
GAATTAAAAA	CTGGTATCAG	CGATGTTTTT	GCTAAAAATG	ATCTTGCTGT	TGTGGATGTC	180
AGAATTGGTA	TGACTAGGAA	ATTTGGTTAT	GTGGATTTTG	AATCTGCTGA	AGACCTGGAG	240
AAAGCGTTGG	<b>AACTCACTGG</b>	TTTGAAAGTC	TTTGGCAATG	AAATTAAACT	AGAGAAACCA	300
AAAGGAAAAG	ACAGTAAGAA	AGAGCAAGAA	CTCGAG			116

- (2) INFORMATION FOR SEQ ID NO:1041:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 370 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: CDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1041:

GAATTCGGCC	TTCATGGCCT	AGGCTTCCCG	AGCAGTCTCC	AAACATATAT	TACATTCGAA	60
GGTCGCGCCC	GCCCCGCCCC	GCTCGCGATT	TGGCCCTTCG	GGGCCCCCGT	CCTCCACCTC	120
CTTCTCTCCC	ATGATGCATT	GTCATCTGGC	TTTTATCACC	TGTTCTGCCC	TTGAATTTGA	180
ACATGCCAAA	GATATAAGTA	TTGGATTGCA	GTCTTGCAGT	ATTATTTCCT	CACTTTTTTT	240
					TGTTTAGAGT	300
	TTTACCCTTT					360
CCATCTCGAG		1000100111	00.0	CCIAICACAI	CCCTTCCAAT	
CONTCICONO						370

- (2) INFORMATION FOR SEQ ID NO:1042:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 563 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1042:

GAATTCGGCC	TTCATGGCCT	ACGCCATCTT	CCAGTAATTC	GCCAAAATGA	CGAACACAAA	60
GGGAAAGAGG	AGAGGCACCC	GATATATGTT	CTCTAGGCCT	TTTAGAAAAC	ATGGAGTTGT	120
TCCTTTGGCC	ACATATATGC	GAATCTATAA	GAAAGGTGAT	ATTGTAGACA	TCAAGGGAAT	180
GGGTACTTTC	AAAAAGGAAT	GCCCCACAAG	TGTTACCATG	GCAAAACTGG	AAGAGTCTAC	240
AATGTTACCC	AGCATGCTGT	TGGCATTGTT	GTAAACAAAC	AAGTTAAGGG	CAAGATTCTT	300
GCCAAGAGAA	TTAATGTGCG	TATTGAGCAC	ATTAAGCACT	CTAAGAGCCG	AGATAGCTTC	360
CTGAAACGTG	TGAAGGAAAA	TGATCAGAAA	AAGAAAGAAG	CCAAAGAGAA	AGGTACCTGG	420
GTTCAACTAA	AGCGCCAGCC	TGCTCCACCC	AGAGAAGCAC	ACTTTGTGAG	AACCAATGGG	480
AAGGAGCCTG	AGCTGCTGGA	ACCTATTCCC	TATGAATTCA	TGGCATAATA	GGTGTTAAAA	540
AAAAAAATAA	AGAGACACTC	GAG				563

- (2) INFORMATION FOR SEQ ID NO:1043:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 396 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1043:

GGCTTGATTG	TTAGAGAAAT	AATGTTGGAA	GAAGAACCTT	CAATAACATC	AGGTGAAAGC	60
CAGACTACCT	ACTCTACTTT	CAGTGCTCCG	TTAAATAAAG	CAAATAGAAA	AAAGTTAATT	120
GAAAGTCTTT	CCCCAGATTT	TTGTCACCAA	AACAAAGGGC	TGTTGCTGAC	AGTTAATACC	180
AGTAGTCAGA	ATGGAAGGCC	TGGAAGAACA	CTTATTAAAG	AAATCCAGAG	TCCTCTGTCT	240
AGTATCTGTG	ATGGCTCCAT	AGCTCTAGAT	GCTGAGCCTG	TTACCCAGCC	AGCATCGCTG	300
CCCAGACACA	GCAGCACACC	AGACCACACC	AGCACACTGG	AGCCTCCTCG	TTTGCCTCAA	360
AGAAAGAACT	TACAAAGTGA	AAAGGAAACT	CTCGAG			396

- (2) INFORMATION FOR SEQ ID NO:1044:
  - (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 351 base pairs

- (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: CDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1044: GAATTCGGCC TTCATGGCCT AAACTGGAAA TCCTCTAAAT GTCTGTCAAT GAAGGAATAG 60 ATAAATTGTA ATATGTTCAT ATAAAATGCT GCATAAATAA GTGAAATTTA TAAATATACT AACGAATGAA TCTTGAAAAC AGAGTTGGGA GATAAAAGCA AGCTGTTGAA GAACATGGTC AGTATCCTCT CACTTATGTA AGTTAAAAAC TCCAAAGAAC ATTATCTATA TTGGTAATGG 240 CATAGACATG TGTGGTAAAA TATAAAAATA TTAACTAAAA GTTCTATACG CTTCAGGATA TTGTTAGTAT AATAAGGCAG GAAGTGGATA GCATTGGGAT GAGAACTCGA G 351 (2) INFORMATION FOR SEQ ID NO:1045: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 390 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1045: GATTCGGCCT TCATGGCCTA AGCAGCTCGG GGTTCGGCAG CAGCGGTCCC ATCGGCTGAA 60 GTTCGGGGGG GGTGGGGCGC CGAGCGCGCG GGGTGGGGGG GGTCCTGGTC TTTGGCTTCT 120 CGACTCGGTC CTGTTTCGAC AGCGAACATG TCGCGGCCTG TCAGAAATAG GAAGGTTGTT 180 GATTACTCAC AGTTTCAGGA ATCTGATGAT GCAGATGAAG ATTATGGAAG AGATTCGGGC 240 CCTCCCACTA AGAAAATTCG ATCATCTCCC CGAGAAGCTA AAAATAAGAG GCGATCTGGA 300 AAGAATTCAC AGGAAGATAG TGAGGACTCA GAAGACAAAG ATGTGAAGAC CAAGAAGGAT 360 GATTCTCACT CAGCAGAGGA AGCTCTCGAG 390 (2) INFORMATION FOR SEQ ID NO:1046: (A) LENGTH: 381 base pairs (B) TYPE: nucleic acid (D) TOPOLOGY: linear
  - (i) SEQUENCE CHARACTERISTICS:

    - (C) STRANDEDNESS: double
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1046:

GAATTCGGCC	TTCATGGCCT	ATGAAGCATC	TGGATGGGGA	AGAGGATGGC	AGCAGTGATC	60
AGAGTCAGGC	TTCTGGAACC	ACAGGTGGCC	GAAGGGTCTC	AAAGGCTCTA	ATGGCCTCAA	120
TGGCCCGCAG	GGCTTCAAGG	GGTCCCATAG	CCTTTTGGGC	CCGCAGGGCA	TCAAGGACTC	180
GGTTGGCTGC	TTGGGCCCGG	AGAGCCTTGC	TCTCCCTGAG	ATCACCTAAA	GCCCGTAGGG	240
GCAAGGCTCG	CCGTAGAGCT	GCCAAGCTCC	AGTCATCCCA	AGAGCCTGAA	GCACCACCAC	300
CTCGGGATGT	GGCCCTTTTG	CAAGGGAGGG	CAAATGATTT	GGTGAAGTAC	CTTTTGGCTA	360
AAGACCAGAC	GAAAACTCGA	G				381

- (2) INFORMATION FOR SEQ ID NO:1047:
  - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 318 base pairs

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(B) TYPE: nucleic acid(C) STRANDEDNESS: double
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- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1047:

GAATTCGGCC	TTCATGGCCT	AGGGGTAGCC	CTTGACCGCC	TCCTGCTGGC	ACAGGTCTTG	60
GTTCTTGTCT	TTGACGCAGT	CAACAGCGGC	ACAGGCAATC	TTTCGGTCAT	CTTTGAAGGC	120
ATCAGCAGTA	GCAGTAAAGT	GCGGAATGAC	CTTCTTACAG	TGTGGGAACC	AAGGGGCGTA	180
GAACATGACC	AAGGTGTGTT	TCTTCTTCTT	CAGGGTCTCC	CGGAAGTTGT	CCCCCACCAG	240
GTGCAACACG	CTTGTCTGCT	GCTCTTCCCA	CGTGGGCTCT	GGGGGGGGG	GGGCCTCAGG	300
GTTTTGCATC	CACTCGAG		-010000101	000000000000	GGGCCTCAGG	
						318

- (2) INFORMATION FOR SEQ ID NO:1048:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 591 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1048:

GAATTCGGCC	TTCATGGCCT	AGCAAATTAT	TCTTCAAAAT	GATTATAACC	AGTTGCACCC	60
					GAAAAAGAAT	120
					AGGGATGCTA	180
AGAAGAGCCC	ACAAATAGAG	GATTACTCTT	CCCCTGAATC	TCTAAACTCA	GAAACAATTA	240
CCAAAAAATA	CATAACTCTT	CCTTGTAGGG	CCCTTTCCTT	ATTCATTTAG	GTAGTGTGAA	300
CATTAAGTAT	AAAATAAATT	ATGTTCTTAA	TGCCTCTTAA	ACCACTTACA	TTCAAAGGGG	360
AACAGAAATC	ATTCTAAGCG	GGAAAAACTT	CCACCTTTTT	TTTTTTTCAA	GTATCTCTCT	420
AATAACTAAA	TGCCACTTAT	TTGCATTCTC	CTTGTGGATT	TTTTGTCACC	TAAGGAAATG	480
CATTTGATGA	GTGCTGGAAA	CTTCTTAAGT	GCTTTACAGT	TTGTTTTCAT	TGTTTGCAGC	540
				GGAACCTCGA		591

- (2) INFORMATION FOR SEQ ID NO:1049:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 355 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1049:

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GAATTCGGCC TTCATGGCCT AGGTTTCTTG GTGTTTTTGT TTTCTGGCAG GCAGTGAGAG 60
GAGGGGTGAA GGAGGAGTTT GGTGCCATTT CTCTTTCTGC TTTTTCCTCT TCTGATGTCA 120
AACAAATGAT GAAAATCCTG CTATGGGAG CCGGGAGCCT GGGGCCAGGC TGCTGGGGGG 180
ACGGTAGAGG GTGCTCTGCT GACTTGGGGG GTTAGGGGGG TTCTGGGGCG TTGGAGGTCCG 240
ACTGGCCTTG GGCCGAAAGA GGCTGCCCTG CTGGGTGCTG GTGCTGTTGG TGACGGTGGT 300
GTGGTCTGGC TCACCCGAGT CGCTCTCCGT GTAGCTGTAG GCCTGTGCCC TCGAG 355
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(2) INFORMATION FOR SEQ ID NO:1050:

> (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 245 base pairs

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(B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: CDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1050:
GAATTCGGCC TTCATGGCCT AATGTGTTAG AAGACTCCCT CTACCTACCT GTTAAAAAAA
                                                                       60
AAATGACTTT TTTTGCAATT TTTTGCTGTT TCCTTAAAAC TAAAGCTGTG TTCTTCTGTT
                                                                      120
TTGAAGGGTT TCCGCCCCCA ACATATGTTA TCCCCCCGCC TGTGGCATTT TCTATGGGCT
                                                                      180
CAGGTTACAC CTTCCCAGCT GGTGTTTCTG TCCCAGGAAC CTTTCTTCAG CCTACAGCTC
                                                                      240
TCGAG
                                                                      245
(2) INFORMATION FOR SEQ ID NO:1051:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 548 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1051:
AATTCGGCCT TCATGGCCTA GGGAGTTTGA GGGAGTTCTT TGGTATGCCC GCATCCCGGG
GTTGTTTGCT GGTTTATTCT GCCACATTAT CACCTTGTGA CGTTTATGGT ACCGGAGATT
                                                                      120
GTAGGTAAAG TTTGTTTATG CTTCCCACGA CCTCCCTCTG TGCGGTCCGG ATGGTTTGTA
ATTGGGGTTT GCTTTATAGC AGCGAGGCCT GATAGGTAAA GTCTGCTGGC TTCACTGTGG
                                                                      240
CGCCTAGATA AGGGCTTAGA AATGTAAAAA GGCTTGGGGC AGCATGGAGA GGAGTTGCAG
                                                                      300
AGTGGGGAGG GGCAGGCAGC ACCAAGAAGC TTCTTGAGGC AGTTTGTCCC TAACAGATTT
                                                                      360
ATTTTCGGAA AGGAATTCTG AACTCTGAGA CCAAATCAGT ATATTTGTGT ATATTTTTTC
                                                                      420
ATATACTTCC AAAGTCTTTT AATTCTTAAT TAACCTGATA TTTAAGTGAA AAGGGTTTAC
                                                                      480
TCTTTATCCT AGTTAATTAC ATATTCCATT TGTTAATGAA ACTATCCTTT GCTCACTGCA
                                                                      540
TACTCGAG
                                                                      548
(2) INFORMATION FOR SEQ ID NO:1052:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 301 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1052:
GAATTCGGCC TTCATGGCCT ACATAATACT TGCTGCTCTT GGGGTTGAAG CCGTTGTTAT
                                                                       60
TTTCTTAGGA GTTAAGTTGC TTTCCAAAAA GATTGGCGAG CGTGCTATTC TACTGGGAGG
                                                                      120
ACTCATCGTT GTATGGGTTG GCTTCTTTAT CTTGTTACCT TGGGGAAATC AATTTCCCAA
                                                                      180
AATACAGTGG GAAGATTTGC ACAATAATTC AATCCCTAAT ACCACATTTG GGGAAATTAT
                                                                      240
TATTGGTCTT TGGAAGTCTC CAATGGAAGA TGACAATGAA AGACCAACTG GTATGCTCGA
                                                                      300
G
                                                                      301
(2) INFORMATION FOR SEQ ID NO:1053:
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WO 98/45435

PCT/US98/06954 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 642 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1053: CGGAGGCCCT GAATGCCCCA TGCGCACCCC ACAGCTCGCG CTCCTGCAAG TGTTCTTTCT 60 GGTGTTCCCC GATGGCGTCC GGCCTCAGCC CTCTTCCTCC CCATCAGGGG CAGTGCCCAC 120 GTCTTTGGAG CTGCAGCGAG GGACGGATGG CGGAACCTCC AGTCCCCTTC AGAGGCGACT GCAACTCGCC CGGCCGTGCC TGGACTCCCT ACAGTGGTCC CTACTCTCGT GACTCCCTCG 240 GCCCCTGGGA ATAGGACTGT GGACCTCTTC CCAGTCTTAC CGATCTGTGT CTGTGACTTG 300 ACTCCTGGAG CCTGCGATAT AAATTGCTGC TGCGACAGGG ACTGCTATCT TCTCCATCCG 360 AGGACAGTTT TCTCCTTCTG CCTTCCAGGC AGCGTAAGGT CTTCAAGCTG GGTTTGTGTA 420 GACAACTCTG TTATCTTCAG GAGTAATTCC CCGTTTCCTT CAAGAGTTTT CATGGATTCT 480 AATGGAATCA GGCAGTTTTG TGTCCATGTG AACAACTCAA ACTTAAACTA TTTCCAGAAG 540 CTTCAAAAGG TCAANGCAAC CAACTTCCAG GCCCTGGTTG CAGAGTTTGG AGGCGAATCA 600 TTCACTTCAA CATTCCAAAC ACAATCACCA CCACTCCTCG AG 642 (2) INFORMATION FOR SEO ID NO:1054: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 496 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1054: GAATTCGGCC TTCATGGCCT ACCTGTGAGT ACCTGGATGA AGCATACCCA GGGAAGAAGC 60 TGTTGCCGGA TGACCCCTAT GAGAAAGCTT GCCAGAAGAT GATCTTAGAG TTGTTTTCTA 120 AGGTGCCATC CTTGGTAGGA AGCTTTATTA GAAGCCAAAA TAAAGAAGAC TATGCTGGCC 180 TAAAAGAAGA ATTTCGTAAA GAATTTACCA AGCTAGAGGA GGTTCTGACT AATAAGAAGA CGACCTTCTT TGGTGGCAAT TCTATCTCTA TGATTGATTA CCTCATCTGG CCCTGGTTTG 300 AACGGCTGGA AGCAATGAAG TTAAATGAGT GTGTAGACCA CACTCCAAAA CTGAAACTGT 360 GGATGGCAGC CATGAAGGAA GATCCCACAG TCTCAGCCCT GCTTACTAGT GAGAAAGACT 420 GGCAAGGTTT CCTAGAGCTC TACTTACAGA ACAGCCCTGA GGTCTGTGAC TATGGGCTCT 480 GAAGGGGACA CTCGAG 496 (2) INFORMATION FOR SEQ ID NO:1055: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 316 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1055:

120

GAATTCGGCC TTCATGGCCT AATGTGCTTA ACCCTCAAGA AATTGTCACA ACTGAAAGAC

CTTCCTTGGG GTAGGGCCGG AGAGCAATAC AAGTGGCGAT ATTCTCTGGT TGCTCAAGCC	240
ACAGCATGTG GTCAATGTTC TTCTGTTGCA GGGTCTCGGC CAGCTCCTTT AGGGTGGTCT CATCTGGGGC CTCGAG	300 316
(2) INFORMATION FOR SEQ ID NO:1056:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 369 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1056:	
CGGGTTAAGG TAGCATCAGA ACCCTGGACG CGGAGTCAGG GCTGGCAGAT AGCAAGGCAT CTCTCGGAGC GTTCTTGGGA GGCGCCATCT TGCCCGACTC CATGTTATCC AGCCACTCGT CATCCCGCGG AGACAGAGGA GAGAGGAGAG	60 120 180 240 300 360 369
(2) INFORMATION FOR SEQ ID NO:1057:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 540 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(11) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1057:	
GAATTCGGCC TTCATGGCGT ATCTCATTCT GTCTCCCAGG CTGGAGTGCA GAGAAACAAT	60
CTTGGCTCCT GCAGCCTCAA CCTCCCAGGG TCAAGTGATC TTGTTGCCTC AGCTTCCCAT	120
ACAGCTGGAA GCACAGGTGC ATGCCACCAC ACTTGGCTAA TTTTGTATTT TTTGTGGAGA	180
TAGGATCTCT CTATGTTGTC TAGGCTGGTC TTGAAACTCC CTGACCCCGT GATCCACCTG	240
CCTCGGCCTC CCGAAGTACT GGGATTATAC GCATGAGCCA CCGTGCCCAG CCGTCATTCT	300
TATATTATTA TTTCCTAGGT GTCTCTCCTG AAGACTATCT TCTGGTCTCG AAATGGACAT	360
GATGGATCCA CGGATGTACA GCAGAGAGCC TGGAGGTCCA ACCGCCGTAG ACAGGAAGGT	420
ATGGCTCTGT TGGAATCCGC ATAGTGTGGA AATGAGTTTG CCCTGGAAAG GGAAAGAACA	480
GCTTCTTGCC CTCAGGTTTC TCACCTTCTC CTCTCCTCAC TCTCACCAAG GACCCTCGAG	540

- (2) INFORMATION FOR SEQ ID NO:1058:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 430 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1058:

GAATTCGGCC TTTATGCNAN NTTCCTTTCA AAAAAAAAA AGAAAAGAAA TTGCAAAAGT

TCTTCTAAAG	TTAAATCCAA	GGTGGTTTGT	CTAGCAGAGA	GCCAGGAATT	CTTTCTAATA	120
GTGGGCAGAG	CCCAGAGACA	AGGGGAAGAA	AGATGACCTT	CTCCCCAGTC	CTTCCCAGCA	180
CCATTTTGT	TTCACACCAG	GCTTGTGGCA	TTTTGGTGCT	CACAGGGGTT	TTGCCTTCTC	240
ACCTCTCCTT	GGAGTAGGCC	ATTCTCATGC	AGGGCTCACC	CTGAGGCAGG	AGGACCAAGG	300
GCTCCCTGCG	TCCACGGACC	ACGTATGCCT	TGGTGGTCAC	TCCCATCGGG	GCTATCAGTT	360
CTGCACTGTG	CCCTGGTGCG	GATTTTAATG	CATATTTTTA	TATATAAATG	TTCCCAAAGG	420
CCGTCTCGAG						430

- (2) INFORMATION FOR SEQ ID NO:1059:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 457 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1059:

~~~~~~~						
GAATTCGGCC	TTCATGGCCT	AACATTAAGG	AAAAAGCCTT	AATGGCCATG	AATAACCTGA	60
GTGAGAATTA	TGAAAATCAG	GGCCGGCTTC	AGGTGTACAT	GAATAAAGTG	ATGGATGATA	120
TCATGGCCTC	TAACCTCAAC	TCACCACTOR	3 3 Cm3 Cmmcc	ACTAAAATTT		
						180
TGACTATTAC	TAATGACTAC	CAACACCTGC	TTGTCAATTC	CATTGCAAAC	TTTTTCCGTT	240
				GAAAATCCTT		
						300
CTGAAAATCC	AGATATGTTG	AAGAAACTTC	TCAGTACCCA	AGTGCCAGCA	TCATTTAGTT	360
				TGCCCTTACT		
				TGCCCTTACT	CTATTTGAGA	420
TTATCTATGA	CAATCTCAGA	GCAGAAGTGG	CCTCGAG			457
			CCICONO			42/

- (2) INFORMATION FOR SEQ ID NO:1060:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 474 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1060:

GAATTCGGCC TTCATGGC	CT ACAACCCCGC	GATAACCACT	GCCGAATGCC	TGAAGGCGCT	60
TGAGCACGTG TTTGGGAG	CG TTGAGAGCTC	TACGGATGCC	CCGATCAAAT	TTCTGAACAC	120
TTATCAGAAC CCGGGAGA	AA AATTGTCTGC	TTATGTCATT	CGTCTGGAGC	CTCTGCTACA	180
GAAGGTGGTA GAGAAGGG	GG CCATTGATAA	AGATAATGTG	AACCAGGCCC	GCCTAGAGCA	240
GGTCATTGCC GGGGCCAA	CC ACAGCGGGGC	CATCCGAAGG	CAGCTGTGGC	TTACCGGGGC	300
TGGGGAAGGG CCAGCCCC	AA ACCTCTTTCA	GTTGCTGGTG	CAGATCCGTG	AGGAGGAACC	360
CAAGGAGGAG GAGGAGGA	GG CTGAGCCCAC	CCTTCTGCAG	TTCGGCCTGG	AAGGGCACTT	420
CTGAGTGCCA GGAAAGGC	AG CTTTAGTGCA	GACCTAGATC	ACAGCTACCT	CGAG	474

- (2) INFORMATION FOR SEQ ID NO:1061:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 365 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1061:

ATGAAATATC AATATACTGT AGGCAAACTA	AGATGGAGCT AGTAACTGTC ATTTTGAGAA CTAACATGCA	TAATGGAGAA TTGGACAGTG ATGGCACAAA TTGTGAGAAT	ATTGCAACTT CTGAAATCAG AACAGGCAGT GCCGTGTATA	TCATTAAAA GTGGTTAAAC CATCTTTAAT CCTCACGTAC	GAAACTCACT ACAAATTCAG GGGTAAACAA GGCTATGCCT TGTGTACTTT	60 120 180 240 300
GTACATATAT TCGAG	TTTACCTTTT	ATACCTATGT	GCCGTGTATA TCGATTTTGT	CCTCACGTAC	TGTGTACTTT CCTGGCGTCC	300 360 365

## (2) INFORMATION FOR SEQ ID NO:1062:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 434 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1062:

60 20 80
40
00
50
20
34

## (2) INFORMATION FOR SEQ ID NO:1063:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 429 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1063:

GAATTCGGCC	TTCATGGCCT	ACTTAATTTC	AGAGCCGGGT	TCGCCGTCGG	ATCAACCTCC	60
AGGAGCTAGC .	AGCGGGCGCG	GACCGGGCAG	TTTCCGCGCT	CAGCACAGGC	AGCTCGCGGT	120
CATGGGCGGC						180
AACTGAGGCT	GCCATCAAAA	ACTTCAGTCC	CTACTACAGT	CGTCAGTACT	CTGTGGCTTT	240
CTGCAATCAC						300
GACCAAGCCA	CCATTGGCGC	CTGGAACTAT	TTTGTATGAA	GCAGAGCTAT	CACAATTTTC	360
TGAAGACATA	AAGAAGTGGA	AGGAGAGATA	CGTTGTAGTT	AAAAATGATT	ATGCTGGGGA	420
GAGCTCGAG						429

## (2) INFORMATION FOR SEQ ID NO:1064:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 368 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1064:	
GAATTCGGCC TTCATGGCTT AGTCTTGGTC ATGCCTGGGG AGCTCAGAAC GCCCCGGCTT	
GGGCCCCAGG CCCATGGACT CCCTTCCCCA TTCTGCCCTC CCATATTCCC CTTTTTTGGT	60
CCCAGACAC AGCACAAAGA AAGGAGGGTT CACAGAGGAA GGCCAGGGCA GAGCCTGGCC	120
CCAGGGAGGG GATGAGGACA TTTCCGGTCC AGGTAGCTGC CGGCTGCTCT GGGAGGAAGA	180 240
GCCATGCGTC TGTAAACTGC TGGGGCTGGC GGCCCGCCCC ACTGCAGGGC CCAGCCTTGA	300
CCCCTGCACG TGGCCATCCA GCTGCCCTCT GGCTGCCCCT GGCCTTGGCA CAGGCATCGA	360
GCCTCGAG	368
(2) INFORMATION FOR SEQ ID NO:1065:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 104 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1065:	
GAATTCGGCC TTCATGGCCT AAGATGGTTG CCAAGCAAGG AAAACTTATT TTATATTTTT ATACTGTATC CAGGCTATGC CTGGGTGTGG AGGGCTTACT CGAG	60 104
(2) INFORMATION FOR SEQ ID NO:1066:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 0 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1066:	
(2) INFORMATION FOR SEQ ID NO:1067:	
(2) INFORMATION FOR SEQ ID NO:1007:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 125 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1067:	
GAATTCCTGG CCTTTGGGAA CTCATATCCT GACCTCAGAT TGAGAAGACC ATCTGTCAAG	60

TCGAG

GCATATTAGT AATCACCTCC GGTAGAAAAG ATTTCACGGG TAACAAGTAG GCCATGAAGG

120

(i) SEQUENCE CHARACTERISTICS:

```
(A) LENGTH: 340 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1068:
GAATTCGGCC AAAGAGGCCT AAGTTCAAAT AATTTCAGAA TGGTGTCTGT TAGGAATGGT
CCAGAGGTTG GTTGGGGGAT GAAAGGAGGA CAGGGACTAC AAGGGATATT GCAAATGACT
                                                                      120
GCCTTAAAAT ACCAACATAA AGCAGTGGAT TCCCAGAGTC CTCCAATCTG TTATCAGACA
                                                                      180
CAAAGATTTG AACAAAAATA AATGAAAGAT AGAAATCAAA AGGTTTTCTT TGAAGTCTCA
                                                                      240
GGGTTATTTG CTTCTGAAAG CAAATGTGTT GTTCTTGCCT CATAGCAAAG TACTTTTCCT
                                                                      300
ATTGATGCAT CACTTTATTG CTTTTCTGTC TTCTCTCGAG
(2) INFORMATION FOR SEQ ID NO:1069:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 432 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1069:
GAATTCGGCC AAAGAGGCCT AGACGGGACC TGTTTGCAGA CAAGATGCAA GGAACACAGC
                                                                       60
CTGCAGTGAT TCACAGCTTT GTTTCAACCC ACAAACCAGA AAATTAGCTC TTGGGTCTGT
                                                                      120
GGGCCCAAAG TGAACTTTAA AGCAATAAAG ACTGGAAGCA GGTCTGGGAA GGCAATACAA
                                                                      180
AATGTGGAGA GTTGAAAAGG AGGCAGAGCT GGCAGGAATG GGTAGGGAGA GTGTTTGGTA
                                                                      240
AATAGCACCT TTGAGTCAAA ATTGAGCAGT TTAGAAATCC AGGAAAGGGG ACTGGCTGTG
                                                                      300
GGGAGGAGAA CCTGGGGGTA GAGGAAGTGG GGTGAAGATT CCTCACTAAG GGGCAACAGC
                                                                      360
AGGAGGGTGG CCATCCTGGC CAAATGCCCT AGCCCTGTCC TTCTTAAGGT GATTCGGTTT
                                                                      420
GGGAAACTCG AG
                                                                      432
(2) INFORMATION FOR SEQ ID NO:1070:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 354 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1070:
GAATTCGGCC AAAGAGGCCT ATTCTAGACC TGCGCAAGCA CGCTGAGGAG AAATTCATTG
                                                                       60
AATTTGAAGA CTCTCAAGAA CAGGAAAAAA AGGACTTACA GACCCGAGTG GAATCTTTAG
                                                                       120
AATCTCAAAC AAGACAACTT GAGCTGAAAG CGAAAAACTA TGCTGACCAG ATTAGCAGAC
                                                                       180
TTGAAGAAAG AGAAGCAGAA CTGAAGAAGG AATATAATGC ATTACATCAA AGACACACTG
AGATGATCCA TAATTATATG GAACATTTAG AAAGAACAAA ACTTCATCAG CTCTCAGGGA
                                                                       300
GTGATCAACT AGAATCCACA GCTCATAGTA GAATTAGAAA AGAACGCCCT CGAG
(2) INFORMATION FOR SEQ ID NO:1071:
```

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 387 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1071:	
GAATTCGGCC AAAGAGGCCT ATTCTGTCTT ATCAAAGGAA GTAAAGAAGT AAAAACAAAA AATGAACGTA TACAAGCACA GATTTTTGAG CTTCGATTGT AGAGAAATGG TAGTTATGTG GCTTGCCAAG AAAGTGCATC ACCTACTTCT GCTTCTGGGG ACAGAGGTGA AGGGGTCTGT TCTGGAAACT TCTAAGGAGG CCATCTTCGT TATTACATCA GGGAAGTTTC TAGTCAAAAT GTTATTCCTG TCTACAGGGA AAAACAAAAG CAAAACACAA AAGAACACTG CTTCTAATGG CATCATAGCA AGGAGTTTAT CTAGAAAGAT GATGCCAGCA GTCACCTCTT TTCCAGGAAG ACAGAAACAA AAACCGTTCT CCTCGAG	60 120 180 240 300 360 387
(2) INFORMATION FOR SEQ ID NO:1072:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 311 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1072:	
GAATTCGGCC AAAGAGGCCT AGAAAGTGCC AAGAGGGAAA AAAGGCACTC TGAGAAGTTA CGGCAAAGAA TTGGGAAAGT TGTCAAAACA AACAACAAA AAATAATAGA TTTGTTTTAG CAAACGACTT GGCTAAAAGT TACAAACCTA ATATATGTAA TACACAAGAC TACTTCATCA TCTTTCTTTC TGACAGTCTC ATGTTCTTTT TCAAGCCAAA AAGGGACATA TTCTTATAGC TGGAAGTTTA AGGGAAAGAC TTCCAACTTA ACTCTGTGTT GAGGGTGCAA ATCATGTGAT GAAGGCTCGA G	60 120 180 240 300 311
(2) INFORMATION FOR SEQ ID NO:1073:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 367 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1073:	
GAATTCGGCC AAAGAGGCCT ACGAAGAAAA AATATTTTTG AGAGAATTTC CCAGATTGAA AGAAGATCTG AAAGGGAACA TTGACAAGCT CCGTGCCCTC GCAGACGATA TTGACAAAAC CCACAAGAAA TTCACCAAGG CTAACATGGT GGCCACCTCT ACTGCTGTCA TCTCTGGAGT GATGAGCCTC CTGGGTTTAG CCCTTGCCCC AGCAACAGGA GGAGGAAGCC TGCTGCTCTC CACCGCTGGT CAAGGTTTGG CAACAGCAGC TGGGGTCACC AGCATCGTGA GTGGTACGTT GGAACGCTCC AAAAATAAAG AAGCCCAAGC ACGGGCGGAA GACATACTGC CCCCCATGAC CCTCGAG  (2) INFORMATION FOR SEQ ID NO:1074:	60 120 180 240 300 360 367

(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 316 base pairs(B) TYPE: nucleic acid

```
(C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1074:
GCTTTATCTA TTTCATTTAA TCTAAATGTT TTCTGCAATT GTTTTTCCTT TAAACTTTGC
                                                                      60
TTCAAAAACT CTTCATCTAC TTGAGATCTG GGCATTGTGG TTTTTGGTCT CGCATTTTCC
                                                                      120
CTGCCTTCTG ATGGCTTAGC AGGGGACCCT TTCTTCTTTG GCTGGTGGGG CTTCTCTGGA
                                                                      180
TCAGTAATGT CCACATGCGG CTTCTGCAGC AAGGTTTTCT CTTTTGCTGA TACTGTAACT
                                                                      240
CGGGGGGCTC TGTTTTCAAA GGAATGAGAG GCCTCTGGTT TTCGAAGCCC CCCTCTGCCT
                                                                      300
TTGCTCACCA CTCGAG
                                                                      316
(2) INFORMATION FOR SEQ ID NO:1075:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 435 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1075:
GAATTCGGCC AAAGAGGCNT AGAACTCGGA GACCAGAAAG TGAACTTCTG GGCAGAGATG
                                                                       60
GNCCTGCAGA GCCAGGTGTG GTCTCTGGCC ACACCCATGC CCATGGCGGA GAGCTCCNTC
TACCGGCAGC GGCTAGAAGT CATCGCTGTA AGTGACGCCC TCCCCGCGCC CTGGGCACCC
                                                                      180
CCAAACTTTC CACCATGCTC CCTTCTCGTC TCTCCGTCAT CTCTGCGGAG AGCGCCCTCA
                                                                      240
GCTCCAGCCC CGCCCAGGGC TCCCCACACC AATTCTCCAG CCCCCTCTGC CCCCCAGTTC
                                                                      300
CTGTCTGGTC ACTACCACCC TCAGAATGGG GAGCTGTGGC CCCCACACTT CCAGAGCCTG
                                                                      360
CATCGGCTAT GCCTCATTCC TGAACCCCAG CCTCCCAAAA ACCCCATGCC TGAGCCGCAT
                                                                      420
                                                                      435
CTCCCGGACC TCGAG
(2) INFORMATION FOR SEQ ID NO:1076:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 310 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1076:
GGAATTCGGC CAAAGAGGCC TAGTGGGAAA AGCTTGGATT ATCAAAACAC ACAACAAATG
                                                                       60
ATAGAACCAA ATATATAGAT GATACAGTGA AGCACAAGGT CAAAATTTTA AAACGGGTGA
                                                                      120
GCTCTTCATT AATGCATTAT TTTGTTTATT TAAGAGCTTT TTGTATGGAC TGACTGCAAT
                                                                      180
AATTTTGAAA TTTCTCTTTA GAAGTTTTAA TGTTCTTTTA CATTTTCAAA TTTAGTTTTC
                                                                      240
CATGAAAGTG AATAGGTTTT TATTTAAAAT TTTTTGTCAG TCTTGGTGAA ATCAGATGGT
                                                                      300
                                                                      310
GACTCTCGAG
(2) INFORMATION FOR SEQ ID NO:1077:
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WO 98/45435

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PCT/US98/06954
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 396 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: double
           (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: CDNA
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1077:
GAATTCGGCC AAAGAGGCCT AGGAAAACAA ATGGCTTCTT CAAGTCCTTG ATTTTTGGAT
                                                                      60
ACACAGGATG CAGGGCTGTG TGTAAGGAAA GGCAGCGTTT TCCTCTCTTA GAGCCTCTGA
                                                                      120
CTGACCTGAG GCGCAGGTGT TCCTGGGAGA CTGGAGGGTG GGCTCCATGG GGGTGTCTGG
                                                                      180
GCCCCACCTG GCAGGGCTCT TGGCAGTGAG CCAGTGGAGG TTGCCTCCCA CGTGTGGCTG
                                                                      240
GCCCTGTAGC CTGGCTCTGG AGAACCTGCA ATTCAGGCTG GAAGAGACTT TGGAGCAGCT
GGAGTGTGAG GTCTGCCTGG GTCTGGTGGG GAGTGTTTTT ACTTTGCCAG TGATAGACTG
                                                                      360
AAATGCCCTC TTTGAGGACA AGGTGGCTAT CTCGAG
(2) INFORMATION FOR SEQ ID NO:1078:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 313 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1078:
AGTGTTTTCC TGTATTTCAG CATATTCTTT GAAACTCTGC TGAAAGGAGG CTGTCAGTCA
GGGTTGTATA AATAGAGTCC TGGGTAAATC CTTGAAGCTT GTCATTCCAC AGCAAATCCA
                                                                      120
CATGTTTCTT CAATGGCTGT TAGCAGCTTT TCATATAGCT TTTCATAGCT TTCATAGGGT
                                                                      180
GGAATGTCTA TTCGATTGAA GCAAGTGTGG GCTTTCGGCA GGTTGTTAGT GCAGGCATCA
                                                                      240
ATCTGGTGTA TGGTAAAGAG TCTCGGGCCT GCAGCACCTT GCAATGCTTT GAAGCCCTGC
                                                                      300
AGAGGCACTC GAG
(2) INFORMATION FOR SEQ ID NO:1079:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 354 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1079:
GAATTCGGCC TTCATGGCCT AAAAATGAAC TATAATAGTT CTAATTTACC TCAAGTTTTT
                                                                       60
CTAAGATAGC AAATAAATTG TAGTGTCACA TTAGCTTCCT AAGTAAGGCA AATTGACCTG
CAATAAAAGG TTCTAGTGTG AGACAAATTA AACCTTCAAC TTCCAACTTC GATTTCTAAT
                                                                      180
ATAATTCAAA TIGTCACTGA AGCTTTTATT AAGAATAAAA ATATATTTAG TCTTTATTAT
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- (2) INFORMATION FOR SEQ ID NO:1080:
  - (i) SEQUENCE CHARACTERISTICS:

300

TTTCTGTAAA TGACTTATTT TCAGATGCAC AATCGTGAAA TAATGAAGAT TTTGATCAGT

TGTTTTTGTC TTTTTCCTTT GAAAGGTATT TTCGCAAGAC CATTAAAACT CGAG

- (A) LENGTH: 641 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1080:

GAATTCGGCC	TTCATGGCCT	ACTCCGGTGG	CTCCCCCATC	TCTCAGGCGC	GATGGCTACG	60
GGCGCGGATG	TACGGGACAT	TCTAGAACTC	GGGGGTCCAG	AAGGGGATGC	AGCCTCTGGG	120
ACCATCAGCA						180
ACACTGACTT						240
GACAAGAAGG						300
AAGGCCAAGT	TGGGCTCCAA	GAAGGTGCGG	CCTTGGAAGT	GGATGCCATT	CACCAACCCC	360
GCCCGCAAGG	ACGGAGCAAT	GTTCTTCCAC	TOCCOACCTC	CACCCACCA	CCCCAACCCG	420
TACCCCTTTG						480
CAGCTTTATC	TCCACGATGA	TGCTTGGACT	AAGGCAGAAA	CTGACCACCT	CTTTGACCTC	540
AGCCGCCGCT	TTGACCTGCG	TTTTGTTGTT	ATCCATGACC	GGTATGACCA	CCAGCAGTTC	600
AAGAAGCGTT						641

- (2) INFORMATION FOR SEQ ID NO:1081:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 415 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1081:

GAATTCGGCC TTCATGGCCT	AGCCCTTTTT	GGTTTTCTAA	TTAGGAATAT	AGCATCTGCA	60
AATAATGACA GATTGTTTCT	TCTTTTCTAA	TTCTTACAAC	TTTTGTTACT	TTTTCTTGTC	120
TAATATGCTG CCTAGAACTG	TAGAGCTTCC	TGCTCTTGTT	CCTCCCTTTT	TTTTATTCTT	180
ATTTTTAGGA GCAACCCTAT	TAACTAAGCC	TCACTCTTAA	AGGGGAAGTT	TTCACCACTA	240
AGTACCTTTC TAATCTAGGT	TTTTTGTGGA	TACCTTTTAT	CAGACTAATG	AAGTTTAATA	300
TTGTTAAATA CTTTGAATTG	TCTATATTAT	GATGATAGTA	TGCTTTTTTC	TTTTATTTAT	360
TAAAATGGTC CCAGGAATTT	GTGAACAGCT	TGGGCAATAC	AGTGTGACGC	TCGAG	415

- (2) INFORMATION FOR SEQ ID NO:1082:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 496 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (x1) SEQUENCE DESCRIPTION: SEQ ID NO:1082:

GAATTCGGCC	TTCATGGATC	CTGATACCAA	ACTCATCGGA	AACATGGCAC	TGTTGCCTAT	60
CAGAAGTCAA	TTCAAAGGAC	CTGCCCCCAG	AGAGACAAAA	GATACAGATA	TTGTGGATGA	120
AGCCATCTAT	TACTTCAAGG	CCAATGTCTT	CTTCAAAAAC	TATGAAATTA	AGAATGAAGC	180
TGATAGGACC	TTGATATATA	TAACTCTCTA	CATTTCTGAA	TGTCTGAAGA	AACTGCAAAA	240
GTGCAATTCC	AAAAGCCAAG	GTGAGAAAGA	AATGTATACG	CTGGGAATCA	CTAATTTTCC	300
CATTCCTGGA	GAGCCTGGTT	TTCCACTTAA	CGCAATTTAT	GCCAAACCTG	CAAACAAACA	360

GGAAGATGAA GTGATGAGAG CCTATTTACA ACAGCTAAGG CAAGAGACTG GACTGAGACT

GAAGAGACTA CTCGAG	480 496
(2) INFORMATION FOR SEQ ID NO:1083:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 342 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1083:	
GAATTCGGCC TTCATGGCCT ATTCACAGGT TTATTGGCTT CTTCTTGAAA TGCCTGTTCA TGTCTTTTGG CCACTTTTA TATGGGTCAT TTGTCCCTTA TTGATTTATA AGGGTTCTTT ATTTTTTCC TAGATATTAA TAGTTTTGGC CAGATGTTT CAGATGTCT TTCCAATAT GGCTTGTCTT TTCAGTTTTG GTGTCTTGAT GATCAGAAGA AGTTCTTCAT GTAGTTGATT TATTGACCTT TTCCATTATG GTTTTCACTC TTTGACTCTA GGAGCTTAAT AAAAGCATGA AATATTTATT GATTGTCCAT TGCTAATCCG AAAACCCTCG AG  (2) INFORMATION FOR SEQ ID NO:1084:	60 120 180 240 300 342
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 374 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1084:	
GAATTCGGCC TTCATGGCCT AACTTACTGA ATGATAAAAC TTGCAGCTAA ATTTGTCTTC AACACACCTT TCTCAGAGCA TCAATTACAT TATTCATTAA GGAATAAATA GCATCCTAA AGCATGTATC AACATCAGAA CTAAGCTTTA TGAATTATAC AGTGCATCTA GTGATTCCTT ATTCTAAAAG ATCTCTGGTG CCATCTACTG AATGCTTTTT AAAGGAAAAA ACATGAAATC AAATAATAGA TTTTCACTTA ATTCAATTTT TTGTTTTGTT	60 120 180 240 300 360 374
(2) INFORMATION FOR SEQ ID NO:1085:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 343 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1085:	
GAATTCGGCC TTCATGGCCT ACTGGAACAC CTTCTCGCTG CCGCCATACC CTGCCTTCTC CAGCGACAGC CGCCCGTTCA TGAGCTCCGC CTCCTTCCTC GGCAGCCAGC CCTGCCCAGA CACCAGCTAT GCCCCCGTGG CCACCGCCTC CAGCTTGCCA CCAAAGACCT GCGACTTTGC TCAGGACTCC TCCTATTTTG AGGACTTCTC CAACATCTCC ATCTTCTCCT CGTCCGTGGA	60 120 180 240

CTCCCTGTCG GACATCGTGG ACACGCCCGA CTTCCTGCCG GCTGACAGCC TCAACCAGGT GTCCACCATC TGGGACGATA ACCCTGCCCC CTCCAACCTC GAG	3 0 C 3 4 3
(2) INFORMATION FOR SEQ ID NO:1086:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 531 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1086:	
GAATTCGGCC TTCATGGCCT AGGGCTGACG CGCCACTATG TAGCGGGTTT CGGGCGGGCC	60
ACGCGTGCGG GACAGGAACC CAACCCCAGC CGACCTTGAG CTCCAGGAGT TCGTCTCTTA	120
CGTCTGCGGA AGTGCAGCTG CCTCAGTTCT TAGCGCAGGT TGACAACTAC AGGCACAAGC	180
CATTGAAGCT GGAATGTCCT GTTGCTGGTA TTTCAATTGA CTTAAGCCAA CTATCCCTTC	240
AGTTACAATA GGAAAGTGCC TCTAATAAGG CCAAATATGC GTACTAACTT GTAGCAACCA	300
CGTGTCCGTG CAGTGCCACA GGAGCTAGAG CAGTGACAAT GCTGGTGGCA ACAGGGCAGT	360
GTAGCAGGTG CTTCATGTTC ACCTTTTCAA CCTTTTCATT TAATTGTCAC AACTCGGAGG	420
TGGATTCTGT TAGGGACAGG CTGCCCCAGG ACCACTCCGC CCCCGCTAAC TCAATGCAGC	480
TGACCCTTAC CCTGAATACT CTGCAGCTGC ATTCCTGAAC CATATCTCGA G	531
(2) INFORMATION FOR SEQ ID NO:1087:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 374 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1087:	
GAATTCGGCC TTCATGGCCT ATGACTAGCC ACCAGGAAGG ACATTCCCTG CTCAGCTGTC	60
CCATTAACGT CACCTGCTCC TCTCCTCCAC GTTAGTTTTT TTCTAGCCTG TTTATTCCTC	120
CCTGTAAGAG AAAAAGAGAA AAGCCTATTT CTATCTGATC TTTGAGATGC TTGCAGATCT	180
TACCTTTGAA GCATTCTCCT TATTGCAATA GTCTCCCTGA CCCTATTGCA ATAGTTCCTC	240
TCTCCCTGTT TGTATTCACC CATTCAGGCT GCTATATATA GCAAAATACC ATAAGCTGAT	300
AGCTTATAGA CAATATAAAT TTACTTCCCA CAGTTCTGAA GCCCGGGAAG TCAAAGATCA	360
AAGTAGGCCA TGAA	374
(2) INFORMATION FOR SEQ ID NO:1088:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 288 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1088:	
	_
GAATTCGGCC TTCATGGCCT AGGAATGTTC CCTTTTGGTT CATTGTAGGC ACATCTGAAA AAGAAGTTAT GAGTCACTCG TAGTGAGGTT TTACTTGACC TGTGACTTGG GATCTCTGGG	120

GATCATTGGC AGTCTGTCTT ACACTGTTAT TTATAATTCA TGTCTGATCA TCTTCTTAAG GAAGTCTGCA TCGTTTGCCT TATGTAGAGC ATTAAACACA AGGATCTGNC ACATTACTTC TGTTGCCATT TTTGCTTCTC ATATCCCTGA CCACCCACCA CACTCGAG	180 240 288
(2) INFORMATION FOR SEQ ID NO:1089:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 336 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1089:	
GAATTCGGCC TTCATGGCCT AAGTAGTTAA ACTCATAGAG TTGCAAACTA GAAAGGTGGC CCCCAGGGGT GGGCAAGAGA GAGAGTGGA CAGCTTGGTG AATGGGTGC ATTTCCATTT TGAAAGATAA AACTGTTCCG GAGACGATGA CAGTGGAAAT TGTAAACAA TGTGAACGTA CTTAATGTCA TGAAACTGTA AACTGAAAAA CAGTGGAAAT TGTAAATGTT TATACTGGCC ATTCTATATG AACTAATATA TATTTATAAT TTTTAATATT TATACATGGT ATATTTCCC ACAATAAAGA TGAAAATTAA AGCAGTTGGT CTCGAG	60 120 180 240 300 336
(2) INFORMATION FOR SEQ ID NO:1090:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 559 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1090:	
GAATTCGGCC TTCATGCCTA CAGAGGCGAA AGGAGAGTCC AGTGAGAAAC CAGCCATTGT CTTCATGTAC AGGTGCGACC CTGCTCAAGG CCAGCTCAGT GTGGATCAGA GACAGACCAG GCAGCAGTCA TGGAGAAGGG TAGAGCAGAG AATGCATTAC TACAGGACTC AGAGAAGAAG AGGAGTCATT CTTCTCCATC ACAGATTCCT AAAAAGATTC TCAGTCACAT GACCCATGAA GTAACAGAGG ATTTTCTCC TCGGGATCCA AGAACTGTTG TTGGGAAGGA AGATGGCAAG GGCTGCACTT CAGTCACAAC AGCATTGTCC CTACCTGAAC TGGAAAGGGA AGATGGAAAA GAAGACATTT CAGATCCTAT GGACCCGAAC CCTTGTAGTG CAACATACAG CAACTTAGGG CAATCTAGAG CAGCCATGAT ACCTCCCAAG CAGCCACGAC AGCCCAAGGG AGCTGTGGAC CCATTGGAGG GAAAACAGAC CAAGAAGCAC CCAATGCTTC CCCAACCTACA CCACTCGAG	60 120 180 240 300 360 420 480 540
(2) INFORMATION FOR SEQ ID NO:1091:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 398 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1091:	

GAATTCGGCC TTCATGGCCT ATTCTTATGT GTGTTTCAGG ACGACTGGGT TTGGATTCAG

AAGAGGATTA	TTATACACCA	CAAAAGGTAA	AATCAGAAGC	AACTTATTTC	TAAAACCTAT	120
CTTAAGTCGC	ACAGACTCCA	TAATATCTCC	TOTATOTATO	CCTCTCTTCT	ATCAAGGTGT	
TTATTTCCGA	AGTGTTTCCT	GTTTGCCACA	CTCACAATTT	ACCAMMOCMO	ATTTAGCACC	180
CTGTGGTCTT	GTCATCTCAC	CARAGOGAGA	CIGACAAIII	AGGATICCIG	AGCGACTGTG	240
GACATTGTGA	ACTCACATOR	CAAATCACAG	AAAATTGAGA	AAGTGGATAC	AGCGACTGTG	300
ANCTOR CAMP	MOTCACATCE	TACTCAGGGA	TGACAGCTAA	AATCAGCGTG	TACAGCAGAA	360
MAGICACATA	TAGCTACAAA	TACCCTGGAA	AACTCGAG			398

- (2) INFORMATION FOR SEQ ID NO:1092:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 436 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1092:

GAATTCGGCC	TTCATGGCCT	ACGAGTTTTC	TGCAAGTCAG	CCATGAAGTC	TATGCTCTGC	60
TTCAGGCTCT	GAATTCTTTC	CTGGCTAAGA	ATTTTCATTC	CTGAGTGCAA	CAGCTTCTTT	120
GCAGCTTTAT						180
TTGAAGTTAT	CCTTTAGTTC	TTCTATGGAC	TGATAGTCAT	TGTTCTTGAT	CTTTTCTTTC	240
ATGGTACTAA	AATCCATTGG	GTGTTTAATG	ATCATGGAGT	AGCCAGGAGC	AATAAAATCA	300
GTCACAGGAA	ATGAAAAGAA	AGCACTTGGA	TCTTTTCTCT	GCAATTGTCT	CATCAGTTGA	360
TTCAAAGCTT	CTTGAAGGGG	TGTCTGTTCT	ACTTCTTCTT	GTTTGGCTAA	AGAGCTTGTG	420
AGAGGCTTCG	CTCGAG					436

- (2) INFORMATION FOR SEQ ID NO:1093:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 390 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: CDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1093:

GGGGCAGGGA	GCCTGGCCAG	GCCTGAGACA	CAGAGGCCCA	CTGCGAGGGG	GACAGTGGCG	60
GTGGGACTGA	CCTGCTGACA	GTCACCCTCC	TTCTGCTGGG	ATGAGGTCCA	GGAGCCAACT	120
AAAACAATGG	CAGAGGAGAC	ATCTCTGGTG	TTCCCACCAC	CCTAGATGAA	AATCCACAGC	180
ACAGACCTCT	ACCGTGTTTC	TCTTCCATCC	CTAAACCACT	TCCTTAAAAT	GTTTGGATTT	240
GCAAGCCAAT	TTGGGGCCTG	TGGAGCCTGG	GGTTGGATAG	GGCCATGGCT	GGTCCCCCAC	300
CATACCTCCC	CTCCACATCA	CTGACACAGC	TGAGCTTGTT	ATCCATCTCC	CCAAACTTTC	360
TCTTTCTTTG	TACTTCTTGT	CATCCTCGAG				390

- (2) INFORMATION FOR SEQ ID NO:1094:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 559 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1094:

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AATTCGGCCT TCATGGCCTA GAGGGATTTG TTAACCAGTG CCACCATGTA GTTCTGGAAA
                                                                       60
CGGAGGATGC GGTGGTAGAT GTCCAGTTCT GTCAGCTCAC GTTTGTGGAT GCAGATCTGG
                                                                      120
TGCTCCTTCT GCGTCTGCAC GATCCGGGCC TGCACTTCTT GCCACGTGCA ATACGGAAGG
                                                                      180
GCAGACATAG GGATGCGCAG AGCGTGCAGG TAGAAGGAGT GGATCTCCCA GTAGCAGCAA
                                                                      240
ATGTTATAGA TGAACTTGAT AAGCCGGTGG ATCCAGAAGA CACCAGCAAT GACCAGGATG
                                                                      300
GTGATAAGGG AGCCATTTTC CTGAATCCTG GCACTACAGA CTTGAGCAGG CAAAAAGGCG
                                                                      360
TCTGGCAGAG TGACCTTGAC GGGTTCAGTA GGGTGAAGAC TGTGGTTCAC CATCTTGTTG
                                                                      420
GCAAATAGGA TGTCATAGTC CACGCAGCTG ACCAGGAAGG TAGTGAAGGC AACCACAAAG
AGGAACTGCA TGAGCTCAAA GATCTCCCCG ATGAGCATAC ATGTGAAGCC ATTCTTCTGG
                                                                      540
TGCAGATTAT AAACTCGAG
                                                                      559
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- (2) INFORMATION FOR SEQ ID NO:1095:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 224 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1095:

GAATTCGGCC	TTCATGGCCT	AGGTTTGGAA	AGTAAGACAT	ACTGGCTTCC	TTTATTCACA	60
TTAGCATTTT	CCTATTATTT	TGGAACCAAC	AATTCCATGT	TCATTGAATT	TCCTTTTTTT	120
${\tt TTTTTTTTT}$	AAAGACTGCA	AATTTTGGCT	GGGCACAGTG	GCTTGACTCT	GTAATCCTAG	180
GTACTTAAGA	GGCTAAAGCA	TGAGGATCAC	TTGAGGGACT	CGAG		224

- (2) INFORMATION FOR SEQ ID NO:1096:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 534 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1096:

GAATTCGGCC	TTCATGGCCT	AGTTCTCTCT	GATTTGGTTT	GTTCTGTCTC	AGGCTTCTGT	60
GGCAGGACTG	GCCCAGGGAG	GAGGAAGCCA	GCAGCACACC	TGGGGAATGG	GGTCCCGGCC	120
GGGAGGCTTG	GCCTCTGGGC	GACCTCGTCC	TGTTTTGTTT	GTTTGTTTGT	TTGTTTTTT	180
AAAGGTAAAC	CTCCTGGGCC	GCAGATGGCA	AAGGGAGTGC	CTGGGCCTGG	TGACCCAGGG	240
CTGGATCCAC	CCCTGCGGAG	CCCTGGGCCA	GGCAGGTGTC	TGCTGCTCAC	CTGGCTCTGG	300
AGGGCTGCCC	TGCAGCTGGG	CCTGGGGACA	GGTCGGCTGT	GGGGCAGCTC	AGTACCCTCC	360
CTGAGGCTCA	CGGTGGCTCC	GAGCATGAGC	TCTGCCTCCT	GGGCGAGACC	CAGCAGTGGA	420
CAGCACGGTC	CTCACACCCA	GCTCCCTGCA	CACCCAGGCC	AGCCACCCCT	CCCGCTCGTG	480
CACAGGCACG	CAGATGCGCT	CACACGTACA	CACACACAAA	TGCAACGCCT	CGAG .	534

- (2) INFORMATION FOR SEQ ID NO:1097:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 606 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1097:

GAATTCGGCC	TTCATGGCCT	ACTTTATTGG	TGGACATTAA	GAATGGAGGA	ATGTTTCAAC	60
AAAGGAACAA	TCAACAGTAT	CAAAATACTG	CAGAGGGGTC	AATTTGGGGA	CTAAGAGGGG	120
			TTTTAGTGCA			180
			NACATGTAGC			240
GCTATGATAA	ACTGGCAGAG	GCTCTAAGAG	TGGGAGGTGA	GTTGTTTTCT	CCTTCATGTA	300
AATATATTTA	CCTTTTAAAC	ACTAGGCCCA	ATTTTATATC	CTATTTCATT	TAACTTTATG	360
AACATATTTA	TGTATGTATG	CATGTATGTA	TGTATCTCAT	GTGATGTTTT	AGACACTGAA	420
AAATAACTCA						480
AAGGAGGTAG						540
GATGTAAACA	TGTGTCCATC	AAGCCTTTAA	TTTTTACNTC	TTATCTTCAG	GGCTCTGCCG	600
CTCGAG						606

- (2) INFORMATION FOR SEQ ID NO:1098:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 308 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1098:

GAATTCGGCC	TTCATGGCCT	AGCAGAACAT	GGATATTTTT	CCTTTAATAT	TTAGTACTTG	60
GGCTATCATG	AAACAAGGTT	AGCATAACCA	TCCAAAACCC	CAAGTGCTCC	AAAATCCAAA	120
ACTTTTTAAA	CACCAACACG	ATGCCCAAAG	TGGAAGATTC	CATACTTGAC	CTCATGTGAT	180
GGGTCTAAGT	CAAAATGTAG	GCAAAACTTT	CACGCACAAA	ATTACTTAAA	ATATTCTACT	240
GAGCCAGGCA	TAGTGGTTCA	TGCCTATAAT	CCCAGCACTT	TGGGAGGCTG	AGATGCCAAT	300
TGCTCGAG						308

- (2) INFORMATION FOR SEQ ID NO:1099:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 484 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1099:

GAATTCGGCC	TTCATGGATG	ACCGCAGCAG	GCTGGTCAAG	CAGATGGAGG	ACAAGGTGTC	60
TCAACTGGAG	ATGGAACTGG	AAGAAGAGAG	AAACAACTCA	GATTTGCTGT	CTGAGAGGAT	120
CAGTAGGAGC	AGGGAACAGA	TGGAGCAGTT	GAGGAATGAG	CTACTTCAGG	AGAGAGCTGC	180
GAGACAAGAC	TTGGAGTGCG	ACAAGATTTC	CCTGGAGAGG	CAGAACAAGG	ACTTAAAGAG	240
CCGGATTATC	CACCTGGAAG	GTTCCTACAG	GTCCAGCAAA	GAGGGGCTGG	TTGTGCAGAT	300
GGAGGCCAGG	ATCGCGGAGC	TGGAGGACCG	CCTGGAGAGT	GAGGAGAGGG	ATCGGGCCAA	360
TCTTCAGCTC	AGCAACCGGC	GGCTGGAGCG	GAAAGTGAAG	GAGCTGGTGA	TGCAGGTGGA	420
TGATGAGCAC	CTGTCATTGA	CTGATCAGAA	GGACCAGCTG	AGCTTGCGTT	TGAAACCCCT	480
CGAG						484

- (2) INFORMATION FOR SEQ ID NO:1100:
  - (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 431 base pairs

- (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1100:

GCAGATTGAG	GACCTCCAGA	AATCTTTACA	GGAACAAGGT	TCCAAGTCTG	AAGGCGAAAG	60
	ATTAAAGCAG					120
AAGAATTACA	GAAGAAACAA	GAACTCATTG	AAGATCTTCA	GCCAGATATA	AATCAAAATG	180
	CAATGAACTT					240
TGGAGGAAAG	ATATAAAATG	TACTTGGAGA	AAGCCAGAAA	TGTAATAAAA	ACTTTGGATC	300
CCAAGTTAAA	TCCAGCATCA	GCTGAAATAA	TGCTACTAAG	AAAGCAGTTG	GCAGAGAAAG	360
AGAGAAGAAT	TGAGATTCTG	GAGAGTGAAT	GCAAAGTAGC	AAAATTCCGT	GATTATGAAG	420
AAAAACTCGA	G					431

- (2) INFORMATION FOR SEQ ID NO:1101:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 557 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1101:

GAATTCGGCC	TTCATGGCCT	ACTGGGAATC	TCTCAGCAGC	TTTTTGCCAA	ACAGATGGGC	60
CAGGAGCCGC	GGAACCAGGC	TGAGGAATGT	TGCCTCACGA	TCTCTCATAT	CCATTCCTGG	120
CACCCACCAG	CCCAGGGAAT	GCCTCTACCA	GTTGTCAGCG	AGAGGCTTAC	ACAGCATCTT	180
AAATAAAAGG	GATTATTGAA	CCAAGAGGCC	AGGGACTGAT	GGAAATGCCC	ACCTTGCTGG	240
CTCATTGAAA	AAGTTTGGCA	AGGTTGTCAG	GAGACATGAA	TTAGATGGGC	TTGGGTCTTG	300
TGCCCTTTGC	TAAACCAAGT	GCTGTATTGG	GAAAGAGACG	GGGAGAGAAG	TGTTGGAGAT	360
GCTCTTTAGT	CAGGCCTGAG	TCACTTGCCC	AACCCTGGAG	TTGGAGTTGG	GGATGGAGCC	420
AGGATCTCCA	AACCACATGC	CCCTAGAGTT	TCAGGGAAAA	TATGGATTGT	GAATTGAAGA	480
TGGGGGGTGA	TGTAAGGCAG	ACAAGGACAG	AAAATCCCTC	TTCCAGCTGT	GATTTGGCTG	540
TGAGTTTGGC	GCTCGAG					557

- (2) INFORMATION FOR SEQ ID NO:1102:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 577 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1102:

GAATTCGGCC T	TCATGGCCT	AGTTTTTCTA	GAGTGAATTA	TAGTATTGAC	GTGAATCCCA	60
CTGTGGTATA G	ATTCCATAA	TATGCTTGAA	TATTATGATA	TAGCCATTTA	ATAACATTGA	120
TTTCATTCTG T						180
AGCTCGTGTT A	TGGAAAAA	GTGCACTGAA	TTTATTAGAC	AAACTTACGA	ATGCTTAACT	240
TCTTTACACA G	CATAGGTGA	AAATCATATT	TGGGCTATTG	TATACTATGA	ACAATTTGTA	300
AATGTCTTAA T	TTGATGTAA	ATAACTCTGA	AACAAGAGAA	AATGTTTTTA	ACTTAGAGTA	360
GCCCTAAAAT A	TGGATGTGC	TTATATAATC	GCTTAGTTTT	GGAACTGTAT	CTGAGTAACA	420

GAGGACAGCT GTTTTTTAAC CCTCTTCTGC AAGTTTGTTG ACCTACATGG GCTAATATGG ATACTAAAAA TACTACATTG ATCTAAGAAG AAACTAGCCT TGTGGAGTAT ATAGATGCTT TTCATTATAC ACACAAAAAT CCCTGAGTGA CCTCGAG	480 540 577
(2) INFORMATION FOR SEQ ID NO:1103:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 298 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1103:	
GAATTCGGCC TTCATGGCCT ACATGGACCT CCTGCACAAG AACATGAAAC ACCTGTGGTT CTTCCTCCTG CTGGTGGCAG CTCCCAGATG GGCCCTGTCC CAGGTGCAGC TGCAGGAGTC GGGCCCAGGG CTGGTGAAGC CTTCGGAGAC CCTGTCCCTC ACCTGCACTG TCTCTGGTGC CTCCATCAGT AGTGGTGGTT ACTACTGGAG TTGGATTCGT CACCACCCAG GGAAGGGACT GGAGTGGATT GGGCGAATCT CTCACAGCGG GCACACCAAC TACGACCCCT CCCTCGAG	60 120 180 240 298
(2) INFORMATION FOR SEQ ID NO:1104:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 306 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1104:	
GAATTCGGCC AAAGAGGCCT AGTCATCTC AATATCTCTC TCTCTCATCC CTTCATTAAA TCATTCACCA AGTTTTGACA GTTTTCCTTT GCAATGGTC TCCAAATGGT CATCCTCTTC TCCTTTTTCA GATTAGGATT CTTGTTTTCT TTACTCATTG GTAAAACAAG TTTGGGAAAT GCTAGTTACG CAGTTAATGG TGTAGTTACC GCAGGACTTG ACAAAACCTC TAATGAAAGA ATAAAACATT TGCTATATTT GTTTGATCAG AGAAACTTTT TTCCATCTCA GGGGATCATT CTCGAG	60 120 180 240 300 306
(2) INFORMATION FOR SEQ ID NO:1105:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 535 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1105:	
GAATTCGGCC AAAGAGGCCT ATAGGCCTCT TTGGCCGTCT AAATGAAATG	60 120 180 240 300 360

GTGGTGTTCA	CATTCGGACG	TGTGTTAGGT	AGAAGTGTGT	GTGCACCTGC	GTGTGCGTGT	420
					TAGAAGATTG	480
		ATTTCCTGAA				535

- (2) INFORMATION FOR SEQ ID NO:1106:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 586 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1106:

GAATTCGGCC NAAGAGGCCT	AGAAAAAATT	AAAAAGGGAT	ACAGACGAGC	TGCNAGCTAT	60
GGAACATAGA TATTAACCCC	CAAAGAGTCN	TAACCACAGC	TGACTCTTAG	CTTCACAAGC	120
AGNCCTCNGA ANGTGGTAGO	TTGTTTTAAG	CAGAGGCCAT	GCAGAACCCA	TGAAACCAAA	180
GGACAGAGCC AGTAGGGCTC	GAGTCTGACC	AGAAAGTTCC	ATGCCCTCTG	CTTTCTGCAT	240
GGAAAATGAC CTGGTAGGTT	TTAACCTATC	CAAGACTACA	GAGGATTTCA	GAATTTCAGT	300
TTGAGGTATG CCTCAAAACA	TTCCAGCCTT	GATCATGAAA	GAAAGAAGTG	ATCAAAATAC	360
CATATGTCAC AATGGAAAA	CCAAGCGGCC	CCAGAGCTCT	TCTTCAGTAA	TGAGATTTAG	420
TTGATCTGNA CAGTTATTT	TGCATTGAGG	TCATATTTTG	GCCAATCTTT	TGCTTACAGC	480
TGTCGCCAAA TAAAGCCTTC	TGTNTTAGCA	TTTCTTTTAC	CAAAATCAGG	TTGAGAGATG	540
GTTCTTTGAG AGGACTGTTT	TGTCAGGGAA	TACAGGGAAT	CTCGAG		586

- (2) INFORMATION FOR SEQ ID NO:1107:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 433 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1107:

GAATTCGGCC	AAAGAGGCCT	AGGACTTAAA	AGAACAGCTA	GAAAAGATGA	AAGGTGACTT	60
AGAAAGTAAA	AATGAAGAAA	TACTACATCT	GAACTTAAAA	TTGGACATGC	AGAACAGCCA	120
GACTGCTGTC	AGCCTCAGAG	AACTTGAGGA	AGAGAACACG	AGCTTGAAGG	TCATATATAC	180
CAGAAGTTCT	GAGATTGAAG	AGCTGAAAGC	CACTATTGAA	AATCTGCAAG	AGAATCAGAA	240
ACGATTACAA	AAGGAGAAAG	CAGAGGAAAT	TGAACAACTC	CATGAAGTCA	TTGAGAAGCT	300
GCAGCACGAG	CTGTCCCTCA	TGGGGCCTGT	GGTGCACGAA	GTCAGCGACA	GTCAGGCTGG	360
CAGTCTGCAG	AGCGAGCTGC	TCTGCTCCCA	GGCCGGGGGC	CCTCGTGGGC	AGGCCCTACA	420
GGGCGAGCTC	GAG					433

- (2) INFORMATION FOR SEQ ID NO:1108:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 316 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1108:

```
GAATTCGGCC AAAGAGGCCT ACGTGAATAT TTTTCCATCT GTGTTCATTG ATGTTAACAA
TAAAAATCTT GTTTATGTGT ATAAGCCTAA CATATGCCTG TGGGTCTTAT AACTGCCTGT
TCAAACTCAA TGGGATACCA AAAATGTATC TGCTTACTTT GGGGGTCTAA CTTTAATTCG
GTACATATAA ACATCTCTGG AAAAAAATGT AGTTTTTTC TTCCCCCTGC TGTTTTCCCC
AGGCTTTCTC CTTTGACCTG GCCACGGTTC CCATAGACTA CAAGACGACT TAGAGACATT
GCTGTGACAT CTCGAG

60
120
120
1316
```

- (2) INFORMATION FOR SEQ ID NO:1109:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 368 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1109:

GAATTCGGCC	AAAGAGGCCT	ACTAACATTT	TCCTAATCTT	ATGTGTTTGG	CTCCTCTCAT	60
TTACTCCCCA	CAGCAGCCAC	ATGAAGTTGG	AATTTCGAAC	TCTTATTTAG	GTATGCAAAA	120
GGGTACCAGT	TCTCTTTAAG	GCTTTAGTTC	AGGAGTGGTG	TTAATGTATT	AATGTGTTGG	180
GGCGCGAGAG	GAAGGCGGTG	CTTATTTCGA	ATCATGGTAG	GTAAAGATAA	TTTCAACTCT	240
GACACTTCCA	CTAATAAATT	TTCGCATCTA	GGGAAAATGA	CGTAAGCTTC	CTAGATCACA	300
GATTTGTTTT.	CATCCAAAAC	CCGAAGTCTG	GTTTTGAAAT	CACGCTCTTG	ATACAAAGGT	360
GGCTCGAG						368

- (2) INFORMATION FOR SEQ ID NO:1110:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 396 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1110:

GAATTCGGCC	AAAGAGGCCT	ATCCGGGGGG	AGTAAGGTGA	GGACAAGGAA	CAGAAAGGCG	60
TGAGGTGATG	GAAGGAAGTC	CGGGAGAACC	ATATGAAGGA	GCAGGAGGAG	AGGAAGAAAC	120
TTTTTTTCCT	TCTTTTCCAG	GAGTAGCTGG	AAATTAAGAT	CGGGTTCCTT	TTCTGCCAGC	180
TTGGAAGGGC	AACCCCATGA	CTGATTGCGA	TTCTGAGGAT	GTCTATGCAA	AGTTGGATTC	240
TTGTTACAGT	GTATCCAATC	TGAAGTATTG	CACATCTGAA	CTGGGACTGT	TAACACTGAT	300
GCCAATACAG	TGTGGGGTGC	CAGAAAGTGT	CTGCTGATAT	TTGTGGAAAA	AAAATCTATT	360
TTGTTTACCT	<b>ACTGTATCAA</b>	AGGGGAGGAA	CTCGAG		•	396

- (2) INFORMATION FOR SEQ ID NO:1111:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 427 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1111:

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GAATTCGGCC AAAGAGGCNT AGATTGTTTT CATTAGCAAA CTCATAATTA TCCTTTTCCT
                                                                       60
TAACACTTCC AGTTGAGAAA ACAAGTATTT GTTAATGACC AGTAATAATC TTGATCCAGG
                                                                      120
GTAGGCAAAA TTTTTCTTCC AGGGCCAGAT TGATACTTTA GGCTTTGCAG GCCACGGGGT
                                                                      180
CTCTGGCAAC CCCCAGCTCT GCTGTTGTAG CACAAAAGCA GCCACAGGCA CAAGTAAACA
                                                                      240
CATGGGTGTG TCTCTGTACC AATAAAACTT TATTTACAGA AACACAGGGC AGATGACTGT
                                                                      300
CTGGCCCCTG GTCTTGTCAG CATTTTGTGG TGGTGAACAA AAGAAACTGT TCAGATCATT
                                                                      360
ACATTTACAG TCATTACCAA AAATAGAATC TTCACAGTAG TTGTACTGTT GATGAAGCAA
                                                                      420
GCTCGAG
                                                                      427
```

- (2) INFORMATION FOR SEQ ID NO:1112:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 504 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1112:

GAATTCGGCC AAAGAG	GCCT AGGTTATAAT	AGCAGCTTAC	TTTTGATAAG	CGTACTAACT	60
GGTACATAGT AAATAC					120
CAAATTCAGT ACAATT	TGTA TTCCCGTTTT	ACAGATGAGA	<b>AAGCATATTT</b>	TGGTGAACTC	180
AACCAAGGTT ACATGA	CTAG TAAATTTTAA	ATGAGATTTA	ATTTCAGTAC	TTACTAACCA	240
TTATGCATTG CTAAAT	TTGA ACATTACTTT	AAAATATAAC	TTCTAAAGTG	TTCATATTAG	300
AAACCTATAA ATATAC	ATAG ATTTGTCTCC	TCTCTNACGA	AGAACACATG	AAGGAAAGAA	360
AGATATTAAT TTGGTG	GCTT ATCATATGCC	AGACATAGAT	ATAGATGCTT	GTATGTATGG	420
CATTTAATCC TTATCT	GTGA GGTAGGTCTT	TTTATGCCTT	TCTATAGATT	TAAATTAAAG	480
GTTCAGTTTA GTAACT	TGCT CGAG				504

- (2) INFORMATION FOR SEQ ID NO:1113:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 369 base pairs
    - (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1113:

GAATTCGGCC	AAAGAGNNCT	AGAGGGATAT	<b>AGAAACTTAA</b>	CAGCAGTGGC	TGACATTTTT	60
GCTTATTTGT	TAGGTATTGG	TGGTGGTGTT	AATCGGGTAC	GCATATGCTT	TCCTTAGGAT	120
TTGCATTTGC	TGTTCCCTGT	GTCTAGAACG	CTATTCCTTA	GATAAATCTT	CATTCCTTAC	180
CTCCTTAAAA	TGTTTTCTCA	TCTATCACCT	TCTTAAGTCT	GTACTGATCA	CCCTACTTAA	240
AATTATAACT	GCCCCTCTTT	GCTTGCACTT	CTAAGCTTCC	TTACCCTAGT	CTGTTTAGCA	300
GTTACCTCCT	TGAAACATGC	TCTGTAGAAT	TTACTTATTA	TGACTATTGT	CTCTCTTACT	360
ACCCTCGAG						369

- (2) INFORMATION FOR SEQ ID NO:1114:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 89 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1114:

GAATTCGGCC AAAGAGGCCT AGTTAAAAAT AGAATTTGAG ATATTTAATT TTCTGCTCTT TTTAAGTTAT GAAAACGTAT TTACTCGAG 89 (2) INFORMATION FOR SEQ ID NO:1115: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 495 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1115: GAATTCGCCA AGAGCCTATT AATTTGTAAA CCTTAATATA GTGTAAACTG AATAAAAGTA AATAATTATT ATTAGAATGG TAACTAAGTC ATTAAATTTT TTNGCAGAAC TGAAACTTGT 120 ATGTTATTAG TTTATTTTCT TAGACCAGTG TAATAATGGA CTGTAAATAG AAAAATAAAT 180 GTCACTTTAC AGTTAGATGT ATCACAGTCG TTTCAGGAGA ATTTTTCCTA TATTGTTACC 300 CTTTATCATA AGCCATAATC ATTTTAAGAA TACTTTATTG GATAGATTTT AGTACTTTTT AAATTCTAAA.GTTCTATTTT TCTTTTCACT TCCCCTTCCT TCCCCTTATA AGATCATTTC 420 CATGTCTTTG TTGGTGATCT CAGCCCAGAA ATTACAACTG AAGATATAAA AGCTGCTTTT 480 GCACCAAGTC TCGAG 495 (2) INFORMATION FOR SEQ ID NO:1116: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 522 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: CDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1116: GAATTCGGCC AAAGAGGCCT AGGGAAAAGA AGGGCTTTGG GGACCTGCCC ACTTCAAAAA 60 CAGTITITCT CATCCTTTGC CTTCGGCTCC AAACCCAGCT TGGTGTTTTC CTAAGGGAGC 120 TACAAATTCT GGAGCATCCC ATGAGGATGA TTTGCTGGCC TCGGTCATTA GGGGGAAAGG 180

CAGCTTTTCT CATCCTTGC CTTCGGCTCC AAACCCAGCT TGGTGTTTTC CTAAGGGAGC 120
TACAAATTCT GGAGCATCCC ATGAGGATGA TTTGCTGGCC TCGGTCATTA GGGGGAAAGG 180
ATGTTCTCAG AAAACAGCC CTGCACGCTG GTCAGCAGAG ATCTTGAGGT CGTCGCCACG 240
ACTGGACTTG GTGCAGAGCT GAACCCGAGA CTCCAGCTGC TCGCTGAGTT CGTCCAGAGC 300
CCCGGTGCAG GACTCCAGGC TCTCCGGCCAG TTTCTGAATC TTGGCCTTCA GCACGGCCTG 360
GCTAACCTTG GTGTCCCCCT CCGCCGCCT GGGGATGAGG AAGCCACGTG AGCCAAAGAA 420
GACGATGAAG TAGACAGAAT TGTACAGGGC GATGAGGCG TTCCTCCCGC ACTGCAGCAG 480
CTGGCGGTCC CCGCAGCCCT GCCAGCGGCA GAAAAACTCG AG 522

- (2) INFORMATION FOR SEQ ID NO:1117:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 352 base pairs(B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1117:

GAATTCGGCC AAAGAGGCCT	AAAAATATTT	TACTTGTTCC	ATCCACAGTT	CTCTACAGAA	60
AGAACCAATG AACCCAATAG	GAACAAATTC	TCTGTGGAAA	ACAAAGCATA	GCTGTAGTAG	120
ATACGAATCC AATCACAGAG	GAAACAGGAA	GAGAAAAACA	TCCAAGACTA	TAGTGAAAAC	180
TGGAAATGGT CTGTTTTCGT	GATATTCGTA	TGATTAAGAT	GCAAATTTTT	TCTTAGGAAA	240
ATGTGATTGT TAACTAGCAT	TCTGTTTTAC	ATGTTGACAT	TTCTAACACA	CACACCACTG	300
ATTTGAACTT CAAAATTTAT	TTTCTGATTA	TATATGCTAG	GTCATGCTCG	AG	352

- (2) INFORMATION FOR SEQ ID NO:1118:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 481 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1118:

GAATTCGGCC	AAAGAGGCCT	AGTGCCCACT	CATTTATGTA	CTGTCTATAG	CTATTTTCAT	60
GCTACAATGG	CAAAGCTAAG	TAACACTCAA	GGCCTAAAAT	ATTCACTATA	TGCCCTTTGA	120
AGAAAAAGTT	CACTCAACTC	TGCCCTAAAC	TACAGACCCT	GGCCAAGGTG	GGAGGATCAC	180
TTGAGGCTAG	TAGTTCAAGA	CCAACCTGAC	TCTGTCTCTG	ACTCTGTCTC	TACCAAAAAA	240
AATTAGCTGG	GCGTTGGGCT	TATCCCTGTA	ATCCCAGCTA	CTCAGGAGTC	TGAGGCAAGA	300
GGATCACTTG	AGCCCAGAAG	TTCAAGGACA	CAGTGAGCTA	TGATTGCACC	ACTATACCCC	360
AGCCTGGGCA	ACAGACCAAG	ACCCTGTCTC	TAAAAACATA	AAATAAAAA	TAAAAAATAA	420
AAATAAATAA	TAAAGAAAA	AGAAACAGAA	TTAAAGAAAT	TCTTTTGCTC	AAAGTCTCGA	480
G						481

- (2) INFORMATION FOR SEQ ID NO:1119:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 314 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1119:

GAATTCGGCC	AAAGAGGCCT	AAGTTGTGTC	AGTGTCTCTC	CTAACCTACT	ΤΤΑΚΤΑΤΑΚΑ	60
GACTTATTCT						
						120
TTTAATCTTT	TGGAATATTG	TCTTTCTTTG	TTATAACTAT	TCATTTTTAG	CTTTTGTCTC	180
CAGTGCATGA	TCTCATATTT	TTGCTTTTAT	TTTTAGTATA	AGAACATTTA	TAAAATCATA	240
TTTTTGTTAC	TGCAATTGTT	TTATTTGTTG	TGTGGCAAAT	GAGAAATCCT	TTATTTATTG	300
				0.10.221.001		500
TGCTGTATCT	CGAG					314

- (2) INFORMATION FOR SEQ ID NO:1120:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 199 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1120:

GAATTCGGCC TTCATGGCCT ACCAGATACT GTTTTTTTAA TACATATTCA AAAGAAAGCT
ATTAACCCTG ACAGACATTT CTCAGTCTGT GCTTTTTTCT ATTTTATCAT TTTAAAGTAC
TTAAGATAGA AAGATGAAAA AGCATTTGTT GGCTACTTGG TTAGCTTCAC AAATTTTCCC
180
CCTTCCTACG CAGCTCGAG

- (2) INFORMATION FOR SEQ ID NO:1121:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 295 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1121:

GAATTCGGCC	TTCATGGCCT	AGTAGCATAT	TAACAGTGTA	ATAAAAAATA	AAAACAAACT	60
CTAGTATCCA	GAGGATCACA	TGCTGACCAG	ACCCTGTGTA	GAAAGTGCCG	AAGAGCATCA	120
AGGAAATGGA	AACGTTGGAA	TTCCATCCGT	GCTTGTGGCT	TTCCTTAAAC	TTTTGTTATG	180
GAAAATTTCA	AATATACCCC	GAAGTGGAGA	TTGGCTTAAA	TCAGCCCCAC	GTGCCCATCA	240
CTCGGCTCCA	GTCATTATCC	AGTGTGGTTC	CTCTGATCTT	CACCACCCC	TCGAG	295

- (2) INFORMATION FOR SEQ ID NO:1122:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 410 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1122:

GAATTCGGCC	TTCATGGCCT	AACGGAAGCG	TCTCCTCATT	GATGGAGATG	GTGCTGGAGA	60
TGATCGGAGA	ATTAATCTGC	TAGTGAAGAG	TTTCATTAAA	TGGTGCAACT	CTGGGTCCCA	120
GGAAGAGGGA	TATAGCCAGT	ACCAACGTAT	GCTGAGCACG	CTGTCTCAAT	GTGAATTTTC	180
AATGGGCAAA	ACTTTACTAG	TATATGATAT	GAATCTCAGA	GAAATGGAAA	ATTATGAAAA	240
AATTTACAAG	GAAATAGAAT	GTAGCATAGC	TGGAGCACAT	GAAAAATTG	CTGAGTGCAA	300
AAAGCAAATT	CTTCAAGCAA	AACGAATACG	AAAAAATCGC	CAAGAATATG	ATGCTTTGGC	360
AAAAGTGATT	CAGCACCATC	CAGACAGGCA	TGAGACACAG	GGAACTCGAG		410

- (2) INFORMATION FOR SEQ ID NO:1123:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 308 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1123:

GAATTCGGCC AAAGAGGCCT ACCTTTCTTT CCTCCCTTCC TCCTCCCATG TCCCTCTCTC

CTCCCTCCCA CCTCTCACCC TTCTCCATCC CTCCTCCCTC	120 180 240 300 308
(2) INFORMATION FOR SEQ ID NO:1124:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 445 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1124:	
GAATTCGGCC TTCATGGCCT ACAATTTGC CATGGTTCTG CTCATTTTC CTGCAATTCT CAGCATGGAT TTATATCGAC GCGAGGACAG GAGACTGGAT ATTTTCTGCT GTTTTACAAG CCCCTGCGTC AGCAGAGTGA TTCAGGTTGA ACCTCAGGCC TACACCGACAA CACACGACAA TACCCGCTAC AGCCCCCCAC CTCCCTACAG CAGCCACAGC TTTGCCCATG AAACGCAGAT TACCATGCAG TCCACTGTCC AGCTCCGCAC GGAGTACGAC CCCCACACGC ACGTGTACTA CACCACCGCT GAGCCGCGCT CCGAGATCTC TGTGCAGCCC GTCACCGTGA CACAGGACAC CCTCAGCTGC CAGAGCCCAG AGAGCACCAG CTCCACAAAGG GACCTGCTCT CCCAGTTCTC CGACTCCAGC CTCCACTGCC TCGAG  (2) INFORMATION FOR SEQ ID NO:1125:	60 120 180 240 300 360 420 445
(2) INFORMATION FOR SEQ ID NO:1125:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 314 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1125:	
CAATTGCCTT CATGGCCTAC ACCAGCCTAT TCTCTGCTTC TGTGAGTTTG ACTCTTTTTT CTTTTATGAG ACAGAGTCTC ACTCTATCTC CCAGGCTGGA GTGCAGTGGC ACAATCTCGG CTCACTGCAA CCACCACCTC CCAGGTTCAA GCAGTTCTCC TGCCTCAGCC TCCCAAGTAG CTGGAAATAT AGGTGTGCCC CACCACGACT GGCTAATTTT TGTATTTTTA GTAGAGACAG GGTTTCACCA TGTTGGCCAG GCTGGTCTCG AACTCCAGGC CTCATGTAAT CCGCCCACCT CGGCCCACACT CGAG	60 120 180 240 300 314
(2) INFORMATION FOR SEQ ID NO:1126:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 328 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	

GAATTCGGCC TTCATGGCCT ACACGCCCCC GCCCCGCCTG CTGCCCAGGA ATACTTTCTC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1126:

CAGGAAGGCT	TTCAAGCTGA	AGAAGCCCTC	CAAATACTGC	AGCTGGAAAT	GTGCTGCCCT	120
					TAGCAATGCA	180
TCTGCTCGGA	CTCAATTGGC	AACTCCAGCC	TGCAGATGGG	CACACCTTTA	ACAATGGGAT	240
					GCAAAGTGCC	300
CTGGTCGTTG				_		328

- (2) INFORMATION FOR SEQ ID NO:1127:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 461 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1127:

GAATTCGGCC	TTCATGGCCT	AGTGAGGCTC	CATTATTTTC	ATTTTTAACA	AGTTTCAAAA	60
TGTGGCTGCT	GCTGTTGCTG	GTGGTCCGGA	GCCTGCAGAC	AGGGGGATTT	GCCTGGGAAG	120
GAGAAGTAGA	AAACAACGTG	TACAGCCAGG	CTACAGGGGT	GGTCCCCCAG	CACAAGTATC	180
ACCCCACAGC	AGGCAGCTAT	CAGCTTCAAT	TTGCCCTGCA	GCAACTTGAA	CAACAAAAAC	240
TTCAGTCCCG	GCAGCTCCTG	GACCAGAGTC	GAGCCCGGCA	CCAGGCAATC	TTTGGCAGCC	300
AGACACTACC	TAACTCCAAT	TTATGGACAA	TGAATAATGG	TGCAGGTTGT	AGAATTTCCA	360
GTGCCACAGC	TAGTGGCCAG	AAGCCAACCA	CTCTGCCACA	AAAAGTGGTA	CCACCTCCAA	420
GTTCTTGCGC	CTCCCTGGTT	CCCAAACCCC	CACCGCTCGA	G		461

- (2) INFORMATION FOR SEQ ID NO:1128:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 461 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1128:

GAATTCGGCC	TTCATGGCCT	AGAATTATCA	TGGCATCTGT	AACACACATG	CCTGTGCTAT	60
ATTCTCACAA	TTTTGTTCAG	GTTGTGCATA	TTAAAATATG	GAGCTCCATA	TTTTTTCACT	120
TCCTAGTTGA	TCACAGTTGA	CTGGGTTGTC	TTTTCTGTCA	CCTGTTAGTT	TTGAAGAGAT	180
GTCTCATATG	TAGTGATGTT	AGGTATGATG	CATTCAGCCA	TAGTAAATAC	CTGGTACTGT	240
CTCTCAAAAA	AAGCCTTTAG	CTTTTTTGTA	AAGAGGACAA	CAGAAAACAC	ACCAAAAAAG	300
CAGAAAAATA	TGTGTCGGTG	ATAGTGGGAG	AAACTTATAA	ATCATGGTCA	TATGTTACCC	360
CAGAGAAGGC	TTACACAAGG	TCAGCTACAG	TTTACCCAAT	AACGCTGTGA	TTGTCTGGTT	420
CCTTGGCTTA	GAAAGCTTAG	TCTCTGCCAA	GCGGCCTCGA	G		461

- (2) INFORMATION FOR SEQ ID NO:1129:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 491 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1129:

GAATTCGGCC	TTCATGGCCT	ACAAGAATGA	AGCACTGAAA	AGCGAAGAAG	GCTGCATTCC	60
GAATATCGCC	CCAGACATCT	GCATAGCATA	CAAACTGCAC	CTAGAGTGTA	GCAGGCTCAT	120
CAACCTCGTG	GACTGGTCAG	AGGCTTTTGC	AACAGTTGTG	ACAGCTGCTG	AAAAAATGGA	180
TGCAAATTCT	GCAACCTCAG	AAGAAATGAA	TGAAATTATC	CATGCTCGGT	TTATTAGAGC	240
			AAAACCTACC			300
			AGCAAATAAG			360
			ATTTACATAT			420
			GTTTAACCAG			
AAGAGCTCGA		CCCCATIGAT	GITTAACCAG	AAAAG IACA I	IGCIAACCCC	480
I WIGHT COM	G					491

- (2) INFORMATION FOR SEQ ID NO:1130:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 358 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1130:

GAATTCGGCC	TTCATGGCCT	AGGGCAACAG	GAAACTCTTT	ATTATGGTGA	TGAGATCGAC	60
			CACACTTCAG			120
CGCTGGCCTG	GGCTTCTGCG	ACCCGCGATC	GTCCAGGAGA	GGGCACTCGG	CGCCCTTCCT	180
GGGGCGCTTC	TGGGGCGGAA	TTTGCTAGGC	CGCCGTAGCA	GCGGTGCCAG	GTCAGAAGCC	240
GAGCCGGCCC	GCTTTTCGTT	CTTTAATTGG	ACTCTTGGCT	AAGACGCTAC	CGACACCCCG	300
TCAGGTGGTG	GAGGAAGAAG	GACAACAGGG	AGAGGTCGAG	GGCCGAGACG	GCCTCGAG	358

- (2) INFORMATION FOR SEQ ID NO:1131:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 295 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1131:

	TTCATGGCCT					60
GTACCATTTA	TGTTTCTCAG	AACCAGCAGA	ATCAGTGCCT	AGCCTGTGCC	CAGCAAATAG	120
TTGGCACTCA	ATAAAGATTT	GCAGAATTTA	ATACAGATCT	TTTCAGCTGT	TCTTAGGGCA	180
TTATAAATGG	AAATCATAAC	GTGGTTCTAG	GTTATCAAAC	CATGGAGTGA	TGTGGAGCTA	240
GGATTGTGAG	TGACCTGCAG	GCCATTATCA	GTGCCTCATC	TGTGCAGACC	TCGAG	295

- (2) INFORMATION FOR SEQ ID NO:1132:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 500 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1132:

GAATTCGGCC	TTCATGGCCT	AATGAAAAAC	AAAACAAAGA	TGATGAAGCA	GAGTGGCAAG	60
	AAGCATACAG					120
CACATCCTGT	GTATAGCCTT	TACTTTCCTG	AGGTAGAGCT	GAAGTTTCCT	GCACCAGGCA	180
	TTATCAGTAT					240
AGATTAAACC	ATTGAAGTTG	GAAGTTCATG	AGGCTAAGCC	TGTGCCAGAA	AATCACCCAC	300
AGTGGGATAC	AGCAATAGAG	GGGGATGAAG	ACCAGGAGGA	CAGTGAGGGC	TTTGAAGATA	360
GCTTTGAGGA	AGAAGAGGAG	GAAGAAGAAG	ATGATGACTA	AGCAGTACTC	TGAATGGACC	420
ACAGTGTTTG	CACATATTTG	CAATTTTTTG	CTGTTTTGGA	AGTGTATCAT	AAACCAGAAA	480
CAGTACATAA	CAATCTCGAG					500

- (2) INFORMATION FOR SEQ ID NO:1133:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 420 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1133:

GAATTCGGCC	TTCATGGCCT	AGATTATATT	GCATATATTT	TATAGAACAA	GGCAAGCAAA	60
ATATTTTAGT	ATTTGCAAAT	CATGTTACTA	TAATTATTAG	ATCATAGTAC	CATTTATATA	120
AAGTATTAGG	TTGGTGCAAA	AGTAATTGCG	GTTTTGGACC	GTGAATTTTA	AATCATTATA	180
AGTCGGCTCA	GACACGTCTT	TATTAATCAG	AGCAGGAAGC	ATTATAATCA	ACACATTTTT	240
GCCAATGAGA	AATAAGTTTG	TTCATTCCTG	TAGCTTAAAA	ATTCATGCTT	TGGGATTTGG	300
AAAGCATTTT	CTGCTTTCCA	AAAACCTGCT	GGTTTTGGAA	GCATTTTCCT	TTCAAATAGT	360
TGTCGAGATG	CTTGAAGAAG	TGGTGGTTGA	CAAGAGGTCA	GGTGAATACG	GCGGCTCGAG	420

- (2) INFORMATION FOR SEQ ID NO:1134:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 335 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1134:

GAATTCGGCC	TTCATGGCCT	AACTAGTCCT	GACTGCTTAG	ACAAAGTCAT	AGATTATGTT	60
CCAGGCATTT	TCCNAGAAAA	CAGTTTTACA	ATCCAATACA	TTCTGGACAC	CAGTGATAAG	120
CTGAGTACTG	AGCTCTTTCA	GGACAAAAGT	GAAGAGGCTT	CCCTTGACCT	CGTGTTTGAG	180
CTGGTGAACC	AGTTGCAGTA	CCACACTCAC	CAAGAGAACG	GAATTGAAAT	TTGCATGGAC	240
TTTCTGCAAG	GCACTTGTAT	TTATGGCAGG	GATTGTTTGA	AGCACCACAC	TGTCTTGCCA	300
TATCATTGGC	AGATCAAAAG	AACAACTAGC	TCGAG			335

- (2) INFORMATION FOR SEQ ID NO:1135:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 308 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1135:

GAATTCGGCC	TTCATGGCCT	ACCAATTTT	CCCTCXCCCC	CCCTCCCA	TTCTTACACA	
		VOCWUIIII	CCCICAGGGG	COCICCCAIC	TICITAÇAÇA	60
GAGAGGCAGC	TGAGGCAGGA	CAGTGGGGCT	AACTGTAGAC	CAGGCGAGGG	CACGGGCTGC	120
TGGGGTGGCC	CTGCTTCCCC	AGTGTACATA	TTGTATCTGT	GTAACATTTT	GTATATTCCA	180
GGGGTAGGGC	CGCCCCCTGT	ATCATACCTA	GCAGAGGTTG	GAGCTGGCAC	ATGGGGAGGA	240
COTTOTATO	A THE R THERE CO.				MICCOCKAGGA	
OGITCIAMIN	ATTATTIGGG	GCTGGGAAAC	TTATTTATTG	ATAGCATAGG	ACAGAGCCCA	300
CTCTCGAG						308

- (2) INFORMATION FOR SEQ ID NO:1136:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 497 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1136:

GAATTCGGCC	TTCATGGCCT	ACCGAGGCTT	CAGCGGGTGC	CGCCCGCCTA	GAGGGAGTGG	60
AGCGGCTAGA	CAGCTTTAGG	AACTGAAAGG	TTCACGAGGC	TGTAACGAAG	AGTCGAGTTG	120
CTCCAGAGAG	CCTACGACTA	GATTTGCATC	TTTACGTCCT	GCGCGGAGGC	TGCTACACAC	180
ATGCAGAAGT	CATGCTGGTG	GCCTGGACAG	TGAAGGGAGA	GAAGTGGATT	TGGGAGACAT	240
TTAGGAGGAA	CAGTAAGAGG	ACCTTGTGCA	TGAATAATTT	GTTTCCACAC	TACAGAGTGG	300
GTAATAAGCA	GATTAGTAAA	AACAATTCTG	CTTCACTTCA	ATAACAGCCT	CCTCCAACTC	360
ATTTTTTCTC	AACAAACTTA	TTTTCCAGCA	GAAGAATCCC	AGACTTCTTA	GAGAACCCAG	420
TGACTTTTTG	CACCTTAAAT	CTGTGAAATC	CTCATGTTTT	CTTCTGCCGT	ATCCATAGTT	480
CAAACAAGAA	CCTCGAG					497

- (2) INFORMATION FOR SEQ ID NO:1137:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 310 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1137:

GAATTCGGCC	TTCATGGCCT	ACAATTGTAT	GCTGAAAAAT	GGGAGTAACT	ACATGAAATG	60
AGCAAATGCC	TAGAAACAAA	AAACCTACGA	AGATTGTATC	ATGAAGAAAT	AGAAAATATG	120
AATAGACGTG	TGTATTAGTC	TGTTCTCACA	CTGCTAATAA	AGACGTACCC	AAGACTGGGT	180
AATTTTTTTG	TTTTTAAGAA	AAAAGAGGTT	TAATGGACTC	ACAGTTCCAC	GTGGATGGGG	240
AGGCCTTATA	ATCATGGCAG	AAGGCAAACA	GCACGTCTTA	CATGGCAGCA	GGCAAGAGAG	300
AATACTCGAG						310

- (2) INFORMATION FOR SEQ ID NO:1138:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 466 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1138:

GAATTCGGCC	TTCATGGCCT	AAGCAAATCA	CTTTTCCCGA	TTGAAAATAC	ACTTTACAAA	60
AGTGTTTTCA	GCTTTTGCAT	TGGTTAGGAC	TATACGGTAT	CTTTACAGAC	GGCTACAGCG	120
GATGTTAGGT	TTAAGAAGAG	GCTCTGAGAA	TGAAGACCTC	TGGGCAGAGA	GTGAAGGAAC	180
TGTGGCATGC	CTTGGTGCTG	AGGACCGAGC	AGCTACCTCA	GCAAAATCTT	GGCCAATATT	240
CTTGTTCTTG	GCTGTTATCC	TTGGTGGTCC	TTACCTCATT	TGGAAACTAT	TGTCTACTCA	300
CAGTGATGAA	GTAACAGACA	GCATCAACTG	GGCAAGTGGT	GAGGATGACC	ATGTAGTTGC	360
CAGAGCAGAA	TATGATTTTG	CTGCCGTATC	TGAAGAAGAA	ATTTCTTTCC	GGGCTGGTGA	420
TATGCTGAAC	TTAGCTCTCA	AAGAACAACA	ACCCAAAGCA	CTCGAG		466

- (2) INFORMATION FOR SEQ ID NO:1139:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 473 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1139:

GAATTCGGCC	TTCATGGCCT	AATTTTTTTT	AATAGAGACG	AGGTCTTGCT	ATGTTGCCCA	60
GGCTGGTCCC	AAACTCCTGG	CCTCAAGCAG	TCCTTCCACC	TTGGCCTCCC	AAAGTGCTGG	120
GATTATCAAT	ATGAGCCACC	ATGCCAGATT	TGTTCATTTT	TAAATATTTT	TATCTCTTCA	180
AGTCATCTTT	TGATCTTTTA	AAAAGCACCT	TCAAACAGCT	GCACCTTCCA	TTTGCACTAG	240
GAAATGAAGG	TAGTGATGGG	ATTGGCAATG	TTCCTGGCAG	ATGTTTCAGC	CCAAAAGCTC	300
TTCTACAGAC	CGGTTTAGAG	CTGGTGCCCT	ATGAGAATAT	TAGGGAGCTT	TTATTTTAAA	360
TTGAACTTTA	CCCTTGTCCA	TGCAAGGCAT	TCCTCCTGAA	TGCATCCATG	AATTTGTTTA	420
CTTTTGCGTC	AAACATATGA	GCCATTGTCA	TGCTCAGCAT	GTGCCACCTC	GAG	473

- (2) INFORMATION FOR SEQ ID NO:1140:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 353 base pairs
    - , (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1140:

GAATTCGGCC	TTCATGGCCT	AAATGAAGAT	CAGCTTCGTG	CAAAGGGTTA	TGACAAAACA	60
CCAGACTTCA	TTTTACAAGT	ACCAGTTGCT	GTAGAAGGGC	ACATAATTCA	CTGGATTGAA	120
AGCAAAGCCT	CATTTGGTGA	TGAATGTAGC	CACCACGCCT	ACCTGCATGA	CCAGTTCTGG	180
AGCTACTGGA	ATAGGGTCCC	AATATAACAG	ACAAATGGTG	AAACAGAGGG	ATACTCACTA	240
GGAAACAGAT	TTGGGCCAGG	CTTAGTCATC	TATTGGTATG	GATTTATCCA	GGAGCTGGAC	300
TOCANCOGO	AAAGGGGCAT	CCTGCTCAAA	GCCTGTTTCC	CCACGTCCTC	GAG	353

- (2) INFORMATION FOR SEQ ID NO:1141:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 571 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1141:

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GAATTCGGCC TTCATGGNCT ACCAATTTCT CATGGTTCCC TAGGACCTTC CTAGCTCCCC
                                                                       60
AGGGAAAGCC THTGCTGTTT CCCTTGHTTT CTTTTCACTT GACAAACTCC TACTCAAACT
                                                                      120
TCAAAACCCA ACTCAGGAAA CATCTCCCCT AGGAAGCTCT CCTTAACTTT TTCTGCTGGG
                                                                      180
TCCCGCTGCC TCTGCTAAAG TCCACGTGAG GGACTGCCAA GANGTTTGCT CTGTCTCACA
                                                                      240
GATTGAGTGC CAAGAGGGCA GGGACNTCTC TTTGAGAGAG TTTAACCTCT GTAACATAAG
                                                                      300
CAAGTTTACT TAATCACTGA TTAAACCACT TTGTGCCTCA GTTTCCCCAT TTGTTAAGCA
                                                                      360
TGAATTATCA CTGTCACTAT CTGCCAGGAC TGTGAAGGGG GTGTAAATGC ATGAACATCA
                                                                      420
TAAAGTGCTT AGAAGCATGC CTGGTACAAA GAAAGTTCTC TAGGNAAACA ANAAACAAAC
                                                                      480
AAAAAAAAC AAAACAGAAA TGTATCTAGA GGTCAGATAC CAGTCCCACA TCGAGTGCAG
                                                                      540
ATAATGGGCT AAGTAACCAA TGAGTCTCGA G
                                                                      571
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- (2) INFORMATION FOR SEQ ID NO:1142:
  - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 316 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1142:

GAATTCGGCC	TTCATGGCCT	AGTAAGGAGA	GCCTCTATCA	AAGGGTGGCC	TGGAGCAGAA	60
TATCAGGCTA	TGTGTATTAG	TTCGTTTTCA	CACGCTATGA	AGAACTACCT	GAGACTGGGT	120
AATTTATAAA	GAAAAGAGGT	TTGATTAACT	CAGAGTTCCC	ATGACTGGGG	AGGCCTCAGG	180
AAACTTACAA	TCATGGTGGA	AGGCATGATA	GCAGGAGGGG	TGGAAAGAGG	GGAGTGTCAC	240
ACTTTAAAAC	CATCAGATCT	TGTGAGAACT	CACTCACTAT	CATGAGAATA	GCAAGGGAGA	300
AATCCACCAA	CTCGAG					316

- (2) INFORMATION FOR SEQ ID NO:1143:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 442 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1143:

GAATTCGGCC TTCATGGCCT	ACTCAAGCGT	TTCAGTGTGC	GATATCTGCG	ACTGCTCGCA	60
GTCTTGTCTT CCTTGGTTCT	CCCCTGGGGG	CTCAGGATTA	CGAGGCCTGA	AGCTCCTAGA	120
GGCTAAATGC CAGGGGGATG	GAGTGAGCTA	CGAGGAAACC	ACTATTCCCC	GACCCAGCGC	180
CTACCACAAT CTGTTTGGAT	TACCACTGAT	TAATCGTCNA	GATGCTGAGG	TGGTACTGAC	240
GAGTCGTGAG CTTGACAGCC	TGGCCTTGAA	CCAGTCCACG	GGGCTGCCTA	CCCTTACTCT	300
ACCCCGAGGA ACGACCTGCT	TACCCCCTGC	CTTACTCCCT	TACCTGGAAC	AGTTCCGGCG	360
GATTGTATTC TGGTTGGGGG	ATGACCTTCG	GTCCTGGGAA	GCCGCCAAGT	TGTTTGCACG	420
AAAACTGAGC CCCAAACTCG	AG				442

- (2) INFORMATION FOR SEQ ID NO:1144:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 339 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: cDNA

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1144:

  GAATTCGGCC TTCATGGCCT ACCATCTACA GCTGTATTCT TGTTCCCTTG ATGGCACAAT 60
  TAAACTGTGG GACTATATAG ATGGCATCTT AATAAAGACT TTCATAGTTG GATGTAAACT 120
  TCATGCCCTC TTTACTCTTG CCCAAGCTGA GGATTCTGTC TTTGTTATAG TGAATAAAGA 180
  AAAACCAGAT ATATTTCAGC TGGTTTCAGT GAAACTGCCA AAATCCTCAA GCCAGGAAGT 240
  AGAAGCCAAG GAGCTGTCCT TTGTTTTGGA TTACATAAAC CAGTCACCCA AGTGCATTGC 300
  CTTTGGAAAC GAGGGAGTAT ATGTTGCGCA GTACTCGAG 339
  - (2) INFORMATION FOR SEQ ID NO:1145:
    - (i) SEQUENCE CHARACTERISTICS:
      - (A) LENGTH: 379 base pairs
      - (B) TYPE: nucleic acid
      - (C) STRANDEDNESS: double
      - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: cDNA
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1145:

GAATTCGGCC	TTCATGGCCT	AGGCCAGGGG	ACCCGGCCTC	AGGTCTGTGG	AGGTGCTTCA	60
ACAGCACGAT	GCTCATTCTC	TGTCCGTAGT	GTCTCCATAT	ACTTTCTCAT	CTTCTCCACC	120
ATCCAGGAGG	GTAGGACAAA	GGATTTCAAT	TCCTCTAGCT	TCAGATCCAG	GCATCCTCTG	180
TAATCATCAC	TGGCCGCAAG	GTCCCGGATG	TCCTCCTCGA	TGAGGAGGTA	GGCCATCTTG	240
CCCCCTGTTG	CCCGCATGTG	ATGCTGCTCA	GCCAGCCAGT	GCTTATCCTG	GGGGTCAGCT	300
<b>GCATACTTAA</b>	AGAGGTGTGG	GTGCTTGATG	TAGATTCTTC	CTCTGGTGCC	CCCCATCCCC	360
AGGGCTTTGT	TGGCTCGAG					379

- (2) INFORMATION FOR SEQ ID NO:1146:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 341 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1146:

(	BAATTCGGCC	TTCATGGCCT	AGGAAAGCTG	GGGGCAAGGA	AGAGCCTTGA	ATCTTGAGGT	60
(	GGACGTTGA	CTCTAAGATG	TCCTTGAGCA	GTGGAGCCTC	CGGAGGGAAA	GGAGTGGATG	120
(	CAAACCCGGT	TGAGACATAC	GACAGTGGGG	ATGAATGGGA	CATTGGAGTA	GGGAATCTCA	180
7	CATTGACCT	GGACGCCGAT	CTGGAAAAGG	ACCAGCAGAA	ACTGGAAATG	TCAGGCTCAA	240
1	AGGAGGTGGG	GATACCGGCT	CCCAATGCTG	TGGCCACACT	ACCAGACAAC	ATCAAGTTTG	300
7	<b>IGACCCCAGT</b>	GCCAGGTCCT	CAAGGAAAGG	AAGGGCTCGA	G		341

- (2) INFORMATION FOR SEQ ID NO:1147:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 315 base pairs(B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1147:

GAATTCGGCC	TTCATGGCCT	AGGGGGGCC	ATCTTTAATT	CTGTAAGTTC	ATGGTAAAGG	60
TATCTCCCCC	CACACTGGGG	CAGGCGGCGG	AATAAGCTCC	AGCGTTCATG	CGCCACTCAC	120
					TGTTCACCGG	180
					AACTAAGATA	240
					CACATCCAGG	300
GGTCTATCCC						
GGICIAICCC	I COMO					315

- (2) INFORMATION FOR SEQ ID NO:1148:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 473 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:

GAATTCGGCC T	TCATGGCCT	AGCTCTTTGG	GGAGCTGTTT	CAGAGGGAAA	GTGGATGAAG	60
GCTGAAGTGG AG	GGCCAAATT	AGGTGCTCTA	GTACCCTCTC	TTGGATCTCT	TTCAGCTTTT	120
ACCTGTTTTA T	ATGCTGGGA	TTTTATATAC	AACTATTTGC	AGAACTCAAC	TGCTAAAGTA	180
AAACGGTGGG G	AGGACTATT	GGATTGGGAG	ATCTCTAAAA	TCCCATTGGG	ATTGATGAAA	240
AAGAGAACTA TO	CAGCAGAAA	AGAGGAAGGG	AACAAATGAG	TTGTTAGTAC	CTTAGTTCCT	300
AATTTATGTT CO	CTTTATTGT	AGATTCTTTT	CTTGGCCACT	ACACTCCTTA	GAAATATAAT	360
TCAACACTGT TT	TCTTTTACC	ATTTTTGATG	ATATGCAAAG	TCCAGCTTTA	CTCAGCCACA	420
TTTTGTCCAC TO	GGCTTATAT	TTAATTTATA	TTTTAGGATA	CAGATAACTC	GAG	473

- (2) INFORMATION FOR SEQ ID NO:1149:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 316 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1149:

GAATTCGGTC TTCATGGCCT	ACTCTGGGTT	GCCTGTGGTC	ACTTCTGGTT	GCCTAGGACT	60
AGAAGGCTCA GATTTTCAGT	GTCGGGACAC	TCCCATTCCT	CATCAAAGAA	GATCAATTGA	120
ATGCTGCACA GAAAGGAACG	AATGTAATAA	AGACCTACAC	CCTACACTGC	CTCCATTGAA	180
AAACAGAGAT TTTGTTGATG	GACCTATACA	CCACAGGGCT	TTACTTATAT	CTGTGACTGT	240
CTGTAGTTTG CTCTTGGTCC	TTATCATATT	ATTTTGTTAC	TTCCGGTATA	AAAGACAAGA	300
AACCAGACAA CTCGAG					316

- (2) INFORMATION FOR SEQ ID NO:1150:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 232 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1150:

GCCACGAAAG	GTACCCCTGA	ATTCTGGACT	CATAAAATCT	CTTAGATAAT	ACATATTTGT	60
					GGAGGCAGAT	120
GAAATTGATG	GAGAACAATT	GCAACGAAAA	CAGAATACAC	AATGCACGAG	CCTGTGTCAG	180
GAATGACAGT	GCATTCCACG	GAAGAGTTGC	ACAGAGAGAG	ACGCCGCTCG	AG	232

- (2) INFORMATION FOR SEQ ID NO:1151:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 367 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1151:

GAATTCGGC	TTCATGGCCT	AGCCTTTAAC	ACTTGATATA	AAATCCAAGC	ATTTTTCAGA	60
CCTCAACCC	GAATAGTAGA	TACCTGAAAT	TAAGATTCCT	ATTGGTGAGA	AACAAGATCT	120
GTATATTTC	CTATCCCTAT	CCCCAAATGC	CAGTGGGTCA	TTTTCCCCAT	GCCTAGCTCC	180
ATTCACAGCT	AATATGTGGA	TTGAGGCTTT	ATTCCAAAAC	ATTTAGGTTC	TATATTCTTC	240
CCTAGCCCTC	ATTAGCAGTG	CTCATCTTTG	AAGATCATTG	TGACTTTTCA	GACTATTGTA	300
GTGATGGCT	AACCTGACCC	CTTCTCCTCC	TTTCAGGATT	TGGCAGAGAG	AACGGCCGCT	360
TCTCGAG						367

- (2) INFORMATION FOR SEQ ID NO:1152:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 391 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1152:

GAATTCGGCC T	PTCATGGACA	GCACAGTGGC	CAAAGAAGGC	ACTAATGTAC	CATTAGTTGC	60
TGCTGGTCCT 1	FGTGATGATG	AAGGCATTGT	GACTAGCACA	GGCGCNAAAG	AGGAAGACGA	120
GGAAGGGGAG (	GATGTTGTGA	CTAGTACTGG	AAGAGGAAAT	GAAATTGGGC	ATGCTTCAAC	180
TTGTACAGGG 1	PTAGGAGAAG	AAAGTGAAGG	GGTCTTGATT	TGTGAAAGTG	CAGAAGGGGA	240
CAGTCAGATT (	GGTACTGTGG	TAGAGCATGT	GGAAGCTGAG	GCTGGAGCTG	CCATCATGAA	300
TGCAAATGAA A	AATAATGTTG	ACAGCATGAG	TGGCACAGAG	AAAGGAAGTA	AAGACACAGA	360
TATCTGCTCC I	AGTGCNAAAG	GGAGTCTCGA	G			391

- (2) INFORMATION FOR SEQ ID NO:1153:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 459 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1153:

GAATTCGGCC AAAGAGGCCT	AGCACTTGTC	TCATTTTAAT	GTAAAGATTT	GCTTCCATTT	60
TCCTACAGGC AGTCTCTCTC	TTCCTCACAG	TCCCACTGTG	CAGGTGCTAT	TGTTACTCTT	120
ACGAATATTT TCAGTAATGT	TATTTTCTTC	TAAGTGAAAT	TTCTAGCCTG	CACTTTGATG	180
TCATGTGTTC CCTTTGTCTT	TCAAACTCCA	AGGTTCCCCT	GTGGNCCTCT	CCCTTACCCT	240
GGGAAGGCCT CTTGGAGACC	TTACCCCTTG	CTGTTTGGAC	TTTGTATACT	TTAAATAATT	300
TAACTACCCT TAATTACTTA	AAAAAAAAA	AAAAAAGCTT	TATGATTTTC	ATAACTTATT	360
GCTGATTTTA ATGGATTGTT	AATTTCAGTC	CTGTAGTTTT	ATTTTATGTT	TAGATAGGGC	420
TGGGCAAGGA AAAAGAAAAT	AAAGACAACC	ATACTCGAG			459

#### (2) INFORMATION FOR SEQ ID NO: 1154:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 390 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1154:

GAATTCGGCC	AAAGAGGCCT	ACTCCTTCAG	ACTACAAGCT	CCACAGAGCC	GCGGGAGGAC	60
				GCGCGCGTGG		120
GCCTCCCGGA	GAAGGATCAG	TGGTCAATTG	GTCAGGACAG	GGACTACAGA	AATTAGGTCC	180
				GATAAAAATC		240
				TCAGTAGCTA		300
				GTATTAAATT		360
TAGCATTGGC	TGTGTGGAAG	GGCTCTCGAG		•		390

- (2) INFORMATION FOR SEQ ID NO:1155:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 534 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: CDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1155:

GAATTCGGCC	AAAGAGGCCT	ACGAATGTGG	CCGGGTGGGA	CCCGGACATA	CGAGAGATTG	60
TCCTCATCGT	GGCCATGATG	ACATTGTCAA	CTTCGAGAGG	CAGGAGCAGG	AGGGAGAGCA	120
GTACCGTTCC	CAGAGGGACC	CACTGGAGGG	CAAGCGGGAC	CGGAGCAAGG	CCAGGTCTCC	180
GTACTCGCCA	GCCGAGGAGG	ATGCCTTGTT	TATGGATTTA	CCCACTGGCC	CAAGAGGCCA	240
GCAGGCACAG	CCCCAACGGG	CAGAGAAGAA	TGGAATGCTG	CCTGCCTCAT	ATGGCCCAGG	300
AGAACAGAAT	GGGACTGGTG	GGTACCAGCG	GGCCTTTCCT	CCCAGGACCA	ACCCTGAAAA	360
ACACAGCCAA	AGGAAGAGCA	ATCTGGCCCA	GGTGGAGCAC	TGGGCAAGGG	CCCAGAAAGG	420
GGATAGCAGG	AGTCTTCCCT	TGGACCAGAC	GCTTCCTCGC	CAGGGTCCTG	GCCAATCCCT	480
GTCCTTCCCA	GAAAACTACC	AGACTCTTCC	CAAGAGCACC	CGAAACGCCT	CGAG	534

- (2) INFORMATION FOR SEQ ID NO:1156:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 505 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1156:

GAATTCGGCC	AAAGAGGCCT	<b>AATGGATCTA</b>	GTCACTTTCA	GATTTCAATT	TGAGGTTAAG	60
TATATAAAGC	ACATCCCAAT	TTTATATGCT	GCCTTGAGAA	<b>AATTACAGGA</b>	TGCACGGCAA	120
TTTGTAGGAA	TTTCAAATGG	GATCATTTAA	ACATTTGAAA	AATTATTTTA	AAAACCATCT	180
AGTTTGCTTT	TGGATTTTAG	ACATTAAAGC	CTATGTTGTC	TTGTTAACAG	GGGTGGAATG	240
TATAACCATC	AGATTCAGCA	TGTGATTTCA	CCTTTGAATC	TGAGTATTTC	TTCCCTATCT	300
TCTTTGAGTC	ATTTTTGGAG	CAGACTGTCA	CCAGTATTGA	TAACTAAGCA	TTAAAGGGAA	360
AAGTTGCATT	GCAACTATGC	ATTGGTTTCC	TGGAAGAACT	TTTCTTTTGT	TTTAGTGAAT	420
GAAGAGGCTT	GATGGGATCA	CTTACTGTAA	CTCCTTCTAC	ATAAGGACCC	CTTCTGCAAG	480
CAGAACACAA	AAGAACACGC	TCGAG				505

- (2) INFORMATION FOR SEQ ID NO:1157:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 441 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1157:

GAATTCGGCC	AAAGAGGCCT	ATGTTATTGG	GAAGGACCCA	GAGAACAAAA	AGTTGAATAC	60
GGAAAAGAAA	ATAGGATTTG	CAAGAAGCAC	NTTTTTTTT	TTTTTTTTT	TTTNGAGACA	120
AANTCTCGNT	TTGCANTCCA	GCCTGGGTGA	CAAGAGCAAA	ACCTNGTNTC	CAAGNAAAAA	180
AAAATACAGT	TTTGGTGATA	ATACAGTTTG	AAAGTAATTA	GCATGTGGAT	AGTCATAGAA	240
ACCACAGGCA	TCAATGAAAC	TGGCTAGGAG	AAAGGACACC	AAGAGGAAAT	GGCCAGAGGT	300
AACAGGAAAA	TCAGGGGAGT	GTGGTTCACA	GAAGCCTGGG	AAGTGCTATT	TCAAGAAGAG	360
AGTGGGTGGA	AATTGTTAAG	TGTCTAATGC	TGCTCAGAAG	CCAAGCAAGA	TAAAGACAGA	420
AGAATCTAGT	GGGAACTCGA	G				441

- (2) INFORMATION FOR SEQ ID NO:1158:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 382 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1158:

GAATTCGGCC	AAAGAGGCCT	AGCAGAACCC	GACCAGGGGA	GCCTTGCCTG	TGTGTTTCAG	60
GTGCTCTGCG	ACCACTTCTA	TAAAACCTAA	AAAAGGAGAT	TGCTCTGATT	GCAACAGGTG	120
TGGGGGACCA	GTATCCCATC	CCATTGGCCC	TGCCCTCCCA	CCTGTAAGGC	AGAATATGGT	130
TGGGAAATCA	TTGCCATATG	CAGAAGGGGT	CACTGAGGGG	TTTTAAACAA	CAGTGACATG	240
CTCAGTTCTC	TGGGTTGAGG	CATCATCACC	CTGGTGGCCA	TGTGGAGGAT	GGACTGGAAA	300
AGGCATTCAG	TTAGAAGACC	TCTGCAGGAG	TCCAAGGAAG	AAACAGGCAA	ATCTGCAGGA	360
<b>GGCAGGCATA</b>	TCCAAGCTCG	AG				382

(2) INFORMATION FOR SEQ ID NO:1159:

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 348 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1159:	
GAATTCGGCC AAAGAGGCCT AGCCTCGGTG ATTTCCAGTG GAAGAATGTA GGTCCCAATA CCACAAGCAC AGTCATTAGC ACAGATGCTT TTAGGCCAGG AGTTCGATAT GACTTCAGAA TTTATGGGTT ATCTACAAAA AGGATTGCTT GTTTATTAGA GAAAAAAAAC AGGATACTCT CAGGAACTTG CTCCTTCAGA CAACCCTCAC GTGCTGGTGG ATACATTGAC ATCCCACTCC TTCACTCTGA GTTGGAAAGA TTACTCTACT GAATCTCAAC CTGGTTTTAT ACAAGGGTAC CATGTCTATC TGAAATCCAA GGCGAGGCAG TGCCACACCG ATCTCGAG	60 120 180 240 300 348
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 313 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1160:	
GAATTCGGCC AAAGAGGCCT AGAAAAACTG AAAAAATAAG AAACTTTAGA GAAAAAGAGG AATCAGTGCA GGCTAGGGGA ATGAACTTGG TAATCCAGTA GTCTTTCCCT GCCAGCATTT TGATTGATAAC GCTAAGTGTC TGCTTTTTCT CATCCCTTAT TTTTTGGCAG GAAACCAGTA TTTTGATACT TGAATGCCTT CTTTCTATCT TAAGGGAGAA GCCTTCTTAA ACTTCAAGTG TGAAGTAGAT CCTTTAGGTA TAGGATGAAA AATTAAGTGG GACTATTTGT GAATTACTAA ATCGCAACTC GAG	60 120 180 240 300 313
(2) INFORMATION FOR SEQ ID NO:1161:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 92 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1161:	
GAATTCGGCC AAAGAGGCCT AGGAGCCTAG AAAAGAAGAA AGGTCTATTT TTATAAA;AC TGATGAAATA CTTGTGGCAG GGAGTCCTCG AG	60 92
(2) INFORMATION FOR SEQ ID NO:1162:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 296 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1162:

GAATTCGGCA AAAGAGGCCT AGTGCATAAG GAATCACTGT GTACAAACTG GCCAAGTGCT 60
TCTGTAGATA ACGTCAGTGG AGTAAATATT CGACAGGCCA TAACTTGAGT CTATTGCCTT 120
GCCTTTATTA CATGTACATT TTGAATTCTG TGACCAGTGA TTTGGGTTTT ATTTGTACTT 180
TGCAGGGTTT GTCATTAATA ATTAATGCCC CTCTCTTACA GAACACTCCT ATTTGTACCT 240
CAACAAATGC AAATTTTCCC CGTTTGCCCT ACGCCCCTTT TGATACACCA CTCGAG 296

- (2) INFORMATION FOR SEQ ID NO:1163:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 378 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1163:

GAATTCGGCC	AAAGAGGCCT	ATTAAAAATA	AGTGTCTAAT	ACTGTGTATT	CATATAGCCT	60
TTATATCTCA	ATACGTGCTT	ATCTGTTGGT	ATACCTTAGA	GAAATAACCC	ACCATCAATG	120
AGAAGAAGGA	AAGGCAGGAG	GAAAAAAGTT	TATATAACAC	TTTAAAATGG	TAGATTATTT	180
GTGGCCATTT	GAATTTACTG	ATTTGAAGTT	CTTAAAGATG	CTGAGCCATG	CCTTACATAG	240
TTATTTTAGA	ATCTAAAGTT	GTTCTGTATT	TGCATAACGT	TTCTGTTCTT	TTTCTTCTTT	300
AAACCCTGAA	AGTGATAGAT	GGGAAGGAGG	<b>AACCAGATAT</b>	TTGGCATGGT	CTGACAAAAA	360
TTAACTTGTC	AACTCGAG					378

- (2) INFORMATION FOR SEQ ID NO:1164:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 356 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1164:

GAATTCGGCC AAAGAGGCCT	ACTCCAGGGT	ACTTTTCCCC	TAGGCCTGAC	CTTTTAGTGT	60
CTTTTTGTCC ANACATATTT	AAGACCAGAG	GAAAAAAGCA	ATTGCTTTAG	TTTCTATGTT	120
TGGGTAACAA AATCTACCCA	CAGACAAGAG	AATAACAAAA	ACCAAACAGT	ACAGTGGGAA	180
ATATACCAGA AAGGAAAAAA	AAGATCATCA	CATTAAATGT	AAATGAGGTA	AATTTTTATA	240
ATAAAGAATC TTTTATGAAG	AATGTCTCAA	ACCAAATATT	GTACTTTCCA	ATTTCTTGGG	300
CACTGGGGAT GCTGAAGTGT	AGTTAGATGA	GTATATAACC	CTATAGGGCT	CTCGAG	356

- (2) INFORMATION FOR SEQ ID NO:1165:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 357 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1165:

CAATTCCCCC	*****					
GWALLCOGCC	AAAGAGGCCT	AGTCTTCTGC	CCCCCTATGA	AGTTTGAGTT	TCAGCCCCAC	60
ATCCCCCATA	TOCOTTOCOL					00
AIGGGGGAIA	IGGCTTCCCA	GCTCTGTGCC	CAGCAGCCTG	TCCAGAGTGA	GCTGGTACAG	120
ACATOCOBAC	******				GC1001ACAG	120
AGAIGCCAAC	AACTGCAGTC	TCGCTTATCC	ACTCTAAAGA	TTGAAAACGA	AGAGGTAAAG	180
***********					UNDO I NAMO	190
AAGACAATGG	AGGCCACCCT	GCAAACCATC	CAGGACATTG	TGACTGTCGA	GC A CTTTC AT	240
				- GILCIGICON	GONCILIONI	240
GTGTCTGACT	GCTTCCAGTA	CAGCAACTCC	ATGGAGTCCG	TCAAGTCCAC	COTOTOTORA	200
				* CONG I CONC	GGICICIGAA	300
ACCTTCATGA	GCAAGCCCAG	CATTGCTAAG	ACCACACCCA	ACCAGCAAAT	Compose	
			UCCUUCA OCCA	UCCUCCUUMI.	CCTCGAG	357

### (2) INFORMATION FOR SEQ ID NO:1166:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 375 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: CDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1166:

GAATTCGGCC TTCATGGCCT AGACAGGCGG ACCCAGAGAG ACTTGCAGTA CGTGGAGAAG	60
ATGGAGAACC AAATGAAAGG ACTGGAGTCC AAGTTCAAAC AGGTGGAGGA GAGTCATAAG	120
CAACACCTGG CCAGGCAGTT TAAGGGCTAA CTTAAAAGAG TTTTTTCAAT GCTGCAGTGA	180
CTGAAGAAGC AGTCCACTCC CATGTAACCA TGAAAGAGAG CCAGAGAGCT TTTTGCACCA	240
TGCATTTTTA CTATTATTTT CCAATACTTA GCACCATTTC ACTAAGGAAC CTTGAATACA	300
ACGAGGATCC TCCTTTGCAT GCGACTGTAG CTGCATTTCA TGAATAGTTT GAACCCTTGT	360
CAATGCAATC TCGAG	375

### (2) INFORMATION FOR SEQ ID NO:1167:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 375 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1167:

GGCTTATTGA	TGACTCTTAT	TTTAATTATG	TTTTTAGCAA	TGATAAGTTA	CAATATAATA	60
GCTGGAGATA	CTTTGAGCAA	AGTTTTTCAA	AGAATCCCAG	GAGTTGATCC	TGAAAACGTG	120
TTTATTGGTC	GCCACTTCAT	TATTGGACTT	TCCACAGTTA	CCTTTACTCT	GCCTTTATCC	180
TTGTACCGAA	ATATAGCAAA	GCTTGGAAAG	GTCTCCCTCA	TCTCTACAGG	TTTAACAACT	240
CTGATTCTTG	GAATTGTAAT	GGCAAGGGCA	ATTTCACTGG	GTCCACACAT	ACCAAAAACA	300
GAAGACGCTT	GGGTATTTGC	AAAGCCCAAT	GCCATTCAAG	CGGTCGGGGT	TATGTCTTTT	360
GGGGACGTTC	TCGAG					375

#### (2) INFORMATION FOR SEQ ID NO:1168:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 552 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1168:

GAATTCGGCC	TTCATGTCTC	TGCAATCTGA	AAATAGTGCC	TTTTACCAAG	AAGAGGACAG	60
AATTGGCGTT	TGGAAGGCTG	AGGGTCATGG	TGTAAGGGCT	TTTGAGTCAA	AATCTTGGTG	120
TCAAGCAGAT	GAGGCTGCAA	CACAGACCTG	TGACCAAACT	TGTGTGGAGC	GTGTGGTGGA	180
CACGCAGGGG						240
CCCCGATGGC	AAGTCTCCCA	GTCAACTCCA	GATCTCTTCA	CAGTAACTGT	GTTTCCTCCG	300
CATTTATTTT						360
GAGGGTGAAA	TATGTGTGAA	GAGTTCAGTC	AGTGTGTCAC	GAGACCAGCT	GAGTGACCCT	420
CAAAGGTTAG						480
GATGACATAG	AGACTGTCAA	GTCAGATTCT	AAAACAACCT	ATGAGTGGGA	AACAGGNACA	540
CAAAAACTCG	AG					552

#### (2) INFORMATION FOR SEQ ID NO:1169:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 566 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1169:

GAATTCGGCC TTCATGGCCT	AGAGCGGAGT	AAATTCTCCA	CAAGCTGGGA	ACAAACCTCG	60
TCCCAACTCC CACCCACCGG	CGTTTCTCCA	GCTCGATCTG	GAGGCTGCTT	CGCCAGTGTG	120
GGACGCAGCT GACGCCCGCT	TATTAGCTCT	CGCTGCGTCG	CCCCGGCTCA	GAAGCTCCGT	180
GGCGGCGGCG ACCGTGACGA	GAAGCCCACG	GCCAGCTCAG	TTTTCTTCTA	CTTTGGGAGA	240
GAGAGAAAGT CAGATGCCCC	TTTTAAACTC	CCTCTTCAAA	ACTCATCTCC	TGGGTGACTG	300
AGTTAATAGA GTGGATACAA	CCTTGCTGAA	GATGAAGAAT	ATACCATATT	GAGGATATTT	360
TTTTTCTTTT TTTTTTCAAG	TCTTGATTTG	TGGCTTACCT	CAAGTTACCA	TTTTTCAGTC	420
AAGTCTGTTT GTTTGCTTCT	TCAGAAATGT	TTTTTACAAT	CTCAAGAAAA	AATATGTCCC	480
AGAAATTGAG TTTACTGTTG	CTTGTATTTG	GACTCATTTG	GGGATTGATG	TTACTGCACT	540
ATACTTTCA ACAACCAGAA	CTCGAG				566

- (2) INFORMATION FOR SEQ ID NO:1170:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 347 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1170:

GAATTCGGCC	AAAGAGGCCT	AGGGAGTCAA	TCATGATCNT	TTCATATATG	CTGGCNATAG	60
AAAATGGTCT	CGGTGAAGTA	ATGGTCTGTC	TGTCAAGCAT	GACATCCTTG	CCTGTGTTAA	120
GTTTTTGTTG	CTCTTCTGGG	ATGTTGATCG	TGACGTCTTG	TCCGGGATTG	AGAAGCTTCT	180
GTTGCTCTTC	TGGGATGTCA	TTCATGATCT	CTTCATATAT	GCTGGCTATA	GAAATTGGGC	240
TCTGTGAAGA	AATAGTGTGT	CCAAAACCTT	GGTACAGGCC	CCCTGGGGAG	GGTACCTTTG	300
AAGAACCAGA	AGTTAGATCT	TGTGAAGAAG	AAGAAAGTAG	GCTCGAG		347

- (2) INFORMATION FOR SEQ ID NO:1171:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 338 base pairs

(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1171:	
GAATTCGGCC TTCATGGCCT ACTTTTTGGG GACTGGTACT GGAGAAAAAT CTGAGAGCAA	60
AAGTGCTTGG CTAAATTCCC TTTTTTTTCT TTTAGTTTTT GAAATCATGA ATCCTGTTTA TAGTCCTGGA TCTTCTGGGG TTCCCTATGC AAATGCCAAA GGAATTGGTT ATCCAGCTGG	120 180
TTTTCCCATG GGCTATGCAG CAGCAGCTCC CTGCCTATTC TCCTAACATG TATCCTGGAG	240
CGAATCCTAC CTTCCAAACA GGTTACACTC CTGGCACACC TTACAAAGTG TCCTGTTCCC CCACCAGCGG GGCTGTGCCA CCGTACGTCC CCCTCGAG	300 338
(2) INFORMATION FOR SEQ ID NO:1172:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 294 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1172:	
GAATTCGGCC TTCATAATCT CCTGCTCTTG AGAATGTGCC GATATGTCAA AATATCTACT	60
GAAACTGAAG AAACTGAAGG ATCCCTACAC TGCTGTAAGG ACCAAAATAT TAATGGGAAT	
GGCCCAAATG GCATACATGA AGAAGGCTCA CCAAGTGAAA TGGAAACAGA TGAGCCAGAT GATGAATCCA GCCAGGATCA AGAACTTCCC TCAGAGAATG AAAACAGTCA GTCTGAAGAT	180 240
TCAGTTGGAG GAGATAATGA TTCTGAAAAT GGATTATGTA CCGGGATACT CGAG	294
(2) INFORMATION FOR SEQ ID NO:1173:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 286 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1173:	
GAATTCGGCC TTCATGGCCT ACATAAAAGA ACGAAAAGGA AGGAACTTCA GTCAACATAT	60
TTTCATTGAC TCCTTAGTAC AAGGGAACCT TAATGACCAA CAGATCCTAG AAGACAGTAT GATATTTTCT CTGGCCAGTT GCATAATAAC TGCAAAATTG TGTACCTGGG CAATCTGTTT	120 180
TTTAACCACC TCTGAAGAAG TTCAAAAAAA ATTATATGAA GAGATAAACC AAGTTTTTGG	240
AAATGGTCCT GTTACTCCAG AGAAAATTGA GCAGCTCAGA CTCGAG	286
(2) INFORMATION FOR SEQ ID NO:1174:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 421 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1174:

GAATTCGGCC TTCATGGCCT AAATATGAAA AGACTAGACA TACAGAGATA TTTATCATAG
CAAAAAGTTG CAAGTACTGG GGATTGACAA AATTATCACA ATGGTTATAT TATTATTATT 120
ATTATTATTA TTATTTAATC AATCAGTGTC TTGCTTTGTT GCCCAGACTG GTTTCAAATC 180
CCTGGCCTCA CGTGATCCTC CCGCCTCAGC TTCCCAAATT GCTGGGGATTA CAGGCATGAA 240
CCACCGCGCC TGGCCTATTG TTCTGCCACA TCTTTCTTTT ATTTTTGAGA GAGAGTCTTG 300
CTTAGTCCAG GCTGGAGTAG AGTTGTGCCG TCATAGCTCA CTGCAGTCTC AATTTCTTGG 360
GCTCAAGCAA TCCTCCTGCC TCAGCCTCTT GAGTAGCTGG GAATACAGGC ACACTCTCGA 420
G

- (2) INFORMATION FOR SEQ ID NO:1175:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 339 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1175:

GAATTCGGCC	TCATGGCCTA	GTGCTTAAAA	GCTGTTCTCA	TAAGAATTCT	ACTGGCCTGT	60
ATCTACCCAA	CCACTTTCTA	TACCTCTCTT	CCAACCAAAA	GTCTTAATAT	GGGAATATCC	120
CTCACCACGA	TCCTAATACT	GTCAGTAGCT	GTCCTGCTGT	CCACAGCAGC	CCCTCCGAGC	180
TGCCGTGAGT	GTTATCAGTC	TTTGCACTAC	AGAGGGGAGA	TGCAACAATA	CTTTACTTAC	240
CATACTCATA	TAGAAAGATC	CTGTTATGGA	AACTTAATCG	AGGAATGTGT	TGAATCAGGA	300
<b>AAGAGTTATT</b>	ATAAAGTAAA	GAATCCAGGT	GCACTCGAG			339

- (2) INFORMATION FOR SEQ ID NO:1176:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 418 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1176:

GAATTCGGCC	TTCATGGCCT	AGGGTCACCG	GGTTCCGGGC	TAAAGAAGCC	CCCGCGCTCC	60
CTAGAATCCA	GGAACGGGGA	CTGGCAGAGG	CCTGGGTAGG	AGTCCATTGG	GCTGCTGGAG	120
GGCAGATTGC	CCAAAGGGAG	TCCACCTTGA	AGAAAGGGCC	TCTGCAGTGG	CGTACGGCTG	180
CCTTNTAGGC	CAGGGGTTCC	ACAACCCAGA	TGCTGTTCTC	GTTCAGAGCC	CAGAACATCC	240
TTGAAGAGCT	GCTGCAGGTC	CTTGGATTCC	ATCTTGGGCA	GTTCTCTGTG	GAAATCCTGT	300
CTAAGTCAGA	GCTAAGCATC	CCTTCACCTG	GGGTGCCTGG	CTTCTCAGGG	TCACTGGGCA	360
CTGGGGATGC	CTTCACGCCC	CCATCCTCAG	GTCCTGGTGT	ATCGGCTTTG	CCCTCGAG	418

- (2) INFORMATION FOR SEQ ID NO:1177:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 433 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1177:

GAATTCGGCC	TTCATGGCCT	AAAGAACCCC	GTGGTGATGG	TGGACGAGAT	TATGAGCTCC	61
				TCATGATCAC		120
GGACCTAGGA	CCCGACTACG	GATGGCCAGC	AGGATCATCA	TTAATGAGCG	GCAGAGACTG	186
ATCAACTCGG	CCAATGGTGT	GAGCAGTAAG	CCGCTTCAAA	ACGGGAGGCA	CGAGAACATT	240
GAGAACGGGA	ATGTTCCTGT	GGAAAACCCC	GAAGACCCTC	AGCAGAATCA	GGAGCAGCAG	300
CCGCCGCCAC	AGCCACCACC	GCCAGAGCCA	GAGCCGGTGG	AGGCTGACTT	CCTGTCCCCC	360
TTCTCCGTGC	CGGGCTGGAG	TGTAGTGGCA	TGATCTCCGC	TGACTGCAAC	CTCCGCTTCC	420
CGGGACTCTC	GAG					43:

- (2) INFORMATION FOR SEQ ID NO:1178:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 370 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1178:

GAATTCGGCC	TTCATGGCCT	AGTTGTTGTA	AGCATATTTA	TGGTAATTTG	TTACTGCACC	60
CTTGGGAAAC	TAACACACCA	AGGTTCATGG	ACAGCATGAA	AAAGAAAAAC	CATAGGCCAA	120
TATTTGTTAG	GAAAAGACAC	AAAAGATCTA	AACAAATATT	AGCTCCTACC	CCTCCAAAAA	180
AGCAAATTCA	ATCCAGTAAG	GCATTTGAAA	AATATGTCAT	GACTAATGAA	CTTATTTAAG	240
TTTACCCCAC	AATACAAGGA	TGGTTTAAAT	TTTACAAAAA	GTATTCATTT	AATTCATCAT	300
ATTGATAAAG	GAGGAAATTT	AATTAAGATA	ATCTCTTGAT	TGTCTCTTCA	TATCTTTTGA	360
TTATCTCGAG						370

- (2) INFORMATION FOR SEQ ID NO:1179:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 305 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1179:

GAATTCGGCC	TTCATGGCCT	AAAAAATACA	AAAAAAAAAC	NNNANNGAAG	AAAAAAGAAA	60
AAACTACCAG	CCTGAAAATG	CATAGTGTTT	GCTACCTTAT	TGCTTTTAGC	ACATCTAGAA	120
AGACACTAAA	CCCAGTGAGA	TTGCAAGTTT	CAAAATATTG	TGTTGTATAT	GGCTTTGCTT	180
AAACGGATAT	ATTTGTTTCT	GAGTGAAAAC	TTTTTACGTA	GAGGTTTATT	TGTAGAGGCT	240
TGTAAACTTA	AGTGTAAGTT	TTAGTGTGTG	TGTTAAGTTG	TTCTTACCCC	GCATTAGCAC	300
TCGAG	•					305

- (2) INFORMATION FOR SEQ ID NO:1180:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 605 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1180:

GAATTCGGCC	TTCATGGCCT	AGCTGGGAGG	TGTAGGTTGT	AGCGAGCCGA	GATCACGCCA	60
CTGCACTCCA	GCCTGGGCAC	TATTGAGCAC	TGAGTGAACG	AGACTCCGTC	TGCAATCCTG	120
GCACCTCGGG	AGGCTGAGGC	TGGCGGATCA	CTCGCGGTTA	AGGGCTGGAG	ACCGGCCCGG	180
CCAACACAGC	GAAACCCCGT	CTCCACCAAA	ACCAGTCAGG	CGTGGTGGCG	CGTGCCTGCA	240
ATCGCAGGCA	CTCGGCAGGC	TGAGGCAGGA	GAATCAGGCA	GGGAGGTTGC	AGTGAGCCGA	300
GATGGCAGCA	GTACAGTCCA	GCTTCGGGCT	CCGCATGAGA	GGGAGACCGT	GGAAAGAGAG	360
GGAAACCGTG	GGGAGAGGGA	GAGGGAGAGG	GAGAGGGGAG	CGATTCTGGT	GTATCTTAAC	420
TTGGATTTCT	ATCCTGTTTG	GGTTTGCTCA	GCTGAATCTA	TAGGTTTGTG	TATAATACCA	480
AAGTATTTTG	TATTAGTGGT	TACAACGCAA	AGTTGGATCG	TGAAGTCAAT	TTTGTGGCTT	540
	TTATGATTGG	TTTTTAATAG	AATAGAAAAT	GAAAATATAT	CCCAGGTATC	600
TCGAG						605

- (2) INFORMATION FOR SEQ ID NO:1181:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 444 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1181:

GAATTCGGCC	TTCATGGCCT	AGGAGAGTGG	TGATGGTGGC	ACAACAATGT	GAATGTAATT	60
AATGCTACTG	AGTTGTATGC	TTAAAAATGA	AAAATTTTAT	GTTATACACA	TTTTATGACA	120
AAAATTAATA	GATGTATTAA	TAAGATTAAA	TGGGTTGTTT	TAATGTTCTG	TTAAAATCAA	180
ACGCTGAGGG	CATTAATAGA	GATTCTTATT	TACCCACATG	TCCTTTTAAA	ACAAGAACCC	240
TCTTTAATAT	GTGTTTTCTT	CTGGTTTATA	GAACATATTT	TAAAACGGGC	TTACTATTCA	300
ATAATATCAA	TTGATTATTG	AGGAATACAA	GTTAATTAAA	TTGTGCAAGT	CAGTTGTTTG	360
GCCTTACTTC	ATGCTTTTGG	TGAACACTGA	TGCAGTACTA	GAATTACTCT	TTTTGATAAA	420
TTGCCAAAAG	CAGGCCACCT	CGAG				444

- (2) INFORMATION FOR SEQ ID NO:1182:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 276 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1182:

GAATTCGGCC	TTCATGGCCT	ACTGTTTCAA	AAAAAAAAA	AGGAATCCAA	AGAAAAAAAT	60
ACATCACCTG	CAAAAGGTGA	AGAGAGAAAG	GAAGCTTTTT	CTCTAAAAAT	GGTGCAGCTA	120
TCCTCTGAAC	CAATTTCCTT	CGGTTTAATG	TACCTGTATC	TTGGGGTTTT	TTTCCACTTA	180
ATTTATCCTG	GAGCTCTTTC	CATAACAACA	CTTGGAAAGC	ACTCTCATCC	TTTTTTCACT	240
GCTGAACAGA	ATTCCACTGT	GCGGATGGAA	CTCGAG			276

- (2) INFORMATION FOR SEQ ID NO:1183:
  - (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 291 base pairs

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1183:

GAATTCGGCC	TTCATGGCCT	AGCATGTTGA	GATAACTTCT	GGGATTAAAA	TAGTCTTTTG	60
CTTTACTTTT	TTGGTTTCCT	AAAACAACTT	TATTGACTTT	TAGTCCATAC	TGTTATATTT	120
TTGTCTTAAA	GAAAATTTAA	ACTACAAATA	CCAAAAGAAA	ACATTTTAAA	TTTAGGGATG	180
AGACTTTGGT	GTATCGTGGG	TCTAGGTTTA	ATGAACACAT	CTGGGGTTAA	GTTGGCATTT	240
				AAAATCTCGA		291

- (2) INFORMATION FOR SEQ ID NO:1184:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 364 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1184:

GAATTCGGCC TTCATGGCCT	AAGGGGAGGC	AGAGGCTGTA	GTGAGCCGAG	ATCGCGCCAC	60
TGTACTCCAG CCTGGGCAAC	AACAGTGAAA	CTCCGTCTCC	AAAAAAAAA	AAAAAAAAA	120
AAAACTTGTT TTCCCTTTGT	AATTTGGTTT	TCCTAAAAAT	TTTAGTATTT	CTAGAGAACA	180
TTTTTTTCCC AGGCTGTTAA	CTGGTTCTGA	AAACAATCTT	ACAGTAAGTA	TAATTTAAAA	240
CATACCTCCT TTTCCAAAAG	CTCATTGTGT	ACCAAGCAAG	CACGTCTGTA	GTTAAAATTT	300
GTTACTGAGG TTGGTTCAAG	GTAAGAAGAA	TGGAGAATAT	TTACAACATC	TTCAAATTCT	360
CGAG					364
					202

- (2) INFORMATION FOR SEQ ID NO:1185:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 384 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1185:

GAATTCGGCC TTCATGGCCT	AGAGTAAAGG	TGGGATTACA	GGTGTGTGCC	ACCACGCCTG	60
GCTAATTTTT TTGTATTTTT	AGTAGAGACA	GGGTTTCACC	ATGTTGGCCA	GGCTGGTCTT	120
AAACTCCCGA CTTCAAGTGA	TCTGTCCACC	TTGGCCTCCC	CAAGTGTGGG	ATTACACGTA	180
TGAGTCACCA AGCCCGGCCT	GTATCCTTTA	TTAAAAGAAA	CAAACAAACA	AACAAAAAAC	240
CCTTTTCTTG ACTGACATCC	CTTTTCAGCT	GCAGCCCTGT	TTCTTTGCTA	CCTTTGTAGC	300
AAAATTCACT AGGTTGTTCC	TACTTGCTGT	TTCCAGTTTT	TTGGTTTTTT	TCCTTTCCTA	360
GGAAATGAGA GGCCCATGCT	CGAG				384

- (2) INFORMATION FOR SEQ ID NO:1186:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 344 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
  (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1186:

CTCGAGGGGG	TCAATTCCTG	GGGGCTCTTG	ATATTGCTCA	GAGCTCTGGA	GAAGTGTTCA	60
TCCACTACGC	TGCTGATGTC	CCCTTGGAAG	TAGGTGAAAA	GGACACACCG	GGAATTCCAT	120
TCCGTCTTTA	TAGGCTTCTG	TTTGCCTTTG	GGCAGCCGGA	TGGCAGTCTT	CTTCATTTCT	180
TCCATTGTGA	GTGAATGACA	CAGGTGACAG	CTCTTAATTC	TGGACCATCA	CCTGATTCTG	240
TGGCTGGGAA	AAGATGGCCA	GAGCTGCCTG	GCTCACTTCA	GAGCAGGTTA	GTGCTTGCGG	300
AAGCAGGAGC	TGAGGATTTG	TACTAGGCCA	TGAAGGCCGA	ATTC		344

- (2) INFORMATION FOR SEQ ID NO:1187:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 0 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1187:
- (2) INFORMATION FOR SEQ ID NO:1188:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 394 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1188:

GAATTCGGCC	TTCATGGCCT	AGCGATGGCT	CACATCAGCA	CTTTGGGAGG	CTGGGGCAAG	60
AGCATCACCT	GAAGCCAGGA	GTTCAAGCCC	AGCCTCGGCA	ACACAGTGAG	ATCTCATCTC	120
TACAAAAAAT	TTAAAAATGA	GTTTGGCGTG	GTGGTACATA	ATCGTGTAGT	CCCTGCTACT	180
TGGGAAGCTG	AGGCGGAAGG	ATCACCTGGG	CTCAGAAGTT	CAAGGCTGCA	GTGAGCTATG	240
ACTGCACCAC	TGCACACCAG	CGTGGGTGAC	ACAGTGAGAG	CCTATTAAAA	AAAAAAACAA	300
AACCAATAAA	CCAAACAAAC	AAAACCTAAA	ATACAAAAA	TTAGCTGGGC	GCAGAGGCAC	360
GGGCCTGTAG	TCCCAGCTAC	AAAGAAACCT	CGAG			394

- (2) INFORMATION FOR SEQ ID NO:1189:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 355 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1189:

GAATTCGGCC	TTCATGGCCT	AGGAGATGTA	CCTGATAGCA	ANTTACTGCN	TCTCAGCTCA	60
AAATTCACCC	TTCAAAACCT	TTTCTACACC	AATGGATAGA	ATTCCTGTCA	GCATTTCTCT	120
TNNAACGTTG	AACACAATGT	TAAGCTTCCT	CAGTGAAGGA	CCCTAGATGG	ACATTGCAGG	180
AAGAAGGGAC	TTCCCCTGTT	GGACCTAGAG	GTTGTACCAG	CATTGTAGGT	GGGAGGACAT	240
CCACTGGCTC	TTTGCAATAG	CCATGTGTCC	ATAAAGTATA	GTTTCTCAGC	AATCTCATTG	300
CCCAGTCTAG	GCNTGGCAAT	CACCCTCCTG	CAGCCTTATC	AACACATTGC	TCGAG	355

- (2) INFORMATION FOR SEQ ID NO:1190:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 451 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1190:

GAATTCGGCC TTCA	TGGCCT ACTTGGAGAG C	CCTCATGCCG TCTC	TACCTT CGCACACTY	GG 60
TCAAGTATCT GCTG	SAGCTTC TTGGCCGCAA G	GATGCAGAA ATAG	GCTGAG GGTCCATG	3G 120
AAGAAAGACA CAAT	GAGGCA GTAGGAGGTG G	GAAGAAAAG AAGA	CAGACT TTCAAAAT	GG 180
AATTAGGCAC TGGG	GAGAGA TCAGTTTCCC C	CACATCAGGG AGAA	GAAGGT ATAGGTGG	GG 240
AAGGGGGTGG CCAG	GAGCAG AAGGAAGAAG A	ACTCAAGATG GAAA	GGGAGC CGCTGTGC	<b>T</b> 300
GTGGCAATAC CACT	TGGAGA GGTCGACTTC A	ATACCTTCAA GCCT	TTTCCC CTGGGCTT	TT 360
GATTGTGTCT GTGC	CCCCTT TCTTGTCCTC 1	CTGCAGATG CCCA	GTAGGG GCTACCTC	AT 420
CCTCGTGCTG TTCT	TTGTGTA GCATTCTCGA G	3		451

- (2) INFORMATION FOR SEQ ID NO:1191:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 338 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1191:

GAATTCGGCC	TTCATGGCCT	AACAGAGATG	GCTTAGACTT	CAAGACTTGA	TTTGTAGCTA	60
TGTTCTACCA	GCCTCCAGCT	GTCTATGCGT	TGGCCTCACG	CATGTCCCAA	ACGTGGTCCC	120
ACACATGTTT	ACACATTGGT	CCCACATATG	CTGAGAGTAA	TTACTTTCTA	TTCATCAGAG	180
GTCAGAATAG	AATAAAGAAT	GTTTATGTCA	TAGTATGACT	TTTTAGGTGA	TTTTGAAAAG	240
CAAGAATATG	AATTCTATGA	AAAAAATCTA	TTAGGAAATT	ATGGAAATGA	CAGAATGCAG	300
AGGTATTTGG	AAATAGAAAA	AAAACGGGTG	ATCTCGAG			338

- (2) INFORMATION FOR SEQ ID NO:1192:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 322 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1192:

GAATTCGGCC TTCATGGCCT ACCGACCACA TTTCACTCTC ACCGCTGTAG GAATCCAGAT	60
GCAGGCCAAG TACAGCAGCA CGAGGGACAT GCTGGATGAT GATGGGGACA CCACCATGAG	120
CCTGCATTCT CAAGCCTCTG CCACAACTCG GCATCCAGAG CCCCGGCGCA CAGAGCACAG	180
GGCTCCCTCT TCAACGTGGC GACCAGTGGC CCTGACCCTG CTGACTTTGT GCTTGGTGCT	240
GCTGATAGGG CTGGCAGCCC TGGGGCTTTT GTTTTTTCAG TACTACCAGC TCTCCAATAC	300
TGGTCAAGAC ACCGCACTCG AG	322
(2) INFORMATION FOR SEQ ID NO:1193:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 396 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1193:	
CTCGAGGGGT GCTGAGCATT TTTTTCATGA ACCTGTGGTC ATTCATATGT CTTCTTTTGA	60
GATGTGTCTA TTCAGGTCCT TTGCTTATAT TTTAATCAAG TTATTTGTTT ACTATTGAGT	120
GAAAGAGTTC TTTATGTATT TTGGTTATTA GCCCCTTAAC AGATATATGT ATAGCTTGCA	180
AAATATTTTT CCCAGTCTGT GGGTTGTCTC TTCAATTTGT TAATTCTTTT TTTTTTTTT	240
GTTGCTGGGC AGAACGTTTT TAGTTTGATG CAATCCCATC TGTCTATTTT TGCTTTTGTT	300
GCCTGAGCTT TTGGGGTCAT AGCCAAAAAA TCCTTGCCCA AACAGCAGTG TTATGGAGCT	360
TTTCCCCTAA GTTTTTAGGC CATGAAGGCC GAATTC	396
(2) INFORMATION FOR SEQ ID NO:1194:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 302 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1194:	
GAATTCGGCC AAAGAGGCCT AGGTAGGGAA TGCAAGCAGG CACTGGGGAG AAATNGGGCN	60
GGAAAGTAGT CTCATGGAAT AAGCCTTTTT TACTTTAATT CAGCATTTAT TGCTTTGATT	120
AAAAAATAAT TTCAAAAATC TTTCTGCTTA CTGAATAAAG AATGCNTTGG AAAGAACAAG	180
AATGGATAAA GGAGAGTGCT TAGGAGGCTC CTGGAGCAGG AAGAGGTGGT GGCGAATAGA	240
CTACCGGAGC AGTGGAGGGT GGAGATGGAG AGACGTGGAA AGACTGAAGA CATATCCTCG	300
AG	302
(2)	
(2) INFORMATION FOR SEQ ID NO:1195:	

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 377 base pairs

  - (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1195:

GAATTCGGCC AAAGAGGCCT ACTCAGAAAC ACAAGGGAAA GGACAGAAGA GGGACCGGGG

60

AGGAAGAGAG	TGAGGAGAGA	GGTATGTAAG	GTGTTTAGTA	CACAGTAAGT	GCTCAAAATG	120
TGTCCACTCC	CTCTGCCAGG	AGAGAGCAGA	AAGTCAGAAA	GGAGAGGACA	CCAATAGAGA	180
GGAAAGAAAG	GGGCCAGGCG	CCGTGGCTCA	TGTCTGTAAT	CCTAGCACTT	TGAGAGGCAG	240
AGGTGGGAGG	ATCGCTTGAG	CCCGAGAGTT	CGAGACCAGC	CTGGCCAACG	TAGAGAGACC	300
CTGTCTCTAC	AAAAAATACA	AAAATTAGGC	TGGGTGCGGT	GGCTCATTCC	TGTAATTCCA	360
GCACTAGGGA						377

- (2) INFORMATION FOR SEQ ID NO:1196:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 341 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1196:

GAATTCGGCC	AAAGAGGCCT	AGTGTTACAC	AGCACTCACA	CTAAAGATGA	AAAATTCCAT	60
TAGCTCATCC	TGGTTCTTCT	GCTTACTTAC	CTAATCATCT	GTTTATGATT	TAAAAAAATA	120
GGGTTACTGT	GAAGAGAGTG	CTTGTGTGTG	AGACAGAGAG	GGAGGGTTGT	TTTTCAAATG	180
TATAGAATAT	ACCAATGTAG	TTTTTGGTTG	GGTATTTTTT	TAAATCATGA	CTTTATTAAA	240
TTTACTTAAT	TAATATTCAT	TTTTATCCTT	TTTTTTATGTT	TTTAAAGTTT	TTATTATTTA	300
TTAATTTATT	TGAGATAAGG	TCTTGCTCTG	TCACCCTCGA	G		341
	TAGCTCATCC GGGTTACTGT TATAGAATAT TTTACTTAAT	TAGCTCATCC TGGTTCTTCT GGGTTACTGT GAAGAGAGTG TATAGAATAT ACCAATGTAG TTTACTTAAT TAATATTCAT	TAGCTCATCC TGGTTCTTCT GCTTACTTAC GGGTTACTGT GAAGAGAGTG CTTGTGTGTG TATAGAATAT ACCAATGTAG TTTTTGGTTG TTTACTTAAT TAATATTCAT TTTTATCCTT	TAGCTCATCC TGGTTCTTCT GCTTACTTAC CTAATCATCT GGGTTACTGT GAAGAGAGG CTTGTGTGTG AGACAGAGAG TATAGAATAT ACCAATGTAG TTTTTGGTTG GGTATTTTTTTTACCTTAAT TAATATTCAT TTTTATCCTT TTTTTATGTT	TAGCTCATCC TGGTTCTTCT GCTTACTTAC CTAATCATCT GTTTATGATT GGGTTACTGT GAAGAGAGTG CTTGTGTGTG AGACAGAGAG GGAGGGTTGT TATAGAATAT ACCAATGTAG TTTTTGGTTG GGTATTTTT TAAATCATGA	GAATTCGGCC AAAGAGGCCT AGTGTTACAC AGCACTCACA CTAAAGATGA AAAATTCCAT TAGCTCATCC TGGTTCTTCT GCTTACTTAC CTAATCATCT GTTTATGATT TAAAAAAAATA GGGTTACTGT GAAGAGAGTG CTTGTGTGTG AGACAGAGAG GGAGGGTTGT TTTTCAAATG TATAGAATAT ACCAATGTAG TTTTTGGTTG GGTATTTTTT TAAATCATGA CTTTATTAAA TTTACTTAAT TAATATTCAT TTTTATCCTT TTTTTATGTT TTTAAAGTTT TTATTATTTA TTAATTTATT TGAGATAAGG TCTTGCTCTG TCACCCTCGA G

- (2) INFORMATION FOR SEQ ID NO:1197:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 363 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1197:

GAATTCGGCC	AAAGAGGCCT	ACAGAAATTT	AAATTAATCT	CTCATCCATT	GGCTTTTGCT	60
ACTTTAGGTT	AATATTAAAA	TATAACATAC	ATTTTTGGGG	TTTATGCTGT	TAGCTCCAAA	120
CCAAAAGATT	TTGGAAATTT	ATTTTGGAAA	TTTTGTGTTT	AGAATATGAA	TAAATCTGCT	180
TATTCAGAAA	AATTAAACCT	TGATAACTTG	GGACCTCCTA	TTCCTGTATG	TTCTCTGACA	240
TACATTGAGG	GATTTGGCTC	TCTTTTGTTT	ATTTGTTTTA	CTAGTCAGAC	ATTCCTTTGG	300
CTGCCCATAC	TTAATTCTGT	TGGGTGTTTC	CGCCCCCGCC	CTCAGCTTCT	GAAGCTACTC	360
GAG						363

- (2) INFORMATION FOR SEQ ID NO:1198:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 169 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1198:

GAATTCGGCC AAAGAGGCCT ACCTGACAAG TGTTAAGCAG ACACATAGAG AAAGTTAAAA

TTTGTTTTGA GTCCTTAAGA GTGAAGTTAA GGAATAAGAC CTATAAATGG ACACCATGTG

ATGAGTGCTG TCATCAAAGC ATGGACAATG GGCTTTGAGA GTACTCGAG

120

169

(2) INFORMATION FOR SEQ ID NO:1199:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 82 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1199:	
GAATTCGGCC AAAGAGGCCT ATAAAAACGT TATGTTATTT TTGGAAGTTT TTCTCATATC TCTGTTGCCA GGGTCACTCG AG	60 82
(2) INFORMATION FOR SEQ ID NO:1200:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 349 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1200:	
GAATTCGGCC AAAGAGGCCT AAGGTGGTGC AGTGGGGACA GCACCTCCGA CCCTATGGGG TGTACCTTCA AGTAGCAAGG CTGACAATGA TGTCTAGAAA GGTCTCCACT TCTGCCTGAG TTTTGCCAAA CCCAGTGGTC TATAGGGATG TGGCAAAAGA ATGACCTACC GCAGTGTGAT TATCAGTGTT TTTTAAAATA AAGAGCACAG TTTTGCCTTT AAAATAATTC ACATCAACGG TATTTGGGAG AACATGGAGC TGGCATAACA TTGGCGTAGA AAGCAGGGCC AGGCCCACCC ACGGGGCCCT CGTGTGGGGA CGGGTGCCTG AGCCCCTGAG CCCCTCGAG	60 120 180 240 300 349
(2) INFORMATION FOR SEQ ID NO:1201:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 318 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1201:	
GAATTCGGCC AAAGAGGCCT AGGGGAAGAG GTTCAAATGT GGGGCTGGAC GTGGCCTTGG GGTGCGGATC CCTCACAAAN ANTTCGTCTT CATAATCTTN ATGAGGTNGC GGGGAGTCCC GCAGGACAGA CTCAGATATT CGGAGGGAGA TCCTCCCTGG AGTGCTCGGG GCCCCAAGAG GTGTGTCTGG GTCAGAAGTG CTGCATAAAC TTGGAAGACT CTGCTGTTTT TGATAGTGCT TCAGGTTTGC AAAATCAGGG GCTGAGGATT CCTCAGGAAG GNTGTCCTCT CTGGCTGCGT GGGCCCCACTT TGCTCGAG	60 120 180 240 300 318
(2) INFORMATION FOR SEQ ID NO:1202:	
(1) SPONENCE CHARACTERISTICS	

- (A) LENGTH: 293 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1202:

GAATTCGGCC AAAGAGCCCT A GTCATAAACA AGAAAGAACT G CAATTTGTGG AATTCTTGAT T ATGAAATTCA AATGAGATCT T	AAATCCTGG ATATTGAAG	TGCATATTGG ACCAGCAAAA TTAATTGTGT	AGCGATCTAA GGACATTAGT CAGTGTACAT	AGAAGTATTA GGGAAAATTG TTCCTGGTTT	60 120 180 240
ATGAAATTCA AATGAGATCT T	TATATTGAAG	TTAATTGTGT	CAGTGTACAT	TTCCTGGTTT	240
TCATAATTGC AAGTGATTAT G	TAAGGTTTG	TTAATATTGG	GAGCAACCTC	GAG	293

- (2) INFORMATION FOR SEQ ID NO:1203:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 306 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1203:

GAATTCGGCC						60
AGAACAGTGC	CTGGCACATA	AACACTCAAT	AAATGTTAAT	TGATACTATA	ATTTATCTAA	120
TTTATCTTTA	TTCCTCCTGC	AAAGATTCCT	TGGACTATTT	AGAATCTCTG	GTCACTCTAA	180
TGAGATGGTG						240
CAGCTGTAAT	TTACTGCTAA	ATAATCTCTT	GTAGTTATTA	TTTTCAGTCT	ACTTGGGATC	300
CTCGAG						306

- (2) INFORMATION FOR SEQ ID NO:1204:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 598 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1204:

GAATTCGGCC	TTCATGGCCT	ACGAGATAAT	ACTGGAGTCA	ACTGTACATT	AACTTGCTTG	60
GAGGGCTATG	ATTTCACAGA	AGGGTCTACT	GACAAGTATT	ATTGTGCTTA	TGAAGATGGC	120
GTCTGGAAAC	CAACATATAC	CACTGAATGG	CCAGACTGTG	CCATTTCTAG	AAAAACGTTT	180
TGCAAACCAC	GGGTTCAAGT	CCTTTGAGAT	GTTCTACAAA	GCAGCTCGTT	GTGATGACAC	240
AGATCTGATG	AAGAAGTTTT	CTGAAGCATT	TGAGACGACC	CTGGGAAAAA	TGGTCCCATC	300
ATTTTGTAGT	GATGCAGAGG	ACATTGACTG	CAGACTGGAG	GAGAACCTGA	CCAAAAAATA	360
				ATTGGACCAG		420
				GACACTGTGC		480
CACAAGCATC	GGCAATGCCA	AGTCCTCACG	GATTAAAAGA	AGTGCCCCAT	TATCTGACTA	540
TAAAATTAAG	TTAATTTTTA	ACATCACAGC	TAGTGTGCCA	TTACCCGATG	ATCTCGAG	598

(2) INFORMATION FOR SEQ ID NO:1205:

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 325 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1205:	
GAATTCGGCC TTCATGGCCT AGTCTAACCA TTATGGAAAG AGAACAGTCC CTTCAATATC CCACTATCTG TAGGGCATGA CACAGCCAAA TCCAAGTCAG ACCATCCCTT TGATCAATTT CTACCAATAA CTGTTCATTG CACACCCTGT ACAGAGCACT GCGACCAAGC TGTTCCTTGA CCTTCTCCTT TCCTAGTGTT TGGTCACAAC ACTCCCTAAA GCCCTAACTC AAGTTCTTGG GATGATACCA CCAGAAGAGG GAAAAAAGGA GCCGTCTTCC TGAAGTCACC TGGGTAGAGC AGCTGGGGAT TTTTCCCTCC TCGAG	60 120 180 240 300 325
(2) INFORMATION FOR SEQ ID NO:1206:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 126 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1206:	
GAATTCGGCC TTCATGGCCT ACCCACTGCA ATGATGTTTA CCAGCACTAT TAACTTACTG CAGACTCTTT GTCTGTCTGC TGGAGTTCAT GCTGAGATCA TGCAGAGCGA AGCCACCAGA CTCGAG	60 120 126
(2) INFORMATION FOR SEQ ID NO:1207:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 349 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1207:	
GAATTCGGCC TTCATGGCCT ACTAATGTGG TTTTGTGAAG TTGGTGTCAA ATTTACGAGC ATAAAATTGT TTGTAATATT CCCTTATATT CTTTTAAAAC TGCTATAGGA TCTGTACTGA TGTTCTGTTT CATACCTGAT GTTTTGTGTC TTCTGTTTGCT TAATTGATTT TCTCTATTTT CCTCTTTTAT TTCTTCTTTT AATAATTCCT TCCTTCTTGC TTTTGGCTTCA TTTTGCTCNT TTTTTAGTTTC TTTTGGTAAT TCAATTACTG GTTCGACATC TTTCTCGAG	60 120 180 240 300 349
(2) INFORMATION FOR SEQ ID NO:1208:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 198 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
494	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1208:

GAATTCGGCC TTCATGGCC	R AGAGTGATTG	TGGGTTATAA	TAGAGCAGAT	TGTTTTAAAA	60
AGAGACTTGT GAGCCAAGAG	TAAATCCTGG	TTTTACTATT	TATTAATCTG	TATAGCTATA	120
GCCAAGCTAT TAAAACTCC					180
CTAAAGGTTT ATGTTGAG					198

- (2) INFORMATION FOR SEQ ID NO:1209:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 546 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1209:

GAATTCGGCC	TTCATGGCCT	ACAGGGGATG	ATTCAGTCCG	ATACAGTCAG	GGAACCGTAC	60
ATAGAATAGA	ATGACTAGAG	TATAATCTGC	AAAGGATGGA	ATGGCAGAAG	TAGTCAGAAG	120
AGGTATGCAA	TGGTTGGATC	AAAAAGAGCT	TTGTATCCAG	CGTCACAGGG	CCTCAAATTG	180
TACTGTAATC	ATATGTCTTT	TACCTGTTCT	CTGGCATTTA	<b>AATATTCTTG</b>	TAAAGAGCTA	240
AGCCATTACT	GATAAAATGT	CTGTTGTGTA	CAGTTGTACA	AATTAAATTC	AGTCACAAAA	300
CTGAAAGAAC	AGCAGTGGGA	CATCTATCCT	AGTGAAAGTT	AGAATACACT	TTTGTGGTCT	360
TTAATAACAG	AGTTGATTGT	TTACCTTCTC	CTTTGGTTAG	AAGACTGGTA	TGGGGATTGT	420
TTGGAATGAA	GAGGTAGGAG	AGAGAAATAA	TTCAATTCTG	TATTCTCCCA	TCATCTTTAT	480
ATTTGAACTG	AGAAATGTGT	GTTTCTATCA	TTCATTCAAA	TTATTAAACA	AAAACAGAGA	540
CTCGAG						546

- (2) INFORMATION FOR SEQ ID NO:1210:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 314 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1210:

GAATTCGGCC	TTCATGGCCT	AAAGATATTT	TAGCTAACAG	GAGAACGGCC	CAAGGGGGCA	60
TTCTCATGTT	AATTACCAAA	TGTGGGCTTG	TCAAAATCAA	ATAGCTCCAG	GAATAATGCA	120
AGTAGCTCTG	CATCATTATA	TTGTTTGGCC	CTCAACCCAA	TATTAGCTAC	TTTTTAAAAT	180
CTGGGTTCAT	TAGGCTTTTA	AATTTAAAAG	AGGAATCACT	ATTGGGAGCC	TTCAGAAGAA	240
TGTAAAGCAC	AGCCAGCAGT	GCCAGAGTTT	AATGTAAATG	ACATTAAAAA	ATAGTTTCAT	300
ATCACACACT	CGAG					314

- (2) INFORMATION FOR SEQ ID NO:1211:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 416 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1211:

GAATTCGGCC	TTCATGGCCT	ACGCATGAAA	ATTACTTAAA	CGTTGCACAC	AACGTTTCAC	60
AAAATCTTTT	GTGAAAGAAG	AAAAGGAAAT	TCAGTGTGTG	AGTCTCAGCA	GGAGTTAAGC	120
TAATGCAGCT	TAAAATAATG	CCGAAAAAGA	AGCGCTTATC	TGCGGGCAGA	GTGCCCCTGA	180
TTCTCTTCCT	GTGCCAGATG	ATTAGTGCAC	TGGAAGTACC	TCTTGATCTG	GTACAGCCTC	240
CAACCATCAC	CCAACAGTCT	CCAAAAGATT	ACATTATTGA	CCCTCGGGAG	AATATTGTAA	300
TCCAGTGTGA	AGCCAAAGGG	AAACCGCCCC	CAAGCTTTTC	CTGGACCCGT	AATGGGACTC	360
ATTTTGACAT	CGATAAAGAC	CCTCTGGTCA	CCATGAAGCC	TGGCACAGGG	CTCGAG	416

- (2) INFORMATION FOR SEQ ID NO:1212:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 328 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1212:

GAATTCGGCC	TTCATGGCCT	AAGGGAAGCC	TGAGCAGGCC	AGTGGGCTGG	GCGCAGAGCG	60
GGGTGTGGGG	GCCAGGCTGT	GTGACCATGA	CAGAAAGAAC	CCCAGCTAGC	CCAGCTTGCT	120
CCCTGGGGCA	GGACTCACCA	ACCCCGTGAG	GGCCTGGGGT	AACAGTGGTC	CAGTGGCCAA	180
GACCAGCAGT	CGCCAGGTAC	CCACTGGCCA	CAAACCAACC	AGAATACTTG	CCGCTGGAGG	240
CCCCAGCCCA	GGGTCAACCC	AGCCGCCGCC	CTGTCTTTGT	GTGTGGGTGG	GTCAGCCCCA	300
TCCCTGCCTT	TCGGACTAAA	AACTCGAG				328

- (2) INFORMATION FOR SEQ ID NO:1213:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 471 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1213:

GAATTCGGCC	TTCATGGCCT	AGAGGCATTA	ATATATTTTA	CATTACTGGG	ACCATAGTAC	60
AGAAATTTCT	AAATGGTTTG	TAAAATAACT	TGTTATTTGT	GTTGTTGTAA	AAGCAGTTAA	120
TACAATGGAA	AAACTCGTAA	TAAGAAGATA	CAGTTTAACA	TCAAAAAGTT	TACCCAAGGT	180
AATTATGAGT	ACTACCTGGC	AAAACTTCAC	GGAAGCTGTG	GTATCACTTT	TATGATGGAA	240
GAATGGTGTT	TGCATTTTGT	GTAAAAGTAC	TTGCGGCTGG	GCGTGGTGGC	TCATGTCCCA	300
GTGCTTTGGG	AGGCGAAGGC	AGGTGGATCA	TCTGAGCCCA	GGAGTTCGAG	ACCAGCCTAG	360
GCAACGTGGC	AAGAGCCTGT	CTCTCCAAAA	CCTACAAAAT	TTAGCCAAGC	TTGGTGGTGT	420
'GAGCCTGTAG	TCCCAGCTAC	TTGGGAGACT	CACGCTGGAG	GATCTCTCGA	G	471

- (2) INFORMATION FOR SEQ ID NO:1214:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 585 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1214:

GAATTCGGNC	TTCATGGCCT	AGTCAATGAA	AGAATTCCTG	CAGTTTCATT	ACCTATGAAN	60
ATTGTGGGGT	CCTCTTGTGG	GACATGAAAG	GGGGACAGAT	AGATGAATAT	TGTTTGGATT	120
TTTGGTCCTC	AGTGCCATCC	ACAGACTCCA	GAAGGGATCA	GCTATTTGCT	GAACAATCTT	180
TCAGTTCTCA	TAGAGCCCTG	ATATGTTTTC	AGGGTCCACA	AATGCCTGTG	ACGGTGGCCT	240
CAAGAACCCA	GTGTCCCCTT	GTAGGTGGGA	TAGCATACCT	CTTAAAGGTC	AGCATGAGAT	300
TCCACCCATG	TCATCCCCAG	CATTGGTGGG	GTCAGCAGAT	CCTCTCTCTG	GGGTTTCNTT	360
TTCTGCTCAA	CCTCCCTGCT	TTGATGGACT	GCACAGACAA	GCCCCATCTT	GGTGGAAGGG	420
TCTCCCCATG	GGCTGTCCTG	GAGGGTCACT	CCCACAGATA	TGCCCCATCC	TGGTGGAAGG	480
GTCTCCCTGG	GGGCTGTCCT	GGAGGGTCAG	TCCCACAGAC	AAGCCCCATC	CTGTGGGAGG	540
GTCTCCCCGT	GGGCCATCCT	GGAGGGTCAG	TCCCACAAAC	TCGAG		585

- (2) INFORMATION FOR SEQ ID NO:1215:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 529 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1215:

GCGATTGAAT	TCTAGACCTA	CCTCGATAAC	CCAAGAGACT	ATGAGCAGAC	ATGACATCAT	60
TGCATGGGTT	AATGACATAG	TATCTTTAAA	CTACACAAAA	GTGGAACAGC	TTTGTTCAGG	120
AGCGGCCTAT	TGCCAATTCA	TGGACATGCT	CTTCCCTGGC	TGCATTAGTT	TGAAGAAAGT	180
AAAATTTCAA	GCAAAGCTGG	<b>AACATGAATA</b>	TATTCACAAT	TTTAAACTTC	TGCAAGCATC	240
ATTTAAGCGA	ATGAACGTTG	ATAAGGTAAT	TCCAGTGGAG	AAGCTAGTGA	AAGGACGTTT	300
CCAGGACAAC	CTGGATTTTA	TTCAATGGTT	TAAGAAATTC	TATGATGCTA	ACTACGATGG	360
GAAGGAGTAT	GATCCTGTAG	AGGCACGACA	AGGGCAAGAT	GCAATTCCTC	CTCCTGACCC	420
TGGTGAACAG	ATCTTCAACC	TGCCAAAAAA	GTCTCACCAT	GCAAACTCCC	CCACAGCAGG	480
TGCAGCTAAA	TCAAGTCCAG	CAGCTAAACC	AGGATCCACA	CTTCTCGAG		529

- (2) INFORMATION FOR SEQ ID NO:1216:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 627 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1216:

GAATTCGGCC	TTCATGGCCT	ATCGGCCCCG	CGGCGGAGGG	ANANGATCCT	CCACAGTGCT	60
CTCTTCAGTN	CCCCTTCAAA	TGCTGTTTTA	TCTCAGCGGA	ANGTACTACG	CCCTGTATTT	120
CCTCGCCACG	CTCCTGATGA	TCACGTATAA	AAGTCAGGTG	TTCAGCTATC	CTCACCGGTA	180
CCTGGTCCTC	GATCTTGCTC	TGCTGTTTCT	GATGGGGATT	CTAGAAGCAG	TTCGGTTAAA	240
CCTGGATACA	CCCCTGATGC	CCGATGTCCA	GTGAGGAACC	AAGGCTGCGG	GGAAGGGTGG	300
CCCCCACCCT	TCCTCTTGTT	ATCAGGCCTC	AGACACACTA	GGAGGATGGA	GGCGAGTTCT	360
CTCAGCTGCC	CATCCCACTG	AGGGGTGCCC	GGCCGTCAGT	GTCTTGTGTG	CACTCACGTC	420
CCAGAACCTC	TAGAGCTTGC	CCCCCAGGGC	GGGCACTGCT	GGGAGGGTGC	GAGCACCGCT	480
GCGGCACAGA	GGCCCGGTTC	TTGGNTGATC	TTCTGGGGCC	TGGGCCTGCC	CTGAGGTGGT	540
GGGGACAGGG	TGTGGCCTGG	CCCTGCTGGG	GGCTGCTAGG	CCAACGGGAC	CCTCCCCAAG	600

CGCGCCGCAC ACTGCAGGTG CCTCGAG 627 (2) INFORMATION FOR SEQ ID NO:1217: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 486 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1217: GCAAATATTG AACATAATCT AAAATCTGAG GAAGAAAAGG ATCAGGAAAA GCAACAGATG TTTGAAAATA AGCTTATAAA ATCTGAAGAA ATTAAAGATA CTATTTTGCA AACAGTAGAT 120 TTAGTTTCTC AAGAGACTGG AGAAAAAGAG GCAAATATTC AGGCAGTTGA TAGTGAAGTT 180 GGGCTTACAA AGGAAGACAC CCAAGAGAAA TTGGGGGGAAG ACGACAAAAC TCAAAAAGAT 240 GTGATCAGCA ATACAAGTGA TGTGATAGGA ACATGTGAGG CAGCAGATGT GGCTCAGAAA 300 GTGGATGAAG ACAGTGCTGA GGATACGCAG AGTAATGATG GGAAAGAAGT GGTCGAAGTA 360 GGCCAGAAAT TAATTAATAA GCCCATGGTG GGTCCTGAGG CTGGTGGTAC TAAGGAAGTT 420 CCTATTAAAG AAATAGTTGA AATGAATGAA ATAGAAGAAG GTAAAAATAA GGAACAAGCA 480 CTCGAG 486 (2) INFORMATION FOR SEQ ID NO:1218: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 497 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1218:

GAATTCGGCC	TTCATGGCCT	ATGAATTCTA	GACCTGCCTC	GAGATCTGAG	CAGGAATTAC	60
TCTCAGATGA	CGCTTCATCT	GTTTCACAAA	TTCAGTCTCA	AACTCAGTCA	CCGCAAAATG	120
TCCCTGAAAA	ATTAGAAGAA	AACCATGAGC	TGTTTTCCAA	GAGCTTCATC	TCCATGGAAG	180
TGCCTGTCAT	GGTAGTAAAT	GGCAAGGATG	ATATGCATGA	TGTTGAAGAT	GAGCTTGCTA	240
AGCGAGTGAG	TAGGTTAAGC	ACAAGTACAA	CCATAGAAAA	CATCGAGATT	ACTATTAAGT	300
CTCCAGAGAA	AATCGAAGAA	GTCCTGTCAC	CTGAAGGCTC	CCCTTCAAAA	TCGCCATCCA	360
AGAAAAAGAA	GAAATTCCGC	ACTCCTTCTT	TTCTGAAAAA	GAACAAAAAA	AAGGAGAAAG	420
TTGAGGCCTA	AATAAAGTCT	TTTTATAATT	ATTATTATAA	CAATGTGACA	TTGCACATCT	480
AAATACCACA	TCTCGAG	•				497

- (2) INFORMATION FOR SEQ ID NO:1219:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 524 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1219:

GAATTCGGCC TTCATGGCCT AAAAGATGGC GGAGGTGCAG GTCCTGGTGC TTGATGGTCG

1 COCO1 MON-						
AGGCCATCTC	CTGGGCCGCC	TGGCGGCCAT	CGTGGCTAAA	CAGGTACTGC	TGGGCCGGAA	120
GGTGGTGGTC	GTACGCTGTG	AAGGCATCAA	CATTTCTCC	AATTTCTACA	CARACRACTE	
C11CE1CE-			CHILICIOGC	MATTICIACA	GAMACAAGII	180
GAAGTACCTG	GCTTTCCTCC	GCAAGCGGAT	GAACACCAAC	CCTTCCCGAG	GCCCCTACCA	240
CTTCCGGGCC	CCCAGCCGCA	TCTTCTCCC	C1 CCCCCCC	GGTATGCTGC		
	CCCHOCCGCA	101101000	GACCGTGCGA	GGTATGCTGC	CCCACAAAAC	300
CAAGCGAGGC	CAGGCCCCCTC	TCCACCOMOR	G11666			
0.2.000	cycoccocic	IGGWCCGICI	CAAGGTGTTT	GACGGCATCC	CACCACCCTA	360
CCACAAGAAA	AACCCCATCC	20022000				200
COLICIANOISM	MOCOGNIGG	IGGITCCTGC	TGCCCTCAAG	GTCGTGCGTC	TGAAGCCTAC	420
AACAAACTTT	CCCTXTCTCC	555555555				720
MOMMOTIT	GCCIAICIGG	GGCGCCTGGC	TCACGAGGTT	GGCTGGAAGT	ACCAGGCAGT	480
CACACCCACC	CTCCLCCLCL					460
GACAGCCACC	CIGGAGGAGA	AGAGGAAAGA	GAGAGCCACT	CGAG		524

- (2) INFORMATION FOR SEQ ID NO:1220:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 444 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1220:

GAATTTCGGC	CTTCATGGCC	TATGATAAGT	TCATTCTGGC	TGGAGTATGG	TGGAGAGCCA	60
TGGAGTACTG	GTAGGTGAGG	GGCTGGAGGA	GGGATAGGTT	GGAGATGTTG	AGAAAGGCTT	120
TAAAGATCGT	GGTGAGTTGT	TTGGGTTTGT	GTTGGCTGTG	AGGAGTCATC	AGAGGTTTTA	180
ATGCAGGAAA	GTGGTTTGTA	CTCTATACTC	CAGCAGCAGA	GGTTGGTTGA	GTGGTGCTCA	240
AACTTTGTTG	TGTATTGGAA	TCATCTGAAG	AGCTTATAAA	AATACCAGTA	CCCAGGCTAC	300
AAACAGTAAA	ATCAGATTTT	CTGAAGGAGA	GGCCCAGATA	TTGGATTTTT	GATAATTTCC	360
CAGGTGATTC	CAGTGCGTAT	CTGAGTTTGA	GAACTACTCT	TTTAGAGGGG	TCTGATGGAG	420
TAAGGAATTC	AGAGGCCACT	CGAG				444

- (2) INFORMATION FOR SEQ ID NO:1221:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 354 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1221:

GCTTGAACAA	CACAGGTTTG	AACTGTGCAG	GTCCACTTAT	CCATGAGTAT	TTTCAACCAA	60
ACTAGTATCA	AATATACAGT	ATACGCGGGA	CTTGAAACCC	ACGTGTAAGG	AGGACGAAGT	120
TTTCGTGTAA	GTCAGCTCCG	AAGCACTGAC	TTTGGGACTT	GAATTTGCAC	AGATTTTGAT	180
				ATATACTGTG		240
AGTTTGATTC	TGGAGTGATA	TATGGAAGAC	ATAATTCTTC	CCATAAAAAA	TCATAATCTT	300
GGTAGTCTAT	CATAGTCTAG	CATTAAGAGC	ATGAACTTTG	GAGCCGTCCT	CGAG	354

- (2) INFORMATION FOR SEQ ID NO:1222:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 312 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1222:

GAATTCGGCC	TTCATGGCCT	AGCTAGTTCA	TGCTTGCGTT	GAAAGAGTGG	TCGTTTGCGC	60
TGGGTCATCA	CTGTGTAGTA	TTGGGGATAC	TTAGGTGAGA	AAAAAACTTA	ACGCTAGAGA	120
CGTTCACGCA	CTAGTGGAGA	AGCCAGGATT	GTTGCCCTAG	AGTTACAGTA	GATAAAAGTA	180
CCTCAGAGAA	CTGCGGGGGC	TCCCAACCTG	GACGCTTGCA	CCGGAGTATT	AAATCCAGCT	240
AGAGAATGGC	ATGTGCAAAG	ATACAGAGCT	TTTAGAAGTT	GCCTGCATTC	CTTGGCCCCA	300
TCCTCACTCG	AG					312

- (2) INFORMATION FOR SEQ ID NO:1223:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 371 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1223:

GAATTCGGCC	TTCATGGCCT	AATAAAAACT	GGCTGGGCGT	GGTGGCGGCA	CCTGTAATTG	60
CAGCTATTTG	AGAGGCTGAG	CCAGGAGAAT	CGCTTGAACC	TGGGAGATGG	GGGTTGCAGT	120
GAGCCGAGAC	CGCCCCATCG	CACTCCAGCC	TGGGCAACAA	TAGTGAAACT	CCGTCTCAAA	180
AAGAAAAAA	GTTTCCTTAG	AATGGAAAAT	ATTCATTCAT	GAGCTCTTTT	GGCAATCCGT	240
CATCAGTATA	TTCTGAAAAC	CAATAAGATG	TTGCCAAGTT	GGGGGCGAGA	GCTATGTAAT	300
GCAAGGCATA	TGCCTGATGA	AGTATACAAA	TACACCTGAC	CAGAAACTTT	GTCTCCCAAA	360
TAAGTCTCGA	G					371

- (2) INFORMATION FOR SEQ ID NO:1224:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 404 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
    - (b) lorogodi. linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1224:

GAATTCGGGC	TTCATGGNCT	AAAGAAAAGT	GCTGTAAATG	AGGATGTGGC	TTGCTGGGCA	60
ATAATCATTG	TAGAGTGGTA	CACCCAGTGC	CTTCACAGGA	TGCTTGAATA	CTGCCTGCAA	120
GCCTCGTGTC	ATTAGCCCAG	TAGGCATATG	ATAAGCCTCT	GGTCATCATT	TCCACTGTTA	180
AGAGTTAGTG	TCAGATATGG	AGCACCAATA	GGCTTGTAAG	TGAGAGCATC	CCTCAAAGTT	240
GTCACCTTAG	GAGACTCTGA	TGACCATGAT	GCTGCCATTG	TCCAAATGTG	CACTCATCTG	300
TCTTTTGGGG	AGTGATTCCC	GACAATTTAT	AGATTACAAG	AGAAAAGCAG	TCTGTATTTT	360
CATCAAATGA	TAGTTTTAAT	GGAAAATGAA	TCAGAAGTCT	CGAG		404

- (2) INFORMATION FOR SEQ ID NO:1225:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 395 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1225:

GAATTCGGCC	TTCATGGCCT	AGTTGGGGTT	AATTATGGCA	CCTAACTTAT	AGAAGAGGAA	60
ACCAATTTAG	AGACATTAAA	ATACTTGTTC	AAGGTTACAC	GGCAGGGAAA	AGGCAGAGTC	120
AGGATCTGTA	TTCTGTAGTC	TGAATCCAAA	GCGAATCCAA	AACTCTGAGG	TGCTNTGCTC	180
			GCTCAACCAC			240
TGCACTGGAG	GTCGAGGGTC	TGCATTCTCC	TTCTGTCGTA	AAATCACAAC	GTCCCCATCT	300
TTCAAGCCAT	AAGAAGCCAA	TGATCTGTGG	TTGTCTGTGA	GAGGTCTTTC	CGCATAGACG	360
ATCTGGCTCT	CGGCTGCGGG	GATGCCAGAC	TCGAG			395

- (2) INFORMATION FOR SEQ ID NO:1226:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 284 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1226:

TCAAAGGTCC	TTTTGTGGAA	GCGGAGGTGC	CCGATGTTGA	TCTGGAGTGT	CCTGATGCAA	60
AGTTGAAAGG	GCCCAAGTTT	AAGATGCCTG	AGATGCACTT	CAAGGCCCCC	AAGATCTCCA	120
TGCCTGATGT	GGACTTACAC	CTGAAAGGCC	CCAAAGTCAA	AGGGGATGCG	GATGTGTCGG	180
TGCCAAAATT	GGAGGGAGAT	TTAACAGGCC	CCAGTGTGGG	TGTGGAGGTG	CCTGATGTTG	240
AGCTGGAGTG	TCCTGATGCA	<b>AAGTTGAAAG</b>	GCCCTTGTCT	CGAG		284

- (2) INFORMATION FOR SEQ ID NO:1227:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 718 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1227:

GAATTCGGCC	TTCATGGCCT	AAGCAGACGG	GCAGTAGGTC	CCAGAGTTAT	ACTTCGGAGC	60
ACATGTTCAA	GAGGGAAATG	ACGACCGGCC	CCCACGGTCC	TGGGATGCAG	GTGTGAGGAC	120
TGAGAATGCT	GGACGGGGTG	TGGTCGAGGC	ATGGTCAGGG	TGGCCCCGAG	CTGTGCCCCA	180
CCCCAGGGAT	GCAGCAAGGG	TGCTCTGTGC	AGGACCCCGA	ACTTGGGCTC	TGCCCACTTT	240
CAGTGTCTGT	TGCATGTCAC	GCTGGCATCT	TCGGCATGTC	CACAGTTTGT	CACCCCCAT	300
TTGGAGAAGC	TGCAGCGGAA	GATGGTTTCC	TCTGTGCCTT	GCAGGCAACG	TCATCCATCC	360
AGATCCTCCC	AGTGCCTTGC	CCGAATCGAN	CTGTGCGGTA	CACTCCTCCA	NACCGCGGAA	420
GCCGAGCATG	CGGCACACCA	CGTCTCCGTC	CTTCTTGTCC	CAGCCGTCGT	CACACACAGT	480
GCCCCAGCGC	CGGTCGTGGT	ACACTTCCAC	GCGGCCCTCG	TGCGGACCTG	AGCCATTCAC	540
CAGGCGGATC	ATCATCGGGG	CCTCCACGCC	ACTGGCATCC	CCAGCTCTGT	CTCCTTTCTC	600
TCCTTTCTCT	CCTTTTGGGC	CTCGGTCACC	TAAAACAGAG	GAGGAAACTG	GCATTAGAAA	660
TGGAAAGAAA	TCCTAATTGT	GAATAAAATA	TTACCTGCAG	GAGATTGATG	AACTCGAG	718

- (2) INFORMATION FOR SEQ ID NO:1228:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 389 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1228:

GAATTCGGCC	TTCATGGCCT	AGCTGGGTTG	ACCCTGCAGA	GGCCAGAGAG	CCGAGGGGCC	60
ATGTGTGCTG	GCATGGGGCT	CCCTGCCCCT	TTCTGAGGCT	CAGCACGGAG	GGGAGAAACC	120
			AGAACCAGTA			180
					AGCTCTGTGC	240
ACACAGACAA	TAGACATCAG	GACTTTCATC	TTCACTCGTC	ATCTGGCAGC	AGAGAGCCTG	300
CAGGGCTGGG	CTGCAGGGAG	AAGAGTTCCT	TTCCTCACGC	ATCCAGGCAA	GGGGAGAGCA	360
GCTCTGTGCC	TGCCACTGGC	CCACTCGAG				389

- (2) INFORMATION FOR SEQ ID NO:1229:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 289 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1229:

C	GAATTCGGCC	TTCATGGCCT	ACACAAACAT	GATTTTATTT	TATTATTTTA	TTTTATTTTT	60
7	TTATTTTATT	TTGAGATGGA	GTCTCGCTCT	ATCGCCCAGG	CTGGAGTGTA	GTGGCATGAT	120
(	TCGGCTCAC	TGCAAGCTCC	GCCTCCTGAG	GCGGGAGAAT	TCCTTGGGCC	TGGGAGGCGG	180
Į	GGTTGCGGT	GAGCTGAGAT	TGCCCCATTG	CACTCCAGCC	GAGGCAACAA	GAGCGAAACT	240
C	CTTCTCAAA	AACAAACAAA	CAAACAACAA	CAACAACAAA	ACTCTCGAG		289

- (2) INFORMATION FOR SEQ ID NO:1230:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 600 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1230:

GAATTCGGCC	TTCATGGCCT	AATGTGTTTT	ATGAACGATA	GATCACATCA	GAACTCCTGT	60
GGGGAGGAAA	CCTTATAAAT	TAAACACATG	GCCCCCTTAG	AGACCACAGG	TGATGTCTGT	120
CTCCATCCTT	CCCTCTCCTT	TTCTGTCACC	TTTCCCCCTA	GCTGGCTCCT	TTGGACCTAC	180
CCCTGTCCTT	GCTGACTTGT	GTTGCATTGT	ATTCCAAACG	TGTTTACAGG	TTCTCTTAAG	240
CAATGTTGTA	TTTGCAGGCT	TTTCTGAATA	CCAAATCTGC	TTTTTGTAAA	GCGTAAAAAC	300
ATCACAAAGT	AGGTCATTCC	ATCACCACCC	TTGTCTCTCT	ACACATTTTG	CCTTTGGGGA	360
TCTGGTTGGG	GTTTTGGGTT	TTTTGTTGTT	GTTGTTTATT	TGTTATTTTA	AAGGTAAATT	420
GCACTTTTAA	AAAAATAATT	GGTTGACTTA	ATATATTTGC	TTTTTTTCTC	ACCTGCACTT	480
AGAGGAAATT	TGAACAAGTT	GGAAAAAAAC	AATTTTTGTT	TCAATTCTAA	GAAACACTTG	540
CAGCTCTAGT	ATTCACTTGA	GTCTTCCTGT	TTTTCCTGTA	CCGGGTTATC	CTGCCTCGAG	600

- (2) INFORMATION FOR SEQ ID NO:1231:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 420 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEO ID NO:1231:

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GAATTCGGCC TTCATGGCCT AGGAGGGCCA CATCTGCCAN AGCCTGGAGT CTGCGAAGGC
CGGGACCCGG TTCCCCGGCC CACAGTGGGG GTGTGCAAAC CCGAGAGAAC TGGGTTGCAA
ATTCGTGAAG AATCAGCATC ATGTTTGGCA GCTGAGTATT GGAGCCAGGA GCCTGCCATG
AACAGAGTGC TGTTTTAGAG CTGGCAGCAG CATCTCAGCC CAAGAGAAGG
CTATATTCCC AGAGGATGTC AGTCCCAAGG ACCAGTAGCT GCCATCAGTT TGGATTCTGA
AAACTAACTG GCATCAACAC TGGGTGTAGA AACATGCTTG CCTTATGTAT CAGAGGACAT
GCTCAGCAGA TCCAAGAGAT ATATTTGGCA ACTTTTTCTA GAAAAGGCAC CTGCCTCGAG
420
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- (2) INFORMATION FOR SEQ ID NO:1232:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 602 base pairs
    - (B) TYPE: nucleic acid

(D) TOPOLOGY: linear

- (C) STRANDEDNESS: double
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1232:

GAATTCGGCC	TTCATGGCCT	ACCACCCGCG	ACAGTTTCCC	AGCAGGGCTC	ACAGCAGCGT	60
TCCGCGTCAT	GGGGATTTGG	CAGCGTCTGC	TGCTTTTTGG	TGGGGTGTCG	CTCCGGGCTG	120
GTGGCGGGGC	CACTGCCCCG	CTTGGGGGAA	GCCGAGCGAT	GGTTTGTGGG	CGCCAGTTGT	180
CTGGCGCCGG	GAGTGAGACC	CTAAAACAAA	GAAGAACACA	AATCATGTCC	CGAGGACTTC	240
CAAAGCAGAA	ACCGATAGAA	GGTGTTAAAC	<b>AAGTTATAGT</b>	TGTGGCTTCT	GGAAAGGGTG	300
GAGTCGGAAA	ATCTACTACA	GCAGTGAATC	TTGCACTTGC	ACTAGCAGCG	AACGATTCGT	360
CCAAGGCCAT	TGGTTTGCTA	GATGTGGATG	TGTATGGACC	TTCAGTTCCA	AAGATGATGA	420
ATCTGAAAGG	AAATCCGGAA	TTATCACAGA	GCAACCTAAT	GAGGCCTCTC	TTGAATTATG	480
GTATTGCTTG	TATGTCTATG	GGCTTTCTGG	TTGAAGAAAG	TGAACCAGTA	GTTTGGAGAG	540
GCCTTATGGT	AATGTCGGCC	ATTGAGAAAT	TGTTGAGGCA	GGTAGATTGG	GGTCCACTCG	600
AG	•					602

- (2) INFORMATION FOR SEQ ID NO:1233:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 571 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1233:

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GAATTCGGCC TTCATGGCCT ACTANACCTG CCTCGTAGTC CAGAAAGATC CCCACGCGCC
TGGGTGGGTC CCGGAGTGGA GCCAAGGCCC GTTCCGAGGA NTTGTAATAG CTCCCUAGGA
                                                                     120
AGACCAGGAT CCAGAAGCCG TTGCCCGCGN ANAGCTCGCC CTTCTCCTTC CTGTTCACGT
TCTCCCTGCA CACCCCCAGG GCCCAGCTGG TGCGGTCCCC AACCTCCACC TCCCAGTAGT
                                                                     240
GGCGGCTGAG GTGAAGCGCT CCTGGCCCAG CACGCAGGGG CCGGGGTCAA AGCGCTCTGG
GCTGTCCGGC ANGGCCTGCC GTANGTCCCC CCGCTGCACG CGTCCGCCTG TCTTCAGACA
                                                                     360
GGATCAGCTC AGGGTTGGCG GTGTCCGGGT CCAAGGTCAC GTCCCCTCGA AACCTCCGCA
                                                                     420
GTGTTTNTAC CAGTCCCGGG ACCCTGCACA CGGTCCTCAG CTCCATAGGC ACAACTTNTG
                                                                      480
GGGGCTGCAG CTTCACATCC TGGACCCTGC NCAGGGCGTC CTTGATGTCC TGCAGCAGCC
                                                                      540
CCAGAGCAGG CAGCTGGCAG CGGCCCTCGA G
                                                                      571
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- (2) INFORMATION FOR SEQ ID NO:1234:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 631 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1234:

GAATTCGGCC	TTCATGGCCT	ACTTAATTTA	TAGTCTTTTT	CTTGTGAAAT	GATCATTGAA	60
GTAGTTACTA	ACAGGTAATG	AAATAAAATA	CCAATTTTGC	TAGTGAAAA	TAGTTTTCAA	120
CTGAGAAAAG	CACTTGGCAG	AAGACCTACA	AACATGCAGG	CTAATGCTAC	ACTCTATTGC	180
AGCTTCAAAT	AAGTTGTTTT	TGATGCCTTT	TGAGAAGAAC	AAACTAAGAT	GAAAATAATT	240
CCTTGAACAT	TTATCAGCAT	TGCTGTTTAG	GTACCCATTA	GAAAGTGATT	AACATTCGAT	300
ACCTACCCTT	TCCAAAACAC	AAAATCACTG	GCAAGCATCA	TCACACACTC	CTAAACCAGC	360
AACATCTGAG	AAGCACAAAA	CACCTTCCCT	TTTGTCTAAT	AACCTGTTGG	TTAGTTATTG	420
GAACTGCAAG	GCTTACAAAC	TCCTCCCCTG	TCCTTTATCC	TTATGTAAGC	TTGCACATTC	480
TCCAGGAATA	GCTATTTTCA	AAGGTAATTT	CAAAAGAATT	AATACAATGA	ATTCTACTGG	540
GCAGTTTGGG	GGAAAATATT	GACGATATTA	AAATTTAAAA	AATGCCTGCC	TGACACATAT	600
AAGGCCTCCC	CAGTCCCTCA	TACAACTCGA	G			631

- (2) INFORMATION FOR SEQ ID NO:1235:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 287 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1235:

GAATTCGGCC TTCGTGGCCT AAGG	ACAGTG TATAAAAAGG	CAGCGTCACA	CAGGTGGGCT	60
CTGGGGTCCT TGGTCCATTA GGAG	ATGGCC TTTGCCTCAG	GAAGGAAGGC	TTCCCAGTAC	120
TTTGCCAGCT GCTGCTGTGA GTAA	AGGAGT GTCTCAAGGT	ACTTGATGAC	GTGGTTCTTG	180
AAGTCCTTGG ATTTCTCTTT CTCA	AACCGT ATCACTTCTT	TTCGGACCAC	TGTTGAAATC	240
CTCTCGAAGT CCCTTTCATA TTGA	GTCACC CGAGAGTCCC	ACTCGAG		297

- (2) INFORMATION FOR SEQ ID NO:1236:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 537 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1236:

GAATTCGGCC	TTCATGGCCT	AGGCTGGCGG	GGTAGGGGTT	GGTTGGTAAG	GCTTGAGCAG	60
AAGGTTCTAG	ATGCATTCAG	GAGATAAAGA	TGCATTTGGG	GTTATTGCAC	TTCTCCTAGA	120
AACATAAACA	TTGACTTCCT	TTTGTGGAAG	AAAAATGTTA	TGTTAGCTAT	TTGACGTTTC	180
AGGAAGGGTG	GCTTCAGCTT	GGNNATTNGG	GATGTTTGTC	TACANGTGGC	CAGGCTGCTT	240
mamaa ammaa	3 3 C 3 C T 3 T T T T T	THE PROPERTY OF A	አ ምምር ምርምር ጥ አ	TCAGACATCA	TGGGAGGAGA	300

TCCAGGGCGA CATCAAAGGG AACATGATTN NCNNAGGACC AGAGGGGCTT GGATGCAGAT GATCATCATC TGGGCACTGN TGGATACTGA GTAAGCCCCA GCTGCACCCC ACCTCTGCGC TCTGAGCATG GGAGGCAGCC TGTGCAGCTA TAACTCAGCC TGACTTTTTC CTTCCCTGCA TACTCTTGAA ATACACTGGA GATGAGTAGG GGCGAGTGAG CTGCACACCA GAATAAG	360 420 480 537
(2) INFORMATION FOR SEQ ID NO:1237:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 306 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1237:	,
GAATTCGGCC TTCATGGCCT ATCTCCANAT AATTTNGATC ATAGGCCGGA GTGAGTCATT CCACCTGCAC CTTTCTGTAC AAATACTAAT TCAATTTTAA GTCTTAAGTC ACTTTTTTAA TATATATGAT CTTCTGGTCT TCCCACTTCC TCCCCNNTCT ACTGCTCTCC CATTTTCCCT TGCTGGGAGT AGCCACATGC TTTTTGCCCC CCAACCCTTG TATATGGGGA CAGTGGGGTC AGTGCAGCTA CCCTTCTTT CCCTCCTGCG GAACAGCGGA CCCAGCAAGA GCATCCACAT CTCGAG	60 120 180 240 300 306
(2) INFORMATION FOR SEQ ID NO:1238:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 320 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1238:	
GAATTCGCCT TCATGGCCTA ATTTCATGCC CCATATTTGG CATATAGTGG AAGGAGAAAG GTAGTATTTT TGCAGTATTT AATAACATTG AGCCTTGAAG CTGTTTGGCA AAAGGTAAGT TTCCTTTGTG GCTTTGCTGA AAAACAAGGC ATAGATTTAC ATAGATACGT GTTTAATTCT CTGCTTCACT AAAGAAAGCA AATGCCTATT AAGCCACTTC AGTTGGGATA ATCCCTGATT ATTGTGAGAT TGAAATTACT TTGTCAATTT TACAAATAGT TTTTATCTTT CCATTTACAT ATTTACCATG ACAACTCGAG	60 120 180 240 300 320
(2) INFORMATION FOR SEQ ID NO:1239:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 328 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1239:	
GAATTCGGCC TTCATGCCTA CAGCGATGAG TGCACGAGTG AGATCAAGAT CCAGAGGAAG AGGAGATGGT CAGGAGGCTC CCGATGTGGT TGCATTCGTG GCTCCCGGTG AATCTCAGCA AGAGGAACCA CCAACTGACA ATCAGGATAT TGAACCTGGA CAAGAGAGAG AAGGAACACC TCCGATCGAA GAACGTAAAG TAGAAGGTGA TTGCCAGGAA ATGGATCTGG AAAAGACTCG	60 120 180 240

GAGTGAGCGT GGAGATGGCT CTGATGTAAA AGAGAAGACT CCACCTAATC CTAAGCATGC TAAGACTAAA GAAGCAGGAA GACTCGAG	300 328
(2) INFORMATION FOR SEQ ID NO:1240:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 279 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1240:	
GGGGATCCTT TTATTTAAT CACAAAAATG CTGAAAATTT TGGGTTGCAA TTTCAATCCA CAGTAAAGCA TGGGCATTTT TTTTTTTTT TTAAATCAGA GTGAACTGCC TCGCGTCTTT CTTTTTAAGG GTTACACTGT ATGTGTTCTG TGTTTTATTT AACTGTTCCC CTCCTGAGGG GCATTCCGCT TGTTTGAGCT TTTCTCCCTC TTGCTGACAG TGCTGCAGTA ATCATTCTTG TCCATTTTAA TCCCTATGTA TTTACACGGT ATTCTCGAG	120 180
(2) INFORMATION FOR SEQ ID NO:1241:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 445 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1241:	
GAATTCGGCC TTCATGGCCT ACGGAAAAGG AAACCTTGGT GGGATTGCTG TGGATGACAT TAGTATTAAT AACCACATTT CACAAGAAGA TTGTGCAAAA CCAGCAGACC TGGATAAAAA GAACCCAGAA ATTAAAATTG ATGAAACAGG GAGCACGCCA GGATACGAAG GTGAAGGAGA AGGTGACAAG AACATCTCCA GGAAGCCAGG CAATGTGTTG AAGACCTTAG ACCCCATCCT CATCACCATC ATAGCCATGA GTGCCCTGGG GGTCCTCCTG GGGGCTGTCT GTGGGGTCGT GCCTGTACTGT GCCTGTTGGC ATAATGGGAT GTCAGAAAGA AACTTGTCTG CCCTGGAGAA CTATAACTTT GAACTTGTGG ATGGTGTGAA GTTGAAAAAA GACAAACTGA ATACACAGAG TACTTATTCG GAGAGCATTC TCGAG	120 180 240
(2) INFORMATION FOR SEQ ID NO:1242:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 329 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1242:	
GAATTCGGCC TTCATGGCCT AATCATGCCT CCTGCTTTTG TCACCTAATA CGTGACAGAC TTCTTGCCAT ATGTGGAAAT AGATAACTCT TTCACTATTC TTAATAATGG ATATTTAGAT GGCTTCCATT TGTCCCTGTT ATTGTGTAA CATATATTCT TGCATACATT TCCTTTCATA CTTACTCAAT TATTAGCTGA ACTTTGGAGT AAAATCACTA AGTAAATACG TTTTAGGCTT TTGCTATGGT TTACAAGATT TCCTGTCAGC AATTTAAGAT ACTTTTATTG CTCCTCACAG	120 180

329

CCTTGCCAGA ACTCATTGGG ACACTCGAG

(2) INFORMATION FOR SEQ ID NO:1243:

(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 433 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1243:	
GAATTCGGCC TTCATGGCCT AAAAATAGTA AATTCCCAGA AATTCAGTGT TTAGACGAGG	60
GAATTTAATT CCTATTTTGT CCATGTTGGT GATGTACTGT ACTTCCCTTC CTTTTCTCTG	120
CATCCCCCAT CACCTCATAG AAGACTCTTT GTTGATCATT GTATGTTAAA AATGTATAAA	180
ATGGCTATCT TGTAAGCGTG CTGTCCTGGT ACTAGTGTAG CGACTTTTTT TCTCCTCTTT	240
CTTCTAGTAC ATATTGATAG GTATAACATA ATTAAGGTTT AAAAAAAATT AGACATAGTT	300
ATTCAGATTT AGGACCAGTA AGGATAGAAC TTTCTCTTAT TTATGAAAAA AAATGCTAAT	360
AATTTTGGGG CAGTTTTTTC CTTTAATTAT TTTTTTCAAT TTCAAGTTTA ATTTTATTTT	420
AGCTGATCTC GAG	433
(2) INFORMATION FOR SEQ ID NO:1244:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 327 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1244:	
GAATTCGGCC TTCATGGCCT ACATGACTGA GTATATTACC TCTGTTTGAG AGAGAACCAT	60
TTTCTTCAGA AATTCATATC CTACCGTTCT GCTGTTTTTC ATGATAATTG TTTTTCTCCT	120
AACATTATAT TTCTGTCTTT TAGATTTTAG TATTTCACCT TTTAGAATAC ATTTTGGATG	180
ATGAAGTTGT TTTTCTTATT TCTCCTACCC CCTTTCCTTC ATCTCAGACA TTATTTCCCA	240
GCTTTCTTTG TTTCAGCTTT TTATTATGAA AAATGTCAAA TGTGCAGAAA AATGGAAAGA	300
ACAGTACAAC ACACCCCCAA TCTCGAG	327
(2) INFORMATION FOR SEQ ID NO:1245:	,
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 397 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(b) lorologi: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1245:	
GAATTCGGCC TTCATGGCCT ACTGAGAATC TTCACCATTA AACTTAGGAG TGTTCTACAA	60
AATAGTGCCT AGAACAGCTA TTGATACTCA AGAGGGCTGT TTAAGTAGCT AGAAAAGTCT	120
AACCTAAAAT CCCATTTGTG ATTAGATTAT GCACTGATGA AAAAATGTTT AATGCCGTTA	180
AAAAGAATCT ATTACATTAT ATTCTTTCAG GCCATGGTAA AGTTACAAAT TTGAACTCAA	240
TAGGCTGTGT GTGTATTTGT ATGTGTGTAT TTTTCTTTCT TTTATTGGCA GTCTCAATAA	300
507	
307	

NTGCACACCA CACACAGCAC AACCACCCAC ACTCGAG

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 440 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:1246:

(ii) MOLECULE TYPE: cDNA

TTGTTAAGCC ACACACTGCA CAGTATACAC ACACACTGCA CACCACACAC ACACCACAGA

360

397

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1246:	
GAATTCGGCC TTCATGGCCT AGTGGGCAGA TCACCTGAAG TCAGGAGTTT GAGAACAACC	60
TGGCCAACAT GGTGAAACCC TGTCTCTACA AAAAATAAAA AAATTAGCCA GGGGTGAGGG	_ 120
CAGGTGCCTG TAGTCTTAGC TACTTAGGAG GCTGAGGCGG GAGAATCACT GGAACCCACG	180
GGGCGGAGGT TGCAGTGAGC CGAGATCACA CCAGTGCACT CCACCCTGGG CGATAGAATG	240
GGACTTTTTA AAAAAAAAA AAACGCCTCA CACGGTTTTA GGTGCTATTA ATACAGTAAG	300
AAACAAATAA ACAAAGCTCA TTGCCCTTGA TGGACTTTAA AAAATGATCC AAGTATATGC	360
TGTCTGTAAA AGATACACCC TAGACTCAAA GACACAAATA AGCAAATCAA AGGATGAAAA AGATACACTA TATGCTCGAG	420
AGATACACTA TATGCTCGAG	440
(2) INFORMATION FOR SEQ ID NO:1247:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 466 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
/ CRANTINGS BUGGETSETON CER IN NO 1015	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1247:	
GAATTCGCCT TTNATGGCCT AGCCNAACAA AATGGCGGCG GCAGCGGTGT CGTTTTGTTT	60
CCGGGGNTCC TGCGGCGGTG GCAGTGGTAG CGCCCTTTGA GCTGTGGGGA GGTTCCAGCA	120
GCAGCTACAG TGACGACTAA GACTCCAGTG CATTTCTATC GTAACCGGGC GCGGGGGAGC	180
GCAGATCGGC GCCCAGCAAT CACAGAAGCC GACAAGGCGT TCAAGCGAAA ACATGACCGC	240
TGAGCCCATG AGTGAAAGCA AGTTGAATAC ATTGGTGCAG AAGCTTCATG ACTTCCTTGC	300
ACACTCATCA GAAGAATTTG AAGAAACAAG TTTTCCTCCA CGACTTGCAA TGAATCAAAA	360
CACAGGTAAA TTGAAAAAGA ATGTGCTATA CCTTCTAGTC TTTTTTCTAT TTTTTTTTAA	420
CACTTATGGA GGTAACCATT TATTTTATTC AGAGAGCACA CTCGAG	466
(2) INFORMATION FOR SEQ ID NO:1248:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 194 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1248:	
TTTTGTTTTG TTTTTGTTAG AGTTGGAGTC TTGCTGTGTT GCCCAAGCTG	60
ATCTCCAATT CCTGACCTCA AACAGGTCTC TCACCTTGGC CTCCCAAAGT GCTGGGAATT	120
508	

180

CAGGGGTGAA CCACCTCACC CAGCCAAGAT CACATTTTGA ATCTAATTTT TTTTTTTTGA AACAGTGTCT CGAG	180 194
(2) INFORMATION FOR SEQ ID NO:1249:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 523 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1249:	
GAATTCGGCC TTCATGGCCT ACCTGTGCAA GAACATGAAA CATCTGTGGT TCTTCCTTCT CCTGGTGGCA GCTC~CAGAT GGGTCCTGTC CCAGGTGCAG CTGCAGGAGT CGGGCCCAGG ACTGGTGAAG CCTTCGGAGA CCCTGTCCCT CACTTGCACT GTCTCTGGTG GCTCCATCAG TGATCACTTC TGGACCTGGA TCCGGCAGCC CCCAGGGAGG ACGCTGGAGT CGCTTGGCTA TATTCATTAC AGTGGGATCA CCAACTACAA CCCCTCCCTC AAGAGTCGGG TCACCTTTTC AGTAGACACG TCCAAGAACC AGCTCTCCCT GAAGCTGAAG ACTGTGACCG CTGCGGACAC GGCCGTGTAT TACTGTGCGA GATTTAGTGG TTATTATACT AACCCTTCCT ACTACTACTA CATGGACGTC TGGGGCAAAG GGACCACGGT CACCGTCTCC TCAGGCCTCCA CCAAGGGCCC	60 120 180 240 300 360 420
ATCGGTCTTC CCCCTGGCAC CCTCCTCCAA GAGCACTCTC GAG	523
(2) INFORMATION FOR SEQ ID NO:1250:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 194 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1250:	
GCCAGAGGGA TGACCGGTGG CTGCTGGTGG CACTCCTGGT GCCAACGTGT GTCTTTTTGG TGGTCCTGCT TGCACTGGGC ATCGTGTACT GCACCCGCTG TGGCCCCCAT GCACCCAACA AGCGCATCAC TGACTGCTAT CGCTGGGTCA TCCATGCTGG GAGCAAGAGC CCAACAGAAC CCATACCCCT CGAG	60 120 180 194
(2) INFORMATION FOR SEQ ID NO:1251:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 503 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1251:	
GAATTCGGCC TTCATGGCCT AAGCCCACTG GCATCAGACA TGCTTTGCTG TAGTGTACAC TTCNTTTTTC NTTTTCNTTT TTTTTTTTTN CACACAGAGC CNGGNTCCGT CCCCCAGGCC	60 120
TGACTGCAGC GGNANAATCC CACCCCACNG CCACNTCCGC CACCCAGGCC CAAGCGGTTC	180
CCTAACGGCT AATGATGTTG AACATCTCTT CATGGGGTTA CATGCCATCT TTATATCCTC	240
TTCAGTGAAA TGTTCCTTAA CATCTTTTGC TGTTTTCTAA TTGGATTACT TGGGGTTTTT	300

TAATACTGAG	TTTGGAGTTA	TTTATATATT	CTAGACAGTA	GTCTTTATTG	GATATGTGGT	360
TCAAAAATAT	TTTCTCCCAG	TCTGTAGTTT	GCCTTTTCAG	CCTTTTAACA	TGGTCTTTAG	420
CAGACCAAAA	TGTTTTAGTT	CTTATGAAGT	CCAACTTACC	AATTTTTCCT	TTTCTAGATC	480
ATACTTTTGG	TGTCAAGTCT	CAG				503

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- (2) INFORMATION FOR SEQ ID NO:1252:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 589 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1252:

GAATTCGGGC	TTCATGGCCT	AATTGAATTC	ATGATTTGTC	TCTCTGCTTG	CCTGTTGTTG	60
GTGTATAGGA	ATGCTAGCAA	TCTTTGCACA	TTCATTTTAT	ATCCTGGGTT	TCAGTATTTT	120
AAAAACTTAC	TTCAGGTGAT	TCTATGTGTG	CAACCATGAT	TGAGATACAC	TGTTATAGAA	180
TCTAGGATGT	GATAAACTAG	AAGAACATAA	CTAAAGTTTT	GCATTTTTCG	GGTGTCTCAG	240
TTTCCTCATT	TATAGATGGA	GTTGGTATGT	GTACCAAGTT	CATAGGCTTG	TTCTGAGTAA	300
ATTAGTGCAT	GTAAAGTGCT	CCACAGAATG	TTAGCTGTTG	TGATGCTTTA	CTTTCCATTG	360
CACTTCCTGA	CTCCTAGCCT	TTCTTTTCCT	TGGCTCTTTT	TATGCTCATG	TCAGATGCCT	420
CTATTGTTTC	TTTCCCCCCA	GAATATCCTC	CACTTTATCT	TGCTCTGCTC	AACATCTTTA	480
AAGTATAGAA	TCAACAGACT	GCCATGCCAC	CCAGTCTGTC	TGACAATTGA	GGCAAATTCC	540
CTAAGTCCTC	TTGTTCTCCT	TCTGAGATTT	CCACCTGCTC	TAACTCGAG		589

- (2) INFORMATION FOR SEQ ID NO:1253:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 702 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1253:

GAATTCGGCC	TTCATGGCCT	ACATTTATCG	AGTCTTTAAT	TAATGCCCTG	GGTAACTATA	60
AGGTTGGAAC	TGTAATTGTC	ACCATATTGA	TGATGAGAAA	CTTGAGAAAG	GATAAGTGAC	120
TTGTCTAAAA	TCACACAGTA	AAACCTCAAA	TCAAACCCAG	GCCCTCTGGC	TCCAGACTCT	180
AAATTATACT	CTGAATGATA	CTCACTGATT	GTCCGAGGAC	ACAAAGACTG	TCGAGGCACT	240
ATCTGCTGGG	TGTCTGCAGA	ACCTTACTGT	TCTAAAGCAA	AACATTTTAC	CCCTGGACAA	300
GAGCAGCAAA	GGTGGCGTTC	GGCCCTCCTT	GGCTCTCATT	TGACTGTTCA	AAGCCAGGTG	360
CTTTTCTTTC	TTGGGTCAGA	ACGTATTTTC	AGCAGCATTT	TGAAGCACCC	CTGGCGTGCA	420
CTGCACAGGG	AAACCAGGAC	CACATTGGTG	TGCTGTGTCC	TCCTTACCAA	CTGGCTCTTG	480
GAGAAGGTGA	GACAGAAGTA	GCTGAGACTC	CATTCCTGAG	ATCTTCACTT	AACAACTCCT	540
GCAGCTTGTG	CAGAGCCTTA	CTAGAAATAC	TGAAGGCAGA	AGTCCCTGGA	AAATAGGGCC	600
CATAACTAAT	TAGTAATTTG	TTTTTGAGTA	ATTTCTTACC	GTTATTTGAG	CACATTCTGC	660
AGTCCAGGCA	TTTTGCTAAA	CTCTTACATG	GCAGGACTCG	AG		702

- (2) INFORMATION FOR SEQ ID NO:1254:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 554 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1254:

GAATTCGGCC	TTCATGGCCT	AAGCAAGTAA	ACACTGTATA	TCTGTAATTG	GAAAGTTGGT	60
GGGAAGATTA	CTTTTCCATT	CTTGATGTGG	CAGCCTTAAG	TGCCATCACA	GCTTGTTCTG	120
	TTTTTTTTGC					180
AGCAATTCCC	CTTCTTCAGC	CTCCCAAGTA	GCTGGGATTT	CTGGTGCATG	CTACCAGGCC	240
	TTTTTTGTAT					300
CCTCAAACTC	CTGACCTCAG	GCAATCTGCC	CACCTCAGCC	TCCCAAAGTG	CTGGGATTAT	360
	CACTGCGCCC					420
	GTGTGTGAGT					480
TAAACATTCT	GATTTTTTT	TTATCAGAAC	CACTAATGAG	ATGAGACCAT	AGTTTGTAAA	540
ACCTCATGCT	CGAG					554

- (2) INFORMATION FOR SEQ ID NO:1255:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 326 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1255:

GAATTCGGCC	TTCATGGCCT	AGCTCCGGCA	CATGGCAGGC	ACTCAGGGAA	AGTATGTAGC	60
CTTATGAACT	GACTGATCTG	AGGGAGGCAC	TTCTGTAAGC	CATAGTATTG	GTCACTGGCA	120
TGAGGCCACC	TACTGGATCC	CTGCCATCCA	GCCCTGGGAG	TAGCATGAAG	CAGCATGGCA	180
CTGGCCTTCT	GGAAGCTTGG	AGAGGAGTCT	TACCCAAGCT	TTGCTCCTAG	ACATTAAACT	240
TCCCAGCTGG	GCACTAACAT	GTGGCTGCAG	AACCTGCCCT	TGCTCAGTCT	GTCCCTGGTG	300
CAGCTGCTGG	GAGAGCCTGC	CTCGAG				326

- (2) INFORMATION FOR SEQ ID NO:1256:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 399 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1256:

GAATTCGGCC	TTCATGGCCT	ACATTAAGGC	AGCTTTGTAA	GTAAGTACAA	AATATATTTC	60
AACCTACACA	ATTTTTATTA	GTTTCCCTCT	CTTTTAGAAG	TACACCGACT	CTAAAATGAA	120
TGAAAGTCTG	ATTACTTGCC	TTAGGTTGGG	GGCTTTATCC	AAGCTCTACT	AAGTGAAGCT	180
AAAATAAAGG	ACATTGTTGT	ATATTGTATT	TTAATGTATA	CATTATTACC	TCCTCAGCAA	240
AGTGAAACAT	AGCTAAAACT	TGAGTATATA	TTTCCTTCAT	TTCTCTTCTT	AGTTCCTTTT	300
TGGCATCTCA	TGCTGAACAA	ATCCAAAATA	GATTTATTAA	TGCCTTCCCC	CAACACAAAC	360
AAAACCAGAA	GAGTCTTTCG	CTTCTAGACC	TGCCTCGAG			399

- (2) INFORMATION FOR SEQ ID NO:1257:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 350 base pairs
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
  (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1257:

GAATTCGGCC	TTCATGGCCT	ACTGAGTACA	GGTTTGGGAT	CTACATACCC	AGATCAACAC	60
CATCTCCCAM	Choomagaga	1000001000		CINCAIACCC	NOW I CHACAG	80
CATGIGGCAI	CACCIGGCCC	AGGTGAGCAT	GACCAGGTAT	ACCCAGATGC	AGCTCAGCAT	120
GGCCATGCTT	TCTCTCTCTT	TGACAGTCAT	GATTCAATGT	ATCCTGGTTA	TCGTGGCCCA	180
GGGTATCTAA	GTGCTGATCA	GCATGGCCAG	GAAGGTTTGG	ATCCAAATAG	AACACGAGCC	240
TCGGACCGAC	GTGGAATTCC	TGCCCAGAAG	GCCCCAGGCC	AAGATGTCAC	TCTTTTCAGG	300
						300
MOTCCAGACT	CCGTCGACCG	AGTCTTATCA	GAAGGGAGCG	AAGTCTCGAG		350

- (2) INFORMATION FOR SEQ ID NO:1258:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 335 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1258:

GAATTCGGCC	TTCATGGCCT	AATTGAATCG	AGCTGGTTAA	GTTTCACTAG	GAGGCGCNAA	60
AAAGGAGCCG	TTTTTGACTT	AACATTTTAA	TTCTAGTAGA	GATAAGAAGA	GCTTGTGTGG	120
GCTTACAGTC	CTTCACCTGA	CTGTCCTTCA	CCAGTGAGTA	GCATACCAGT	TCTTCAAATG	180
TCCTATACTT	TGGAAAGCAG	ACCCGACTCT	GGAGCACTCG	CCTTAATTAG	ATTCTGAATT	240
TCCTTGAATT	TTGGATGGTC	CTTATCAGCT	ACCAGCTGAA	GCAGAACAGC	CTCACTCGTG	300
GTCACTATGA	TCCCGGTTCG	AGCGAGACGC	TCGAG			335

- (2) INFORMATION FOR SEQ ID NO:1259:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 621 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1259:

TCCAGTTGAA	TTTAATAGAA	TTCGGCCTTC	ATGGCCTAGC	CGACCGTTGA	CTATTCTCTA	60
CAAACCACAA	AGACATTGGA	ACACTATACC	TATTATTCGG	CGCATGAGCT	GGAGTCCTAG	120
GCACAGCTCT	AAGCCTCCTT	ATTCGAGCCG	AGCTGGGCCA	GCCAGGCAAC	CTTCTAGGTA	180
ACGACCACAT	CTACAACGTT	ATCGTCACAG	CCCATGCATT	TGTAATAATC	TTCTTCATAG	240
TAATACCCAT	CATAATCGGA	GGCTTTGGCA	ACTGACTAGT	TCCCCTAATA	ATCGGTGCCC	300
CCGATATGGC	GTTTCCCCGC	TGCATGCTAG	TTATATTTCT	CCAACATAGA	TTAAATACAT	360
ACATGACTAT	TAAAATCTCA	GGGTTCTTCT	ATGTGTCCCC	TAAAAGCATG	ATGTATGCCA	420
GTGGTCATCT	GTCCACCACC	ATTTGGGGAC	CACGGCATTT	AGGTAAAGTG	GGTCTCGGAT	480
GACCTCCTTC	AGCTTAACAG	CAGGAGTTGA	GATGGAGCCC	TTGCAATTTC	CCCACTGAAT	540
TCCAGAAGCA	AGGAGAAAGA	CTGAAGTGAC	AAGTACCGCA	AGACAGACTT	CAGGAACAAT	600
TCGTTTAAGC	TGCAGCTCGA	G				621

(2) INFORMATION FOR SEQ ID NO:1260:

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 322 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1260:	
GTTTTGTGAT TCTCCAGGAC AGATGATGAA AAACAGTGTA GATAGTGTCA AAAATTCCAC TGTAGCCATA AAATCTCGAC CTGTTTCAAG AGTTACCAAT GGAACTTCCA ATAAAAAAAG TATCCATGAA CAAGACACTA ATGTAAATAA CAGTGTACTA AAGAAAGTCA GTGGCAAAGG ATGTAGTGAG CCAGTACCAC AGGCAATTTT GAAGAAAAGA GGAACTAGCA ATGGATGTAC TGCAGCTCAG CAGAGGACAA AGAGTACCCC ATCTAATCTT ACTAAAACTC AAGGATCCCA AGGAGAGTCA CCAATACTCG AG	60 120 180 240 300 322
(2) INFORMATION FOR SEQ ID NO:1261:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 276 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1261:	
GCCCTCATGA CTCGGATCCA ACCTGCCTCG CAGGGAGTCG AGCTCTCCGG CCTCTCAGCC GCCATCAGCC ACTTCCTGAA CTGCTTCCTG AGCTCCTACC CAAACCCCGT GGCCCACCTG CCCGCCGACG AGCTGGTCTC CAAGAAGCGG AATAAGAGGA GGAAAAAACCG GCCCCCGGGG GCTGCAGATA ACACAGCCTG GGCTGTCATG ACCCCCCAGG AGCTCTGGAA GAACATCTGC CAGGAGGCCA AGAACTACTT TGACTTCGAC CTCGAG	60 120 180 240 276
(2) INFORMATION FOR SEQ ID NO:1262:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 292 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1262:	
GAATTCGGCC TTCATGGCCT ACAAAGAAAG CAAGCCACAA ACAATAATGA AGCAAAAAAT GGAATCTAAG AATCTTTTTG TATGGAATAT TACTTCTATC AGAAGATGAT CAAGATGTTT CAGTCCAGTG CACATCAGCA TTGCTGACAT TTTATGGATT CTAAACTTGT GTTGTTTCTT TTTTAAATCA ACTTTTTAAA AAAATAAAGT GTAAATTAAC CGACTAGAGT ACTTGGAAAA TGTGATCAGT ACAAGTGAAC TTAGGTTGTT GCCAACAGGG TCCGTACTCG AG	60 120 180 240 292
(2) INFORMATION FOR SEQ ID NO:1263:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 439 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1263:

GCGATTGAAT TCTAGACCTG C	CTTGATGCC	AACTAAGGAA	ATTTGTTTAG	CATTGAATCT	60
CTGAAGGCTC TATGAAAGGA A	TAGCATGAT	GTGCTGTTAG	AATCAGATGT	TACTGCTAAA	120
ATTTACATGT TGTGATGTAA A	TTGTGTAGA	AAACCATTAA	ATCATTCAAA	ATAATAAACT	180
ATTTTATTA GAGAATGTAT A	CTTTTAGAA	AGCTGTCTCC	TTATTTAAAT	AAAATAGTGT	240
TTGTCTGTAG TTCAGTGTTG G	GGCAATCTT	GGGGGGGATT	CTTCTCTAAT	CTTTCAGAAA	300
CTTTGTCTGC GAACACTCTT T	AATGGACCA	GATCAGGATT	TGAGCGGAAG	AACGAATGTA	360
ACTITAAGGC AGGAAAGACA A	ATTTTATTC	TTCATAAAGT	GATGAGCATA	TAATAATTCC	420
AGGCAAATGG CAACTCGAG					439

- (2) INFORMATION FOR SEQ ID NO: 1264:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 486 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1264:

GAATTCGGCC TTCATGGC	CT AGGGGAGGCC	GCGGNGGGGA	AAATGGCGGA	CGGGAAGGCG	60
GGAGACGAGA AGCCTGAA	AA GTCGCAGCGA	GCTGGAGCCG	CCGGAGGTGA	ACACAACCCC	120
AGCGTCGTGG GCAGCGTG	GG ATGCTCCGGG	CCTTTCTTTG	AGCTCCCAAG	GTGGGGGGAG	180
TGGGGTGGGG CGAAAATG	GG CGGATCTGGA	CCTCACCCGG	ACAGGTGTTG	GGCCCAGACC	240
TGCCTCCGGG CNCGCCCC	GA TGCGGCCCTC	CTGGGCTCCG	GGCCTACATC	GCCTCCTTGC	300
CTGGGGAGAG CCGGCCAC	TG TTCGTCACCT	CCTGGCCCCA	GCGGAGGCCC	TGATTCCGAG	360
GAGAAGGGAG ATGGGCGC	CA GAAAGGGAGA	CCGAACTCGG	GGTGGGACCA	GGAGCGGCGG	420
TGCAGGAGCC GCTACCGC	CA CACCGGAGAC	GCACATCACA	CAAAACACAC	ACACCGGATT	480
CTCGAG					486

- (2) INFORMATION FOR SEQ ID NO:1265:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 317 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1265:

GAATTCGGCC AAAGAGGCCT A	AATTTATTGT	TGGATCAATC	AAAATTTTCA	TCACTTAAAA	60
GAACCATGTC TATTAAAGAA 1	CTAGCTCAC	TGGAGTGCAT	TGCCATTCCA	AAAAAGAAGA	120
TGAATTTAAA AGATAAAAGC C	CATGAAGGTG	TTGCTTGTGT	CCAGAAAGAA	AAATCAGTAG	180
TTAAAACCTG GTTCTGTGAA T	rgcaatcagc	GATTCCCAAG	TGAAGATGCA	GTAGAAAAGC	240
ATGTTTTCTC AGCAAACACA A	ATGGGTTATA	AATGTGTGGT	CTGTGGAAAG	GTATGTGATG	300
ATTCAGGGGT TCTCGAG					317

- (2) INFORMATION FOR SEQ ID NO:1266:
  - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 479 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1266:

GAATTCGGCC AAAGAGGCCT	AATCTTTTCC	TTTCTTGTAA	<b>GTTAGAAGAA</b>	ATAACCTCTT	60
CAGTTAAACC TTCAGTGAAG	GTTCTTTTAG	TTTTCTGTTC	TGCTTTCTAA	AAACATAGAC	120
TCTGTTCTTT AGAGCAACTT	ATGACTCTCA	TCTCTGCTGC	ACGAGAATAT	GAGATAGAGT	180
TCATCTATGC GATCTCACCT	GGATTGGATA	TCACTTTTTC	TAACCCCAAG	GAAGTATCCA	240
CATTGAAACG TAAATTGGAC					300
TACTTGAAAC TAGAAGTTTA	CTCAGTTGCT	TTTACGATGT	TAAAAGGAAA	TCAAATTCCT	360
ATTTCTTTGT TTTCTTTTTT	TGTTTGTTTG	TTTTGTTTTT	TGAGACAGAG	TCTTGCTCTG	420
CACTCCAGCC TTGGGCAACA	GAGCAAGGCT	CTCAAAATAA	AAAAGCAGCG	ACACTCGAG	479

- (2) INFORMATION FOR SEQ ID NO:1267:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 615 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1267:

GAATTCGGCC	AAAGAGGCCT	AGGGTTTATG	CCAACAAAAG	GAGAGGGAGC	CATAGGTTCT	60
CTAGATAACA	CTCCTGAGGA	AAGAAGAGCA	CTTGCCAAAA	AATCACAAGA	TTTCTGTTGT	120
GAAGGATGTG	GCTCTGCCAT	GAAGGATGTC	CTGTTGCCTT	TAAAATCTGG	AAGCGATTCA	180
AGCCAAGCTG	ACCAAGAAGC	CANAGAACTG	GCTAGGCAAA	TAAGCTTTAA	GGCAGAAGTC	240
AATTCATCTG	GAAACACTAT	CTCTGAGTCA	GACTTAAACC	ACTCTTTTTC	ACTAACTGAT	300
TTACAAGATG	ATATACCTAC	AACATTCCAG	GGTGCTACGG	CCAGTACATC	GTACGGACTC	360
CAGAATTCCT	CAGCAGCATC	CTTTCATCAA	CCTACCCAAC	CTGTAGCTAA	GAATACCTCC	420
ATGAGCCCTC	GACAGCGCCG	GGCCCAGCAG	CAGAGTCAGA	GAAGGTTGTC	TACTTCACCA	480
GATGTAATCC	AGGGCCACCA	GCCAAGAGAC	AACCACACTG	ATCATGGTGG	GTCAGCTGTA	540
CTGATTGTCA	TCCTGACTTT	GGCATTGGCA	GCTCTTATAT	TCCGACGAAT	ATATCTGGCA	600
AACGAATACC	TCGAG		•			615

- (2) INFORMATION FOR SEQ ID NO:1268:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 515 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1268:

•	GAATTCGGCC	AAAGAGGCCT	ACAGAACTTT	TGTCAAATGG	AGTGTTACCC	ACAGTCAGAA	60
	TCTAGCCACC	AAAATGGGAA	GGGAGTGNAG	CTGCCCTGTC	CACAGGCTTC	TCTATGGGAA	120
	ANGCTGCTGT	TCTGTAAAAC	ATGNTGGGGC	NGGCTGTGGG	GANGAAGGCA	TTTTCTGGAC	180
	CACATGNACG	AATTCGAATT	GGGGGACGGT	CCTACCCCAG	TGAGGAAGCT	GAAAGAAATG	240
,	GGCCTGATTT	GGTGCAGGAC	ANCCCCTGAA	GACCGTGAGG	CCCCTGGCCT	CTGCCGCAGA	300

TGGGAGCCTC AGCAGCANGG TTTAGGGCAG CACCCAGGGC ATCCTTGCCA CGTGAGGCTG

CCGTTGGTGC CTGGGCATCA GTAGCTCAGG CTGGAATAAT TGGAAAGGAA AAGGCAGGAG

360

420

GANCCCCTGA GGCCAGGCCA TTGGGCTGGG GAGCTGTTAA GCTGAGGTGG CCCTAGGGCC TGCCGGGGCT GGGGGTGGCA AGCCAAACTC TCGAG	480 515
(2) INFORMATION FOR SEQ ID NO:1269:	
.(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 229 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1269:	
GAATTCGGCC AAAGAGGCCT AGTGCAACTG ATCTGTCCAG TTTGTGTATG AAATGGATTT GATAAAGTTT TTGCTAGTTA TTTACTACAT TTTGGGATTA ATAAGTGATT TATATGCATA TTTTTCTGTA AATCTACAGT TTTTTGTACA AGATATTCTA CAAGTTATGA AGCTAAGGGA AGAAAATGCC AAAGATACCT CTAGTTATGT TGAACACAGC CAGCTCGAG	60 120 180 229
(2) INFORMATION FOR SEQ ID NO:1270:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 128 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1270:	
GAATTCGGCC AAAGAGGCCT AGTATGCCCT TAAATCTGGT TATTAGGTAA TTCTTTTCCG AGTAGGAGCC CAGATCAACT CACAGTGTTC CTGAGTCCTG GGAGATTGAA TTCTAGACCC GCCTCGAG	60 120 128
(2) INFORMATION FOR SEQ ID NO:1271:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 412 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1271:	
GAATTCGGCC AAAGAGGCCT ATTTAGCACA AATTTCTTTT TGCTTGCCTT TTCAGATTTT AAAACTATTA GAGAAAAACA TACTTGATTG CTAAAATTTG TCAAACATAA ATAGTAGACA CAATTTAGTA ATAATCATAT TAATAATCAT AATCATTAAT ACTCATAATA ATCANACAGA GGACGCCCTA AAATGTACAC TGATTAAATT TTATTTTTTT CCCATGCATA GCTAGCCTGT TTGTACAACT TTACTTTTGC TGCTGCATGT AACCAGATGA TTTTTTAATC AGATTACTGC CTTTCTGATT TATTTAGAAT TTTTTTTCTT TTTTTTTTTT	60 120 180 240 300 360 412

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 480 base pairs

(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(D) TOPOLOGI: Tinear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1272:	
CANTECCCC ANACACCCT ACTOMINATE CANACACTOR	
GAATTCGGCC AAAGAGGCCT AGTTTTAAAG GACAGGTTTA AATAGGCTTA CTTTTTCTT TTAAGTTCAG ATACCTAAGC CTTATGTCCC TAGCCGCAGT TTTCAGATAT TTGCAGCTAA	60
TTAATTCTTA GGAAATCTAA TCTGAATTGA ATTAATTTTC CCTTTTAGGG CACACGAAGC	120
AACTTTTAGG TAAGAAAAA AATGAAAACA GCTTTTGTTG CACATAATTC TTGCAACTAA	240
TGAAAAGTAA TATTGCTGTT CCCTTCAAAT AATGCAATAA CAAAACACCA AATGAGAGCA	300
TTGCATTGTA TTGTTATATT TGCTGTTTAA ATAATTTAGC TGCAAAAATC TGAGGGCTGC	360
TTTAGCTGTA ATTAATTATT CATTAATGAC ATGCTAATTG CACAATACCT TTGAATATTT AACAAAATGC AAAAACCAGG CTCTGAAGTT ATGTTTTTAG TGCAAGGGGG ACACCTCGAG	420
ANAMATOC ANAMACCAGO CICIGAAGII AIGIIIIIAG IGCAAGGGGG ACACCICGAG	480
(2) INFORMATION FOR SEQ ID NO:1273:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 293 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(,	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1273:	
GAATTCGGCC AAAGAGGCCT AAGACCAGCC TGGGTGACAG AGCGAGACTC CGTCTCAAAA	60
AAAAAATTGA ATGAAGCAGA AATTTATTCT TTTAAGCCCA TTTAGCTGTT ACACACATAG	120
TTATAGCATA TTCTCTCTTG AGATAACTTG CTTTTAATTG GAAAACTAAT TCATTAAATA	180
TCCAAACTCT ATATCATTTC TGGAATAAGT GATTTTAGCA ATTTTTGATA CTTATTCTAA	240
CATGATGCAT ATATTGAGTA TGTACTTTTC TTTAAATGCA GGCAATACTC GAG	293
(2) INFORMATION FOR SEQ ID NO:1274:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 194 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1274:	
GAATTCGGCC AAAGAGGCCT ACCGCTTTTT TTTTTTTTTT	60
CAGGAGGAGG CTTGAAAGCT TGAATTTAAT TACTCCTCCA TCTCCTCATT ATTCCACCCA ACTCCCTACT TCCCCATCTC ATTTCACAGC CTCCACCAGC TCTCCCCTCA GGCCTCCTAG	120 180
ACATCGCGCT CGAG	194
(2) INFORMATION FOR SEQ ID NO:1275:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 164 base pairs	
(B) TYPE: nucleic acid	

(C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1275: GAATTCGGCC AAAGAGGCCT AAGAAGAAGA AAGAAAAATT GGAGAGAAAA AAGGAGTCTT TAAAAGTTAA AAAGGGTAAA AATTCAATTG ATGCAAGTGA AGAGAAGCCA GTTATGAGGA 120 AAAAAAGAGG AAGAGAAGAT GAATCATACA ATATTTCAGA GGTC (2) INFORMATION FOR SEQ ID NO:1276: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 465 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1276: GAATTCGGCC AAAGAGGCCT ATTTGGATGG CAACGAGCTC ACCCTGGCTG ACTGCAACCT 60 GTTGCCAAAG TTACACATAG TACAGGTGGT GTGTAAGAAG TACCGGGGAT TCACCATCCC CGAGGCCTTC CGGGGAGTGC ATCGGTACTT GAGCAATGCC TACGCCCGGG AAGAATTCGC 180 TTCCACCTGT CCAGATGATG AGGAGATCGA GCTCGCCTAT GAGCAAGTGG CAAAGGCCCT CAAATAAGCC CCTCCTGGGA CTCCCTCAAC CCCCTCCATT TTCTCCACAA AGGCCCTGGT 300 GGTTTCCACA TTGCTACCCA ATGGACACAC TCCAAAATGG CCAGTGGGCA GGGAATCCTG 420 GGGTCAGATT TTTATTGTGG GGTGGGATGA GTAGGACAAC TCGAG 465 (2) INFORMATION FOR SEQ ID NO:1277: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 302 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1277: GAATTCGGCC AAAGAGGCCT AACTGTGGTT CTTACATCCT AACAAAAGCT GCCCTCCCCG CACATTCTTT TGTATGTTCC TTAAGCTTAA AGATGAATAG ATGCTTAAAG TATGCAACTA 120 TGGCATTTGG AGTGCAAGAC AACTTGAAAA AGAGTGTGAA AACATTGTCA GATATAAAGT 180 TACTTCAATT CTTTGGAGTC TGTTTCCTGT CATGCTTAGA TGTTTGGAAT CTTAAAGTTA 240 CAGAGGAACT GTTCTCTGGT AACAAGACAT GTCTGAGTTT GTGGACTGCA CGCGATCTCG 300 302

- (2) INFORMATION FOR SEQ ID NO:1278:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 401 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1278:

GAATTCGGCC	AAAGAGGCCT	ATAGGCCTCT	TTGGCCGGGT	TAGCCTAAAG	GAGAAAAAG	60
CAAGGCTCAA	GAGAAATTAG	ACAGCAGCTT	TCAAATATTT	TTAGAGAAGT	AGGTTAATTA	120
TGGTAGTCAT	TCAACAAGGT	AGAAATCATA	CCAAGCATGA	AGTCACAGGA	ATGTCCCAGG	180
AGTGTGCAAC	CATTGGAACT	GTCCATAGTA	AAATGGGCCA	GCTTGAGCAA	TAAAAGTCTC	240
CTAGTACCAG	GAAATGCTTA	GAGGTTGGGG	AAAGTGAAAA	AAAGGGGGAA	AGTTTGGTCA	300
GGTTGGGGAG	CAGTCACACT	TCTTCCTGAG	AGGTAGTAAA	TACCAGGCTC	TCCATCTGGA	360
GGAGGGGTCA	GTAAATCACG	TTTGCAAAGG	<b>AATATCTCGA</b>	G		401

- (2) INFORMATION FOR SEQ ID NO:1279:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 391 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1279:

GAATTCGGCC	AAAGAGGCCT	ACCCACCCCT	ACTCCTCAAC	ACTTCTGGTT	TGCCCTGACT	60
TCTCTACGGC	TCTGGCTTCT	TCCCGAAGAG	ATATAGGAGC	CATGTAAGCA	CGCAGTGGGT	120
GAACTGCTTA	ATTTCACTAC	ATGTTGATGT	ACTTGTCTTC	CGTCCTGTAG	GTCTTTTCTA	180
TATAACTTTA	TGCCACCCTT	AAATGAATCA	TTGGGTATAC	CTGTCATGTT	GGATCCTGTA	240
ATCACAGTTT	TCCCTGCTCA	CCTTTTTGTC	TAAGATCTAT	TGAGAAAGGG	AAATATGGGA	300
AGGAGAACCA	TTTGATCAGA	ATACAACCAA	TAGTCTTTAA	GCATTGTTAA	AGTATGAAAC	360
TGAAATACAT	TCAAAACACT	TTACACTCGA	G			391

- (2) INFORMATION FOR SEQ ID NO:1280:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 326 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: cDNA
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1280:

GAATTCGGCC	AAAGAGGCCT	AGGACTCCAC	ACTCCCAGA	TCCCAGTATG	ACTACATCTT	60
GCCTCAAGTT	TCTTTCACCG	CAGTGGGCTA	CCATAAACAC	ATCACCTTGA	TTTTTAATCC	120
CACGAGGAAG	CTGCCTGAAC	AGGACATCGC	ACAAGGATCC	TACATTGCCC	TGCCATTGAC	180
GCTGCTGGTT	CTGCTGGCCG	GTTACAACCA	TGACAAGCTC	ATTCCTTTGC	TGCTGCAGTT	240
GACAAGCCGG	CTACAGGGAG	TCCGCGCGCT	CGGCCAGGCA	GCCTCTGACA	ATAGCGGCCC	300
AGAAGATGCA	AAGAGACAAC	CTCGAG				326

- (2) INFORMATION FOR SEQ ID NO:1281:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 367 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1281:

GAATTCGGCC	AAAGAGGCCT	ACAGATGCAG	ACACGGTGTC	CGACGAGTAT	TCTGACGAGG	60
				CAGTGCCTCC		120
CCCGCACCTG	GGCCGCTGTC	CGTCTAGCGC	TCTAACAGTC	TTACACCTTG	GCTTTCTCTG	180
TCCCTTGAAA	GAATTAACTA	TATCTACTGT	GGACTGTTTC	ATAAAACCAA	CCTATGGTGT	240
				ATGATTGGGT		300
	TAGCTTCAGA	ACAGACCCTT	GTTCAAACAT	CTCATGATCT	TCGCTAACCA	360
TCTCGAG						367

- (2) INFORMATION FOR SEQ ID NO:1282:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 560 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (x1) SEQUENCE DESCRIPTION: SEQ ID NO:1282:

GAATTCGGCC	AAAGAGGCCT	AAGAGAAGTG	TCAGCCTCAC	CTGATTTTTA	TTAGTAATGA	60
GGACTTGCCT	CAACTCCCTC	TTTCTGGAGT	GAAGCATCCG	AAGGAATGCT	TGAAGTACCC	120
CTGGGCTTCT	CTTAACATTT	AAGCAAGCTG	TTTTTATAGC	AGCTCTTAAT	AATAAAGCCC	180
AAATCTCAAG	CGGTGCTTGA	AGGGGAGGGA	AAGGGGGAAA	GCGGGCAACC	ACTITICCCT	240
AGCTTTTCCA	GAAGCCTGTT	AAAAGCAAGG	TCTCCCCACA	AGCAACTTCT	CTGCCACATC	300
GCCACCCCGT	GCCTTTTGAT	CTAGCACAGA	CCCTTCACCC	CTCACCTCGA	TGCAGCCAGT	360
AGCTTGGATC	CTTGTGGGCA	TGATCCATAA	TCGGTTTCAA	GGTAACGATG	GTGTCGAGGT	420
CTTTGGTGGG	TTGAACTATG	TTAGAAAAGG	CCATTAATTT	GCCTGCAAAT	TGTTAACAGA	480
AGGGTATTAA	AACCACAGCT	AAGTAGCTCT	ATTATAATAC	TTATCCAGTG	ACTAAAACCA	540
ACTTAAACCA	GTAACTCGAG					560

- (2) INFORMATION FOR SEQ ID NO:1283:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 284 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1283:

GAATTCGGCC	AAAGAGGCCT	ATTTTCATCA	ATAGTAAGTT	TTTATTGTCT	GCTAATTTGG	60
TAGATAAGTT	GAGACATCTC	ATTGTTACTT	TAATTTGCAT	TTTCTCCACA	TTAGAAAATA	120
TTTTCATTGG	TTTATTGACC	ATTTGCATTT	CTCTTCTATA	AATTGACTTT	TTATATTTAT	180
TTGTCTCTAT	TTCTGTATTC	TGTTGATAGT	CAATTTATAG	GAACCTTCTG	ACAGATATGC	240
ATATTCATTT	TATGTGTGAG	TTATTTTTGT	GGCACTCACT	CGAG		284

- (2) INFORMATION FOR SEQ ID NO:1284:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 344 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1284:

GAATTCGGCC	AAAGAGGCCT	ACTTCGGTTG	CGGGATTCCT	CCTCTGCCTG	GGTCATTCTT	60
					TTGTATAAAT	120
					GCAGTCAAAG	180
					ATGAACTTCA	240
					CTGGATTGAA	300
	GAATTAAATT				CIOCALIONA	344
	~·-·-·		rogramorer	CONO		244

- (2) INFORMATION FOR SEQ ID NO:1285:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 586 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1285:

GAATTCGGCC	AAAGAGGCCT	AGGGAATTTG	TTTTTGCATA	GGGGAATAGG	TAAACCAAAA	60
GTGGTATTAA	AAGCAGTGCT	ATAGTAAAAG	GAGATTTTTT	TTAACTCCAC	AATAAAAAGT	120
TTAGGCCCAA	TTTCATAGTA	AAACTATTCT	AATTAAGGAT	TGAACATATT	ATCACTTGCC	180
TTGATTTTGA	CCAGTGACAT	TTTTTGGCTT	CTTCATTTCA	CCTGTGACCA	TCTGAATGCT	240
TTCTATTTGG	CTCTTTAATG	CCCAGATTTT	ATTGACATTG	GTGGCGAATC	CCTATTCATA	300
CACAGACAAA	GCATCTGACT	TTGTCCAAGA	AGCAAGCATG	CTGCAGGCCA	CTATGACGAA	360
GCAAGAAGCC	GATGACATGA	GCATTCCCAT	CTCCCACATT	GACGATGTTC	TCGACATGGT	420
GGATGTCCTG	GTGGAGGGCA	GTGAAGGCTT	GGATGAGGAA	ATAGGGTTCA	CGTTGAGTGA	480
AGACATGATC	CTGCTCACGT	TCCCATTCAG	TGCGGTAGTC	CCTGCGGCCC	TGGAAGCCAG	540
GAATAAGTTG	CTCCTTGGGA	CAGGCAATGA	AGCAGATACC	CTCGAG		586

- (2) INFORMATION FOR SEQ ID NO:1286:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 497 base pairs
    - (B) TYPE: nucleic acid.
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1286:

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GAATTCGGCC AAAGAGGCCT AGTTGAACAT AACTTGTAGT GTGAATATGG TTAAAACAAA
                                                                      60
GGACACCTGA TGTCTGTGAA GTCTGCTAAG GACAGGTACA AAATTTATGC ATTGCTTTTT
                                                                      120
AAAAGTTTA AAATGAGGAA TGCTTTTGAT AATCAGAAAG ACTAATGTAA AGTGCTGACT
                                                                     180
GATGTCCTGT CTGCAGTTAA GGAAGACACC CAACTCTCTT CTTCCTCATC ATGGTATTCT
                                                                      240
CTATGTATAG ATCTCTAAAA ATGCAAACTT CCTATGGACA AGACAATATG ATTTGCTATA
                                                                     300
ATATGAATTA AGATATGGTA ATATCTAATA GTCTCCACTG CTAGGATTCT GAGTAACACA
                                                                     360
AAAAATAGGT TTTATAAAAA GCCCATGCAC TTCAATTGGT GGGGGAAAAG AATAAAGTCA
                                                                     420
TTTTCAGTCG ACTGACTCTG TAAAACAGAT TACCAATATA ACAAGCTATG TTATCTAAAT
                                                                      480
TGCCCTGGCT ACTCGAG
                                                                      497
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(2) INFORMATION FOR SEQ ID NO:1287:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 329 base pairs

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(B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1287:
GAATTCGGCC AAAGAGGCCT ACAGGAGTTC ATTTTCATCC AAAACAAACA CTGGACTTCC
TGCGGAGTGA CATGGCTAAT TCCAAAATCA CAGAAGAGGT GAAAAGGAGT ATAGTAAAAC
                                                                     120
AGTATCTAGA TTTCAAACTT CTCATGGAAC ATCTGGACCC TGATGAAGAA GAAGAAGAAG
                                                                      180
GGGAGGTTTC AGCTAGCACA AATGCTCGGA ACAAAGCAAT TACCTCACTG CTTGGAGGAG
                                                                      240
GCAGCCCTAA AAATAATACA GCAGCAGAGA CAGAAGATGA TGAAAGTGAT GGGGAGGATA
                                                                      300
GAGGAGGAGG CACTCCCGGG GAACTCGAG
                                                                      329
(2) INFORMATION FOR SEQ ID NO:1288:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 459 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1288:
GAATTCGGCC AAAGAGGCCT ATGCATCGCG GGAGGCGCAT GGCGGGGATG GCCCTGGCGC
GGGCCTGGAA GCAGATGTCC TGGTTCTACT ACCAGTACCT GCTGGTCACG GCGCTCTACA
TGCTGGAGCC CTGGGAGCGG ACGGTGTTCA ATTCCATCCT GGTTTCCATT GTGGGGATGG
                                                                     180
CACTATACAC AGGATACGTC TTCATGCCCC AGCACATCAT GGCGATATTG CACTACTTTG
                                                                      240
AAATCGTACA ATGACCAAGA TGCGACCAGG ATCAGAGGTT CCTTGGGGAA GACCCACCCT
                                                                      300
ACGAAGTTGG AATGAGACCA TCAGATGTGA TAAGAAACTC TTCTAGATGT CAACATAACC
                                                                      360
AACCTTATAA AGACTAAAAT TCATGAGTAG AACAGGAAAA TCATCCTGAC TCATGTGTTG
                                                                      420
TGTTCTTTAT TTTTAATTTT CAAAGAGGCT CAGCTCGAG
                                                                      459
(2) INFORMATION FOR SEO ID NO:1289:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 333 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1289:
GAATTCGGCC AAAGAGGCCT ACTACCTGCC TGAAATTCAA TGCCGTGTTC CTTCTGGACC
AGTTTTAAGC CATCTCTTCT GTTGTTTCTT TCCTCCCAAA GATGTAGACT TTTCCACTTA
                                                                      120
AAAGCATTTC CAAGATTCTA TTTTTTCATC CTTTTTTCTG TCCCTATTCT CTTTCACTCC
CCACACTTGT TCCTAGCCTG TCTCTGTTGC TCTGATGTCC ATGTTGATGG TGGCGGTCTT
                                                                      240
CAACCATGCC ATCCGTGTGC CAACCCAGCA CTTTCCTGCC ATCCCTGTAG CCCTTGCCCC
                                                                      300
AACATCTGTG CATTTGACTC CCCACCACTC GAG
                                                                      333
(2) INFORMATION FOR SEQ ID NO:1290:
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(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 326 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1290:	
GAATTCGGCC AAAGAGGCCT ATCCACCCGC CTCAGCCTCC CAAAGTGTTG GGATTGCAGG TGTGAGCCAC TGCGCCTGGC CTAAACAAAC TTTTTGAAAA GCTGTTTCTA AAAGATTCCT TAAATTCAGA TATGACAGCT AATTACCTCA TCATAAATTA CTTTTATACT AATTGTTTCC AGGGTTTTAG AGTAGTTGAA TGTTTATTTC ACAAGGCACC CTAAATTCTA TAGAAATAAA ACCTCAGATG AGTCTCCTTC TTAGAGTGTT ACAATGAATG GGAGTTTACA ACTTTTATGT GTCATGTTTC CAACAGCTAT CTCGAG	60 120 180 240 300 326
(2) INFORMATION FOR SEQ ID NO:1291:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 281 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1291:	
GAATTCGGCC AAAGAGGCCT ATTGAATTCT AGACCTGCTG CTTCGTGCTC GTCCAGTACA TTGGCTTTGA AATATACTTG AATTTGTGGA GGCAGGGTGT AGAATGACAA AAACAAACAA AAACCCCACA ATACAGACCA AATTGGGGTA CACACGGACA GATTGGTTTT AATTTTATTT TAATTTTTGA GTTTCTATGA GAAGAAGAAT GAGGAGAGAC AAAAAAGGGG AAGAGTGAGA GATAGTATAT TTAGGGTATG ACAAATCAGG GATGGCTCGA G	60 120 180 240 281
(2) INFORMATION FOR SEQ ID NO:1292:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 367 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1292:	
GAATTCGGCC AAAGAGGCCT AATTAAACTA AATCTTAGGG ACTTAGGGAT TTAAACTAAA TCCCCACCAC ATCTGATTC CCCTTCCTCG AAATACCAAT AGTACGTGCA ACACAGACTT GTAGCTCAGA GGTCGCATGC TGTTTCAAAT TCTTGGGATA TGCATGTTAC TTTTTTTTAA AGAAGTGGTA TATCAGACAC CTGAAGGTCA AGTCTCTCTG TGCCACCAAC AAACTCTCGT GACCTTGAGC CCCTCCTCT AATTCCTCTT CGGTAAAAGA AATACCTCAC AGTGGCTGTG CAATCACCAA ATAGGAACTA CAGGTGGCAT TATTTATCTT TTGCCCTTGT GTAAGAAAAG ACTCGAG	60 120 180 240 300 360 367
(2) INFORMATION FOR SEQ ID NO:1293:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 234 base pairs	

(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1293: GAATTCGGCC AAAGAGGCCT AGGATATTTT AAATTTTGTT AATTTTGTTT CGTGGTCTCT 6.0 GCCTGAATAG ACAGGCACTT GCCTGGAACG TAATACTGTT TCACTGCCTC GTTTTTACCT 120 GTTTAATCTA GAACCAAATT GTGTCAATGT GTCAGCCCGT TTGTGCTTTT ATAACAAAAT 180 ACTACAGACA GTAATTTATA AAGAATAGAT ATTTATTTCT TCACAGTTCT CGAG 234 (2) INFORMATION FOR SEQ ID NO:1294: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 562 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1294: GAATTCGGCC AAAGAGGCCT ATACTGATCC TCTCCCCTTG TGCATCACTT TTTCAGTGCA 60 GATATCTTGT AGCTCCGTGT CTAGAGGTAG CCAAGGTATC CTCCTAGCTT GCCTTCTTGG 120 TTTTATACAT GCTTCAGTAT GTAAGACAGC TTGTAGTCCA AACTCATGAG ATGACTATTC 180 TGCCTGCCCC ATCTTACCTC AACAAGTGAG CCTGCATGCA TGTGCTCCTC AGTCTAGTCC 240 CAGGATAGGA GGTAGGGGTC TCACATCGAC CTCAAGTTCA TATGACTTTT TCTAACTCAC 300 CTTTACCACA CAGCCCCTAC TGTGGGGCTT ATAAAGTGTC ATGGAGATTT GTGAAGTCAA 360 TGTTTCCTTT CCTTGTTTAT GTGCTTTATA AATTAGGTCC CTCTCCAAAA CTTTTGCATC 420 ATCCTAAACT GAAACACTAT GCCCATGAAG AAGTCATTAA ATAAAAGACT GATAAATTTG 480 ACTCCATAAA AATTAAAATT TTCTATATAG GAAAAAATGC CTCAAAGTCA AAAGTCAATC 540 ACCAAACTGG GAGTTACTCG AG 562 (2) INFORMATION FOR SEQ ID NO:1295: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 322 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1295:

GAATTCGGCC AAAGAGGCCT AGACACCCGT	CATTGCAATT	TATATTTTAA	CAAAGGCTTC	60
TGATCCTAAT TTCAGGAAAT AGCCTCTAAA	CTCATCTATT	AGTCCCAAAT	TCTTTACCCA	120
TTAAATCTGC TATTTTATGC CTCCTATATT	CTTACCTTCA	GATGTTGAGA	GGTTGGGGCA	180
TAAAACTTTG CAGCACGTCT GCAGTCTTCC				240
TCTTTTATT CTCTTCAAAG TTAAATCATA	TTCCAGCATT	CATGGTATTT	CTCCAGCTTG	300
TCCTCCACAC TCACCCCTCG AG				322

- (2) INFORMATION FOR SEQ ID NO:1296:
  - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 313 base pairs

- (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1296: GAATTCGGCC AAAGAGGCCT AAGCTGTTCG GGTACTTGTC AAAAATGGCT TCCAAATATA TTCCTTTTAA TACAGGATGT GAAAACACTT CCTAATAAAT TCCTGCAAAA TTAGATGATA 120 CTGTATGTAC TTCTGAAGGA CAGACAAGAA AGTAACCTAA GACCAAAACA ATAGAGGTCT 180 CCTACTACTG GGGAGAAGGA GGATTATCAA GAATAGAGGA AAACAGAGCC TGCCTAAGAC 240 TAATACTGGT CTAGAACAAA AGAGAAAGCT CAATTCCTAC CACCACAAAG CTAAACAGCA 300 TCCAAGGCCT CGG 313 (2) INFORMATION FOR SEQ ID NO:1297: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 340 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1297: GAATTCGGCC AAAGAGGCCT AGATTTTTGT CTTTAATTCT CTGTGTTTTC AGNACCTTGC 60 GATTTTTAAA GTATATTAAC CTTTTCTCCT AGATGTTTAC CTTTGAAATA CCTCTCTCT 120 CTAATGATTT AGACCTATGT GTCCAACTAC TTTTCGGACA TGTTTCCCTA GATGTCTCAT 180 GGTTAACTCC AATTTAACAT TTCCAAAGTT AAATTTATTT TATTTTACCA GACTTGGGTT 240 TTTTGTTTTC TTTGTTTTTG CTTTTTCCCT TTTTAAGATA TCCTGGAGTC ACCAGAATCC 300 TATCTAGATA CCCTTGGTTA GAGTTGCTCA TGATCTCGAG 340 (2) INFORMATION FOR SEQ ID NO:1298: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 370 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1298: GAATTCGGCC AAAGAGGCCT AGCTTCTTCT GAGAGAGTCT CTAGAAGACA TGATGCTACA 60 CTCAGCTTTG GGTCTCTGCC TCTTACTCGT CACAGTTTCT TCCAACCTTG CCATTGCAAT 120 AAAAAAGGAA AAGAGGCCTC CTCAGACACT CTCAAGAGGA TGGGGAGATG ACATCACTTG 180 GGTACAAACT TATGAAGAAG GTCTCTTTTA TGCTCAAAAA AGTAAGAAGC CATTAATGGT 240 TATTCATCAC CTGGAGGATT GTCAATACTC TCAAGCACTA AAGAAAGTAT TTGCCCAAAA 300 TGAAGAAATA CAAGAAATGG CTCAGAATAA GTTCATCATG CTAAACCTTA TGCATGAAAC 360 CACGCTCGAG 370
  - (2) INFORMATION FOR SEQ ID NO:1299:
    - (i) SEQUENCE CHARACTERISTICS:
      - (A) LENGTH: 342 base pairs
      - (B) TYPE: nucleic acid

WO 98/45435	PCT/US98/06954
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129	99:
GAATTCGGCC AAAGAGGCCT AGTTGGAGTT TGCTGATAGA A	001001000 1110000000
CTGCAGGAAT TACAAACTGA AGAGGACTCT GTTGGACTGT T	GGACTAGCT AAAGGCGTCA 60 TTTTTTTTC TTTTNCTTTT 120
TTTTAAGAAA AACCCATTTT TTTCCTTAAG GACTTACTAG C	CAAAATTC TTAAACTTCG 180
AGGACTCTAC TAGCCATGGC CGAGCCATTC TTGTCAGAAT A	TCAACACCA GCCTCAAACT 240
AGCAACTGTA CAGGTGCTGC TGCTGTCCAG GAAGAGCTGA A	CCCTGAGCG CCCCCAGGC 300
GCGGAGGAGC GGGTGCCCGA GGAGGACAGT AGGCATCTCG A	
(2) INFORMATION FOR SEQ ID NO:1300:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 217 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130	0:
GAATTCGGCC AAAGAGGCCT ATCTAGACCT GCCTCGAGTT G CGCTAAGAGA GACCACATTT TATTTGCTGT GTCCAACACA G TTTAGGAATG CCTTCAAGTT CCTCTTTATC TTTATATCTC T CTCTAGAGAA GTTCTAGATC TTTCCCCAAC TCTCGAG	GAATTTAAT AAATGTTGAT 120
(2) INFORMATION FOR SEQ ID NO:1301:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 237 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	•
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130	1:
CCTTCGGAGA GAGGCACGCC CGGCCCGGAC AGTTCAGGCT C	TCTCGGCTC CGGGGAGTTT 60
ACTGGCGTGA AGGAGCTTGA TGACATCAGT CAAGAGATTG C	
TATTCACTGG AACAAGACAT TCGAGAAAAG GAAGAGGCAA T	
GTGCAGGAAT TACAAAATGA CCTAGACCGG GAAACAAGCA G	
(2) INFORMATION FOR SEQ ID NO:1302:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 379 base pairs	

- (B) TYPE: nucleic acid
  (C) STRANDEDNESS: double
  (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1302:

GAATTCGGCC AAAGAGGCCT ACAAAGGAGA CCCTTCATAT CAAAATACAG TTATCAAAAT ATTTTAAAGT TATATATAAT TATGTGCTTC TNTACTAATG TCTTAAATAA TGAGATCAAA CAGCAGATCT TAAAAACTGT CATAATATTT GGAGTAGTGA TGGGCATAAA AGTTATTCTG AGATCCTCCG AGGACTGTA ATGTGATATG AAAAAGTCTG TGACTCCTCT TACCAACAAA GTCTCAAGGTC TCAAGTCTAC TACTAGGGTA TGTTACCTAC ATTCCCTAAG TGAGGGAAAT GTTATGTTTC AGTTGAGGCC AAATGATGGC AATGATGTAA TTTTTTTCTC TTTCAAGTTC ACAGCCCCCC CCGCTCGAG	60 120 180 240 300 360 379
(2) INFORMATION FOR SEQ ID NO:1303:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 285 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1303:	
GAATTCGGCC AAAGAGGCCT ATTTTGCTGA TTTCTTCTTA CATATGAATT ATGTGGGTAT GTTTAATTTT AAGTTAGGAT AAACAGGCGT TAAGTAAGGG TTAGTGTAGA ATTTAAGCAT GTCATTTTTG TAATCTCATC GGGCCTTGAT TTCATTAGTT TAGGCCCTCC ATTTTATAGA TAGTGGTTCC CAGACTTCCC GGCTGCCTCA ATCTCCTGGG TCTTTGTTAA ATAACCTTAA GCAAGCTCAT TTCCCCCAGT GTGTTCAGTT CACAGAAAGC TCGAG	120 180
(2) INFORMATION FOR SEQ ID NO:1304:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 356 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1304:	
GAATTCGGCC AAAGAGGCTT AGTTGGTATC TGCCCAGGGA TAATTGCTCT TAGGGTAAGA CTTTTAACAT GTAAGCCAGC CTGTCAAAAG TGCACCTAAA AGTTCTCTTT CAGTCATTTT CTGAGTTACT GATAGGAACA TAGGTACTGT GTGAATCAGA TCTGAGAGGA TTATGAATGT TATAGAATGC CTTTTGTTAG GGAATTTAAG CCCAGAAGAA GTTGGGAAAG TGACAGATTT ATATAAATGC GAGTGACAAA ACCAGTTAAA ATGTTCTGAC TCAACCTGAA ATATGTTGGA CTATATAAATA AATATAATAT TGTGAGATAT TCTGAACTAG ACTCAACTCC CTCGAG	240
(2) INFORMATION FOR SEQ ID NO:1305:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 489 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1305:	
CTCGAGTACG TAGCGTAGAA ATAGAGAATA GGTCATCAGG TTGGAGGTGG AGTGTTTAAG	60

GACAAAGTTA TAAAGAAGTT TTTTGGTTTG AAAAATTAGA GGATAGGTTT GTACCATAGA CAAATGGATA AGTTCGGAAA AAATCTTTT TTTTTTTTTT	120 180 240 300 360 420 480
(2) INFORMATION FOR SEQ ID NO:1306:  (i) SEQUENCE CHARACTERISTICS:	
<ul><li>(A) LENGTH: 315 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: double</li><li>(D) TOPOLOGY: linear</li></ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1306:	
GAATTCGGCC AAAGAGGCCT AAACTCAAAT AAAGAAGAAA TACAGGAAAA GGAGACAATC ATTGAAGAAT TAAACACAAA AATAATAGAA GAAGAAAAGA AAACTCTTGA GCTAAAGGAT AAATTAACAA CTGCTGATAA ATTACTAGGA GAATTACAAG AACAGATTGT GCNAAAGAAC CAAGAAATAA AAAACATGAA ATTAGAGCTG ACTAATTCTA AGCAAAAAGA AAGACAGTCT TCTGAAGAAA TAAAACAGTT AATGGGGACA GTCGAAGAAC TTCAGAAGAG AAATCATAAA GACAGCCAAC TCGAG	60 120 180 240 300 315
(2) INFORMATION FOR SEQ ID NO:1307:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 212 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1307:	
GAATTCTAGA CCTGCCTCGA GTAAAGCCTG TAGGTAAAAT GGAGACAGAT TTGAAAGAAA TTAGAGAAGA AATTTCCCAA AGGGAAAAGG TGCTAGCAGA GATCAGTGCT ATAAGGGAAA AGGAGATTGA TTTGAAAGAA ACTGGAAAAA GAGACATTCC CATGATGGAG AAAGTATCAG GAAAGATGGC TGTTGTTGAA GGACATCTCG AG	60 120 180 212
(2) INFORMATION FOR SEQ ID NO:1308:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 270 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1308:	
GAATTCGGCC AAAGAGGCCT AGAAATATTA ATGAAATCGC TGAAAAGCTT TGCCTTCGAG AGGCCAGAAG CCTCGCGGAA TGTCTGCAAG TCCAAAGACG CGTGTGGGTT GTGCCCTGAA	60 120

CCTTTCTTCC TGTTTTCTGT TTTTTTAATT TGGGGACTGG TGAGGGCTCG TCCATGTCCT TTGTCAGGTC TTCTTGCTCC TCCCCTCGAG	180 240 270
(2) INFORMATION FOR SEQ ID NO:1309:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 186 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1309:	
GAATTCGGCC AAAGAGGCCT AGTCTTATAC CTGGGATGTA GCTGACAAAT TATTGCATTG TAAAATGAGT CACGTGAATC ACGGAAGCTT TAAACTTTTT CTTTTTATAG CCCTACCTGA ACCCATCCTT CCATCCCTCC AAAAAATTTA CCCAGTAAGT GTTTCTTATA AATTATTATA ATACATTTTA TGTCAAGTGT ATGTAGAACT ATTATAAGTA GTATTAATGT GATTATAAAA GTAGTAAGGC TAAGTACATG ATAACATTTT CTATATATAC CAAGAGAACA TTTAAAATGT TTCATATACT GTTTCAGAAA ACTCTCTTAC TTGTTATTTT GTTATTGGCA GACAGTCTGG TCAGTTGTGT TAATGGTGGA CTCGAG	60 120 180 240 300 360 386
(2) INFORMATION FOR SEQ ID NO:1310:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 373 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1310:	
GAATTCGGCC AAAGAGGCCT ACCATTTAG CCTGCAGGCT TCCTTGGGCT TTCTCTGTGT GTGTAGTTTT GTAAACACTA TAGCATCTGT TAAGATCCAG TGTCCATGGA AACATTCCCA CATGCCGTGA CTCTGGACTA TATCAGTTTT TGGAAAGCAG GGTTCCTCTG CCTGCTAACA AGCCCACGTG GACCAGTCTG AATGTCTTTC CTTTACACCT ATGTTTTTAA GTAGTCAAAC TTCAAGAAAC AATCTAAACA AGTTTCTGTT GCATATGTGT TTGTGAACTT GTATTTGTAT TTAGTAGGCT TCTATATTGC ATTTAACTTG TTTTTGTAAC TCCTGATTCT TCCTTTTCGG ATACTATCTC GAG	60 120 180 240 300 360 373
(2) INFORMATION FOR SEQ ID NO:1311:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 402 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1311:	
GAATTCGGCC AAAGGAGGCC TAAACAGATA TTTACTGAGC ATTTACCATG TTCAGTAACC AGGGCCCTGG GAATATAATA GGAGAAGGCA GATGAGATCC TTGCCTTCAC CAAGCTTATG TTTTTCTATT TTAAGTAAAA TTTGCCATGA CAAAATTTCT ATCAGCGGAA GAGCCAGTAA	60 120 180

CTCTTATTGT AATAGGTTTT ACCCAGTTTT AGAAAAGGAA AGTAGCTAAA CTCTTGGTTC CTTGGTGTGT GTTTTTGTTT GTTCATTTCT AGTACTTGTC TATGTCTTTG GGGTAATTTT TGATTTAGAA TTTTGTAGAA ATTACTCGGC ACAGTGTAGT TGAGGTGAAT ATAGGCAAGA AGGCTTAGGA AGCCTACAAC AAAGGAATCT GACACACTCG AG	300
(2) INFORMATION FOR SEQ ID NO:1312:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 519 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1312:	
GAATTCGGCC AAAGACGCCT AATTGAATTC TAGACCTGCC TCGAGTTGGA CCCTGAGTGT ATCACTCCCA AGTGTGTACT ATTTATACAC AGCAGTTTCC AATGTACTCA AATCAACCTC ATGTTCTTTG CTGTAGTAAG CTGAATGAAC ATGACTCTTG AATCACCTTA AATATGCTTG ATAACATGTC AAACTGCAG GGAAACCTGG TTTATGTCCC ATAGCTACTA GAATTCCTAC ACTTGGCCAG CTTATTTTAA TAGACCATTT CTCAACTACT CTAGCTGTTC TGTCTAGTTC TAAATAAAAA GCTAGGTAGT TGGGTACTAA AAGGCAAATA TGAATATATC AGTGGCTCTG TATCATCTGC AGCAGTGGT CTCAGTTGA TTCCTGGACA GGCAGCACAA GCATCATCAG GGAACCAGTC GGTAATGCAA ACTCTGGGGC GCACTCGAG	180 240 300 360 420
(2) INFORMATION FOR SEQ ID NO:1313:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 157 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1313:	
GAATTCGGCC TTCATGGCCT ACGAGGACGT GAGCAGATAT ACCAGCCCAG TGAACCCAGC	
TGTCTTCCCC CATCTGACCG TGGTGCTTTT GGCCATTGGC ATGTTCTTCA CCGCCTGGTT CTTCGTTTAC GAGGTCACCT CTACCAAGAC ACTCGAG	60 120 157
(2) INFORMATION FOR SEQ ID NO:1314:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 449 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1314:	
CTCGAGTTCA CTACCATGAC AATCATTAAT TAATTTGGTT TCTCTAGTGA GGTTAGTTGC TTTCTTCCCT TCCTCCAGCA TCTGACCAAG GTCTGATTCT ACAGCTATTT GGGAAACAGT AGTTTCTGGT GACATAGCTG AAGACCCTGA TGCTGTCATA GTCTGAATTC CAGAATCTTT AGAATCTTGA GTTTCAGTAT CAGTTTGCTT TTCAGTAACA GGTTTTCCTT CTTGAAATAT	60 120 180 240

TAATTTGTCA TCATTACCAA ACATGTCCAG TTTTTCACCG GCTTCAGATG CAGCTGGAGA

CAAACTGTTA TCTTGGAGCT CTGTGGGTAG ATTAGCTTCC TCAGTAGGAC TGCCTTCTAC

TTTCAGTTCC ACATAATCAT CATCTTCCTC TTCCTCTACT ATAGATTTAT CCAAGAATTC

TGGCATCTCT GAGGCAGGTC TAGAAATTC

(2) INFORMATION FOR SEQ ID NO:1315:

F

300

360

420

449

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 411 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1315:	
GAATTCGGCC TTCATGGCCT AGTGGAATAC TAGGATATTT GTTTGGCAGC AATAGAGCGG CAACACCCTT CTCAGACTCG TGGTACTACC CGTCCTATCC TCCCTCCTAC CCTGGCACGT GGAATAGGGC TTACTCACCC CTTCATGGAG GCTCGGGCAG CTATTCGGTA TGTTCAAACT CAGACACGAA AACCAGAACT GCATCAGGAT ATGGTGGTAC CAGGAGACGA TAAAGTAGAA AGTTGGAGTC AAACACTGGA TGCAGAAATT TTGGATTTTT CATCACTTTC TCTTTAGAAA AAAAGTACTA CCTGGTTAAC AATTGGGAAA AGGGGATATT CAAAAGTTCT GTGGTGTTAT GTCCAGTGTA GCTTTTTGTA TTCTATTATT TGAGGCTAAA AGTTGATGTG T  (2) INFORMATION FOR SEQ ID NO:1316:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 274 base pairs  (B) TYPE: nucleic acid (C) STRANDEDNESS: double	60 120 180 240 300 360 411
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1316:	
GAATTCGGCC AAAGAGGCCT ACATCCAACA AGAAGCCATA ACTTTATTTA TGATAGAAAC AGTACAAATT TCAAACCAAG CTGCAGTTAC TCCTTTGAGA CACCAAAAAA AGTTGCCTCC ATATGGTTAC ATTGTTAATT CCATAATCGC ATTTACAATA TCATTACTGT TGTTCTTCAG GGCTCGGACT GCCTTTGCTC TCGACACATT TGCTTGTGAC ATGACCAATT CTATGTCCTT AACTTCTACA CCTGTTTCAC TTCCTCTTCT CGAG	60 120 180 240 274
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 320 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1317:	
GAATTCGGCC AAAGAGGCCT AGGCGGAGGT GCAGGTCCTG GTGCTTGATG GTCGAGGCCA TCTCCTGGGC CGCCTGGCGG CCATCGTGGC TAAACAGGTA CTGCTGGGCC GGAAGGTGGT GGTCGTACGC TGTGAAGGCA TCAACATTTC TGGCAATTTC TACAGAAACA AGTTGAAGTA CCTGGCTTTC CTCCGCAAGC GGATGAACAC CAACCCTTCC CGAGGCCCCT ACCACTTCCG	60 120 180 240
621	

GGCCCCCAGC CGCATCTTCT GGCGGACCGT GCGAGGTATG CTGCCCCACA AAACCAAGCG AGGCCCAGCC GCTCCTCGAG	300 320
(2) INFORMATION FOR SEQ ID NO:1318:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 226 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1318:	
GAATTCGGCC AAAGAGGCCT ATAATTTTTA CCATCATTTA CCCTGATAAT CTGCCTCTTC TCCATTTCTC CTTCCCTTAC TACCTTTCTT TGAATTACTG TAACTGATTG GTCCCACCAA AATTTTAAAG TACATGAAGT ATCTTCATTG GTTCATCCTC TTGCCCCCTC CAGATGTCAA AAAACTTTAT CCTGCCCCCT TGCCTCCACC CGATGGCCCA CTCGAG	60 120 180 226
(2) INFORMATION FOR SEQ ID NO:1319:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 192 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1319:	
GAATTCGGCC AAAGAGGCCT ATGAAGCTTC TGAGTTCTGC GGCCTCACNT CTGAGAAAAC CTCTTTGCCA CCAATACCAT GAANCTCTGC GTGACTGTCC TGTCTCTCCT CGTGCTAGTA GCTGCCTTCT GCTCTCCAGC GCTCTCAGCA CCAATGGGCT CAGACCCTCC CCCCGCTGGC AAATCTCTCCG AG	60 120 180 192
(2) INFORMATION FOR SEQ ID NO:1320:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 210 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1320:	
GAATTCGGCC AAAGAGGCCT ATTTATTACA ACAGATCTTT TAATGACTAT TITTAACATA AAGATTGTTG TITTGGGAAA CATCTATTCT CTTTGAACAT TTCACTAAAT TITCAATGTA TTAAATAACT GACAGAAATA AGTTCTGTGT TCTGTACAAA TTAAAGGTCC CATGAATACA TAACCCCCAC CCCCCCCCG TCCACTCGAG  (2) INFORMATION FOR SEQ ID NO:1321:	60 120 180 210
(1) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 156 base pairs (B) TYPE: nucleic acid	

(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1321:	
GAATTCGGCC AAAGAGGCCT ATTTTTTTT TGATCTATGA ATGATTTATT AGATAAATTC TATACATACA AAGTACAGAT TCTTCATTTA GCATTGATTT ACTTCTTAGT TTTCATCTTT CTGACTATCC AAACCGCTGA CTCGAGGCAG GTCGAG	60 120 156
(2) INFORMATION FOR SEQ ID NO:1322:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 199 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1322:	
GAATTCGGCC AAAGAGGCCT ATTTTTGCTA CACTATGTTA CAGAACAGCT TATAAAACTA GGTATGAACA TTAACTGTGA GTGTAAACAG TAGGACTACC ACTTGTCAAA AGTTTTAAAC ACTTGAACTG GAACTGGTAC TGGTTATTCA TCATTTTCAT TGTTTTCTAT TTCATCCCCC CCACACCCCT CTGCTCGAG	60 120 180 199
(2) INFORMATION FOR SEQ ID NO:1323:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 209 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1323:	
GAATTCGGCC AAAGAGGCCT ACACGGTACC AAACACAACT CAAGCATCGA CTCCTCCGCA GACCCAGACC CCTCAGCCGA ATCCTCCTCC TGTGCAGGCC AGGCCTCACC CCTTCCCTGC CGTCACCCCG GACCTCATCG TCCAGACCCC TGTCATGACA GTGGTGCCTC CCCAGCCACT GCAGACGCCC CGCCACTCAG CGCCTCGAG	60 120 180 209
(2) INFORMATION FOR SEQ ID NO:1324:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 229 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1324:	
GAATTCGGCC AAAGAGGCCT AATCACTACT CACAGTAACC TCAACTCCTG CCACAATGTA	60

CAGGATGCAA CTCCTGTCTT GCATTGCACT AAGTCTTGCA CTTGTCACAA ACAGTGCACC TACTTCAAGT TCTACAAAGA AAACACAGCT ACAACTGGAG CATTTACTTC TGGATTTACA GATGATTTTG AATGGAATTA ATAATTACAA GGCTCCAAAC TCACTCGAG	120 180 229
(2) INFORMATION FOR SEQ ID NO:1325:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 204 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1325:	
GAATTCGGCC TTCATGGCCT AGCTTTCCCA ATCTCTCGGA GCATGCACAT CAGGGCCACG TTGGTCTTCC CAGCACCAGT AGGAGCACAC AGCAGCAGAT TCTCATCCGT CTCAAGGGCA GCACGGTAGA GCTTACTCTG GATCCGATTC AGTGTTTTGA AGCCCTCAAA CCCAGCCTGG ATTGAATTCT AGACCTGCCT CGAG	60 120 180 204
(2) INFORMATION FOR SEQ ID NO:1326:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 192 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1326:	
GAATTCGGCC AAAGAGGCCT AGCCGATCTC CAGCCCAAGA TGATTCCAGC AGTGGTCTTG CTCTTACTCC TTTTGGTTGA ACAAGCAGCG GCCCTGGGAG AGCCTCAGCT CTGCTATATC CTGGATGCCA TCCTGTTTCT GTATGGAATT GTCATTCCCC CAGAGCGTCT CGAGGCAGGT CTAGAATTCG AG	60 120 180 192
(2) INFORMATION FOR SEQ ID NO:1327:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 222 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1327:	
GAATTCTAGA CCTGCCTCGA GAATAGGATA GCATTTAGTA ATTCACTTAA CAATTTTAT TGAATATCTA TTGTTTTATT GAATATGCTT GTTCTCACCT TAGCACATTT GCCCTTGTTC TCCCTGGGAT ACTATTCCCC TAGATCTGAT TTTTGGTTTT TGTGTTTGTT TGTTTTAATT CTCTGCCATC TTTCTCCAGT CAAATGTCAC CACACTCTCG AG	60 120 180 222
(2) INFORMATION FOR SEQ ID NO:1328:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 267 base pairs	

(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1328:	
GAATTCGGCC TTCATGGCCT AAGAAATGTT CACTTTTCCA ACTTAAAAGG ATTTTTAAAA ATACAAACAT AATTGACCTA CCTGGTTCAA AGAACAGAAG TGAGGAGAAC TTGCTTAAAG GTATTGATGT TATATTTTCT CTTGACTGAG TGCTTGAAAA AAAATTTTAT TGAACATATG TTCTCCTTCC GTGGCTTTTT TGTCTTTGTTTT GTTTTTTTT	60 120 180 240 267
(2) INFORMATION FOR SEQ ID NO:1329:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 267 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1329:	
GAATTCGGCC TATGGCCTAA AAAAAAAAG AAAGAAATAG GATTGATACA GGTATAGATA CATAGATACA TGAGAAGGGA TTTATTATGG GAATGGGCTC ATATGATTAC AATGATTACA GAGGCTGAAA ATTCCCACAA TAGGCCATCT GCAAGCTGGG GACCAGGGAA GCCATTTATG TGGTACAGTC TAAGCGTCAA TCAGGAAAGC CAGTTGGGTA ACTCTCAGTC TGCAGCTGAA GGCCTGAGAC CCGGAGGTCC ACTCGAG	60 120 180 240 267
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 267 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1330:	
GAATTCGGCC TATGGCCTAA AAAAAAAAAG AAAGAAATAG GATTGATACA GGTATAGATA CATAGATACA TGAGAAGGGA TTTATTATGG GAATGGGCTC ATATGATTAC AATGATTACA GAGGCTGAAA ATTCCCACAA TAGGCCATCT GCAAGCTGGG GACCAGGGAA GCCATTTATG TGGTACAGTC TAAGCGTCAA TCAGGAAAGC CAGTTGGGTA ACTCTCAGTC TGCAGCTGAA GGCCTGAGAC CCGGAGGTCC ACTCGAG	60 120 180 240 267
(2) INFORMATION FOR SEQ ID NO:1331:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 494 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1331:

ATGGATTGGT	TGCCGTGGTC	TTTACTGCTT	TTCTCCCTGA	TGTGTGAAAC	AAGCGCCTTC	60
TATGTGCCTG	GGGTCGCGCC	TATCAACTTC	CACCAGAACG	ATCCCGTAGA	AATCAAGGCT	120
GTGAAGCTCA	CCAGCTCTCG	AACCCAGCTA	CCTTATGAAT	ACTATTCACT	GCCCTTCTGC	180
CAGCCCAGCA	AGATAACCTA	CAAGGCAGAG	AATCTGGGAG	AGGTGCTGAG	AGGGACCGGA	240
TTGTCAACAC	CCCTTTCCAG	GTTCTCATGA	ACAGCGAGAA	GAAGTGTGAA	GTTCTGTGCA	300
GCCAGTCCAA	CAAGCCAGTG	ACCCTGACAG	TGGAGCAGAG	CCGACTCGTG	GCCGAGCGGA	360
				GCCTGTGGCC		420
				AAAAGATGTG		480
ACGGCTTACT						494

## (2) INFORMATION FOR SEQ ID NO:1332:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 317 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1332:

GAATTCGGCC	TTCATGGCCT	AGCTGATATT	ATTTCTGAGT	TTTTGCTTAT	TTGCTTTCTA	60
CATAGAATCA	ATAAAATTGA	CAACTAGCAT	TGCCTATATA	TGCAGGTGTG	ATACTATTCA	120
GGGTACTAGT	ATATTGGCCA	CTCATTATGA	AACTTTCAGG	TCCTCATATA	TTTTCTTTTA	180
TTACAATGAT	CTACTTATTT	CTGATAAATA	TTGGATTCAT	AGAGGCTAAA	GGGCTGGGAA	240
AGGAAAACAT	TCGTGACTAC	TTACAACCAT	TTGATACGAG	TTGTGTCAAT	ACAGACCTCA	300
CACAGCAGCA	CCTCGAG					317

## (2) INFORMATION FOR SEQ ID NO:1333:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 255 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1333:

GAATTCGGCC	TTCATGGCCT	AGCTTTTCTA	GCCTTTCTCA	AAGAAATGCA	AACAGCTTGT	60
GTTTTTTCCC	CTTGGGTCCT	ATTGTACCTA	CTTTTGTTTG	ATGGTCTCTC	TGTCTCCCAT	120
GATGCCAGTG	AATGTAGCAG	TTTCTCTCCA	CTTCCACCAG	TGCCTGGGGA	AAATTTGGTA	180
TTGGCAAATT	TGAGTTCTGC	CTTTTTGCAG	CTTGCATTGC	TGGATTCAAC	CTTAGGAGCC	240
TCAGTTACCC	TCGAG					255

## (2) INFORMATION FOR SEQ ID NO:1334:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 267 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1334:

GAATTCGGCC	TTCATGGCCT	ACTCTTCCCC	AAAAGGAAGC	ATTTACTCTG	CCTCTTACAG	60
TGCAGAGTGA	CAGAATGGAC	ACAGAAAAAC	ATAGGTGGGT	CAGAACAGAT	CTCAGTTTGA	120
ACCCAGTAGC	TACTGGCTAT	AGGGTCTCTG	GGCAAGTGAT	TTGACCTCTC	TGCGCTCTGT	180
CTTCTCAAAT	GTAAAAACGG	GTCAGGCGCA	GTGGCTCATG	CCTATAATCC	CAACACTCCG	240
GGAAGCCAAA	GTGGGAGGAC	TCTCGAG			chichereco	267

- (2) INFORMATION FOR SEQ ID NO:1335:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 463 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1335:

GAATTCGGCC	TTCATGGCCT	ACAAATGTAA	AAATAACTGG	GCACTGAAGT	TTTCTATCAT	60
ATTATTATAC	ATTTTGTGTG	CCTTGCTAAC	AATCACAGTA	GCCATTTTGG	GATATAAAGT	120
TGTAGAGAAA	ATGGACAATG	TCACAGGTGG	CATGGAAACA	TCTCGCCAAA	CCTATGATGA	180
CAAGCTCACA	GCAGTGGAAA	GTGACCTGAA	AAAATTAGGT	GACCAAACTG	GGAAGAAAGC	240
TATCAGCACC	AACTCAGAAC	TCTCCACCTT	CAGATCAGAC	ATTCTAGATC	TCCGTCAGCA	300
ACTTCGTGAG	ATTACAGAAA	AAACCAGCAA	GAACAAGGAT	ACGCTGGAGA	AGTTACAGGC	360
GAGCGGGGAT	GCTCTGGTGG	ACAGGCAGAG	TCAATTGAAA	GAAACTTTGG	AGAATAACTC	420
TTTCCTCATC	ACCACTGTAA	ACAAAACCCT	CCAGGCACTC	GAG		463

- (2) INFORMATION FOR SEQ ID NO:1336:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 286 base pairs
    - (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1336:

(	GAATTCGGCC	TTCATGGCCT	AAATTCTAGA	CCTGCATCGA	GGGCGGCGAC	CTGATGATGA	60
(	CCAGCTTCGA	GAGGATGCTG	TCCCAGAAGG	ACNTGGAGAT	CGAGGAGCGC	CACAAGCGCC	120
1	ACAAGGAGAG	GATGAAGCAA	ATGGAGAAGC	TGAGGCACCG	GTCCGGAGAC	CCCAAGCTCA	180
1	AGGAGAAGGC	GAAGCCGGCA	GACGACGGGC	GGAAGAAGGG	TCTGGACATT	CCTGCTAAGA	240
I	AACCGCCGGG	GCTGGACCCT	CCATTTAAAG	ACAAAAAGCT	CTCGAG		286

- (2) INFORMATION FOR SEQ ID NO:1337:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 255 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1337:

CTCGAGGGTT TTTGTTTGGC TGGTTGTGT TACACAGTGT ATACAAGTTG AGTTGTACAG AAGCCCAAGA AAGAGCAAGA GACAAAGGGT AGTGGGAGCA GGGGGTGGGG CGGGGGCGAG AACGGGGAGG AGGGGAAAGG AGACCGATAA AAAATAGAAC CACATCCAGA CAACAATGGG GGATGGGCAG TGGGTGGGGG CCAGACACAG ACAAATCGCC GTAGAAAAGG AGTGGGAGGG GCAGAGAGATA GAGGG	60 120 180 240 255
(2) INFORMATION FOR SEQ ID NO:1338:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 259 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1338:	
GAATTCGGCC TTCATGGCCT AAGAGAAAGC ATTTTAACTT TTATAGTAAA CAATAAAAAA GCCTCATAAA GCTTCTCACA ACAACTTCAT TCGTTTCAGA AGTTAAGATA TATTCCTTAT GAATACCAAC ATTGTGACAT TTGTGTTGCC AATTATTTTC TCTGGAATCA TTCTTTTAAC TTCACTTCCT GTTGTTTGGG AAGACTTTGC AGAGAACATA TTTTTAATAG GCTATAATCA CACGGGCAAC AGACTCGAG	60 120 180 240 259
(2) INFORMATION FOR SEQ ID NO:1339:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 286 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1339:	
GAATTAGAAG TATTGTTTAA TAAGTCCTTT TTTTCTACTC AACATTAAGT AGTAATCAAC TTTTACCTCC GCCAGTTTTT CTGCTTTTTT GCTGGTACGA TCTCTCTTTC TAAATTGAAT CAAAGACCTA GGTGAACTG GAAACTTAGG AGGGAAAGAC AAAATGAGGC TTGTTCATGA TCAAATTCTG TGTACTCTAG TTGCTTCTTT CCCCTTGGAGT GACAGGTACT TTTATATCCA GGATGATTAC AGTGATGACA TCCATTCTTT TTTGGGGGCC CTCGAG	60 120 180 240 286
(2) INFORMATION FOR SEQ ID NO:1340:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 240 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	,
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1340:	
GAATTCGGCC TTCATGGCCT AGGAATCAGT AGTGTACTTT GATTGTATTG TATAAGGTAT TTTCAAATAG AAAAGCAGGT AGCAGAAATA CTAAAAGAAT TTTTGCTTT AGTGTAAAGT AGATAATGAG AGGTAGATGC CTAATTTCTT AGTTTTCTTT TTAAAATTAT GCTAAAATAT	60 120 180
ATCATATCAT TTACCATTTT GACTATTTTA AAAGTATACA GTTCCGTGGC AAGTCTCGAG	240

(2) INFORMATION FOR SEQ ID NO:1341:

(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 245 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1341:	
GAATTCGGCC TTCATGGCCT ACAAAATTGT GTCTTTTTTT TGGCAATGTT GTCTTGCCAA	
TCCCATCCCT CCCCCAGCTC TCCGAACAGC AGGATTTCCC AACGGCAGCT TGGGANAAAG	60 120
ACCCAGTGGC AGCTTGGGGA AAAGACCCAG CGCTCCGTTT AGAAGCAACG TGTATCAGCC	180
AACTGAGATG GCCGTCGTGC TCAACGGTGG GACCATCCCT ATTGCTCGGC CAAGTCACAC	240
TCGAG	245
(2) INFORMATION FOR SEQ ID NO:1342:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 134 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1342:	
GCGATTGAAT TCTAGACCTG CCTCGAGACT GACGCCGCAC CATGACCCTC CTGCTGCTGC	60
CCCTTCTGCT GGCCTCTCTG CTCGCGTCCT GCTCCTGTAA CAAAGCCAAC AAGCACAAGC	120
CACCGCATCT CGAG	134
(2) INFORMATION FOR SEQ ID NO:1343:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 381 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1343:	
Chargeson and chooses annual chooses are medical medical management	
GAATTCGGCC AAAGAGGCCT AAAAAGCTTC CAGCAGCAGA TGCAGAATTA CCTTAAAGAC AACAAAACAG CCACTATTTT GGACAAATTG CAGAAAGAAA ATAACTGCTG TGGAGCTTCT	60 120
AACTACACAG ACTGGGAAAA CATCCCCGGC ATGGCCAAGG ACAGAGTCCC CGATTCTTGC	180
TGCATCAACA TAACTGTGGG CTGTGGGAAT GATTTCAAGG AATCCACTAT CCATACCCAG	240
GGCTGCGTGG AGACTATAGC AATATGGCTA AGGAAGAACA TACTGCTGGT GGCTGCAGCG	300
GCCCTGGGCA TTGCTTTTGT GGAGGTCTTG GGAATTATCT TCTCCTGCTG TCTGGTGAAG	360
AGTATTCGAA GTGATGTCGA G	383
(2) INFORMATION FOR SEQ ID NO:1344:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 486 base pairs	
(B) TYPE: nucleic acid	

(C) STRANDEDNESS: double

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(D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: CDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1344:
GACCAGATGG AANGGTCACC GAACAGTTCT GAGTCATTTG AGCATATAGC TCGATCTGCA
                                                                       60
AGAGATCACG CAATTTCCCT TTCTGAGCCT CGTATGCTGT GGGGGTCAGA TCCCTATCCT
                                                                      120
CATGCTGAGC CTCAACAAGC AACTACTCCC AAAGCAACAG AAGAGCCTGA GGATGTAAGG
                                                                      180
TCTGAAGCTG CGTTGGACCA GGAACAGATT ACTGCTGCTT ATTCTGTAGA ACATAATCAA
TTAGAGGCTC ACCCAAAGGC AGACTTTATC AGAGAATCAA GTGAGGCACA AGTACAAAAG
                                                                      300
TTTTTAAGCA GATCTGTGGA AGATGTTAGA CCTCACCATA CTGATGCAAA TAATCAGTCT
                                                                      360
GCTTGTTTTG AAGCACCTGA TCAAAAGACC TTATCCGCTC CTCAAGAGGA GCGGATTTCA
                                                                      420
GCTGTAGAAA GTCAGCCTTC CCGGAAAAGA AGTGTTTCCC ATGGATCTAA CCATACGCGC
                                                                     480
CTCGAG
(2) INFORMATION FOR SEQ ID NO:1345:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 243 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1345:
GAATTCTAGA CCTGACTCGA GGTGCTGGAA TTACAGATAA AAGCCACCAC ACGCAGCCCA
CATAAAGTGT TTATGGGAGC AACTAACAGT TGGTTTGCAG GCAGCCTAAA TAGGGGATGG
                                                                     120
CAAGGTTGGG TTTTCCAAGG TTTTCTAATC TTTCTATTTC TTCTAGTGAG TCTTCAGGTT
                                                                      180
ATTATGACTT GTGTTACCAG ACTATCAACA AAAGTGGGTA CCTCTTTAAA TCAGAGCCTC
                                                                      240
                                                                      243
(2) INFORMATION FOR SEQ ID NO:1346:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 294 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1346:
GAATTCTAGA CCTACCCCAT CCACATGCAC AGCCAGCTGG ACCACCTTAG CCTCTATTAC
                                                                      60
TGCAGGTGTA CTCTGCCAGA GAATCCAAAC AATCACACCC TCCAGTACTG GAAGGACCAC
                                                                      120
AACATCGTGA CAGCAGAAGT CCACTGGGCT AACCTGACTG TCAGTGAATG CCAGGAGATG
                                                                     180
CATGGAGAGT TCATGGGATC TGCGTGCGGC CATCATGGAC CCTACACTCC TGATGTCCTC
                                                                      240
TTTTGGTCCT GTATTCTCTT TTTCACCACC TTCATCCTCC CAAGCACCCT CGAG
                                                                      294
(2) INFORMATION FOR SEQ ID NO:1347:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 240 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
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- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1347:

AGTTTCTCCA TTTTAGAATT TTGTTGTCCT CCTTAATCAT CTGCTTACCT AGTCATTACT
CAATCTGCAG AAACTTCATA AAGGAAAAGT GCTGCATTGT TTTTACAAAT AACAGTTTGT
AGGGAAAATA TGACAAACCT CAACTATGGG AGTTGTCCAC AATACAAAAT TTTGAAAAAA
CATTACATAG TGATAATATC ATACTTGGTT GTTAGGCTTG TTGCTTCCCC ACCACTCGAG
240

- (2) INFORMATION FOR SEQ ID NO:1348:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 356 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1348:

P	AGTATTCTT	TCAATTGCAA	AGTGGCAACA	GCTTTTATAT	GCTAAGTCTG	ACAAGTTTGC	60
P	GTCAGTGAA	TGATGGCACA	TGGCACGAAG	TGACCCTTTC	CATGACAGAC	CCACTGTCCC	120
					TTTTGTGACC		180
					TTATGTGGGA		240
					AGAAATCGGA		300
T	CTCTTACTT	TGAAAATGTT	CATGGTTTCA	TTAATAAACC	TCAGGACGAG	CTCGAG	356

- (2) INFORMATION FOR SEQ ID NO:1349:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 180 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1349:

GAATTCTAGA CCTGCCTCGA GACCTTTCTC CTGGTCTAAT GCTCCTTTTA AGGAAGGTGG 60
AAGGAACAAT GGAAGAATGC TTGTAAAGTA ATGTATTCTT AAGAACTAAA GCTATTTGCA 120
GAAGGGCCGA AGCTATGTGG TGTGAAAGGG AAATGAAGAG GGTGAGTTGG GGGGCTCGAG 180

- (2) INFORMATION FOR SEQ ID NO:1350:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 287 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1350:

GAATTCTAGA CCTGCCTCGA GCTTTCCCTG ATCTTCTTCC ATCCCTTACT GACAGTGTTT ACCAAGGATT TCCCTTGGCC TGCTTCTTTC TTTGACGCTC ATTTAAACCT TTCCCTTCAG TTGCAGACCT CGTCTGCTTC TCCCAGCTAT TCCATTCTTC AGTTGCTTGT TAAACACGGC CCACCATCAC CTCAAAAATG ATGTTAAAAT GTCCCCATTT TTTATCAAAC TTAAGTTTCT TCCTGTGGAT CTGTTGCTCA GTACTCTCAT CTTTCCGATC ACTCGAG	60 120 180 240 287
(2) INFORMATION FOR SEQ ID NO:1351:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 335 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1351:	
GAATTCGGCC TTCATGGCCT AAAAAAATTCT TTTTTAATGG GTTTTAAACA CTAACACTGA GAATTTTTCT TGATTCCCAT CTGTTGGTTT ACTTGATTGC TATAGCTGTA TGGTAAATCT CAAAATTAGG TAATGTGATT TCTTTTTTCT TACTATTTTT ATTTAAAATT CATTTAGCAT TCCTAGTTTG ACTTTCCATA TACACTTTAG GATTGGTTTT TCTGTTTTTC AAATATTCTT GCTTGGATTT TGATAGAAAT TGAGTTAAAT CTATAGATCA ATGTGTTGGA AATTGGCATC TTAGTCTTCC AATTCATGAA CATAGCCTAC TCGAG	60 120 180 240 300 335
(2) INFORMATION FOR SEQ ID NO:1352:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 267 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1352:	
GAATTCGGCC TTCATGGCCT ACGTATGAGA CAGTGTATAT GACACTGTAT ATGTGTGAGA CTGTGTGTGT GAAACACTAT ATGACACTGT ATATGTGTGA CACTGTATAT GACACTATAT GTGGAGACTA TGTGTGAGAC ACTATGTATA TGTGACACTA TGTATGTGT TGACACTGTG AGAGACACTG TGAGACACCA AGACAGTATA TGTATGAGAC ACCCTGTGT TGTGACACAG CGTGTGACTG TGTGAAACAT GCTCGAG	120 180
(2) INFORMATION FOR SEQ ID NO:1353:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 202 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	·
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1353:	
GAATTCGGCC AAAGAGGCCT ACCCAGAACC AGTTATACTG AGGGTCCTGA GATCTGCTAT AACATCACCA TCCTTTCAAC CCAGAGGTGT GTGTTTGTGG GCCATTCATT TGGCCCTCAC CACATCCTGC CTTGTATTGC TAGTTTATCT TTTTATTGTC TTTGTTCTCC CCCAACCTCC	60 120 180

202

TGCGCCATAC AGACTCCTCG AG

(2)	INFORMATION FOR SEQ ID NO:1354:
	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 285 base pairs
	(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
  (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1354:

GGTTTGGATA	TCCTGAAAGA	TCAATGGGCA	GCTGCAATGA	CTCTCCGCAC	GGTATTATTG	60
TCATTGCAAG	CACTATTGGC	AGCTGCAGAG	CCAGATGATC	CACAGGATGC	TGTAGTAGCA	120
AATCAGACGA	GCAAAAATCA	AATTAAAGTA	GATCTTGTAG	ATGAGAATTT	TACAGAATTA	180
AGAGGAGAAA	TAGCAGGACC	TCCAGACACA	CCATATGAAG	GAGGAAGATA	CCAACTAGAG	240
ATAAAAATAC	CAGAAACATA	CCCATTTAAT	CCCCCTGATC	TCGAG		285

- (2) INFORMATION FOR SEQ ID NO:1355:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 306 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1355:

GAATTCGGCC	TTCATGGCCT	AGTTATTTCG	TCACTGTCGC	AAACAGCAGG	CAAAGTTTGA	60
CGAGTGTGTG	CTGGACAAAC	TGGGCTGGGT	GCGGCCTGAC	CTGGGAGAAC	TGTCAAAGGT	120
CACCAAAGTG	AAAACAGATC	GACCTTTACC	GGAGAATCCC	TATCACTCAA	GACCAAGACC	180
GGATCCCAGC	CCTGAGATCG	AGGGAGATCT	GCAGCCTGCC	ACACATGGCA	GCCGCTTTTA	240
TTTCTGGACC	AAGTAAAGAT	GGGTCCGTGG	CCCACACTCG	GTCATGTGCT	CAGACAACAA	300
CTCGAG		•				306

- (2) INFORMATION FOR SEQ ID NO:1356:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 297 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1356:

GGAATGATGT	CACTCACGTC	CAGCAAAGCC	AAAGAGCTGA	AGGACCGGCA	CCGGGACTTC	60
CCAGACGTGA	TCTCAGGAGC	GTATATAATT	GAAGTAATTC	CTGATACCCC	AGCAGAAGCT	120
GGTGGTCTCA	AGGAAAACGA	CGTCATAATC	AGCATCAATG	GACAGTCCGT	GGTCTCCGCC	180
<b>AATGATGTCA</b>	GCGACGTCAT	TAAAAGGGAA	AGCACCCTGA	ACATGGTGGT	CCGCAGGGGT	240
AATGAAGATA	TCATGATCAC	AGTGATTCCC	GAAGAAATNG	ACCCACAGGC	TCTCGAG	297

- (2) INFORMATION FOR SEQ ID NO:1357:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 276 base pairs

- (B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1357:

GTCCCGCTAA ACC	CGGCAGGC GATGAGAAA	G GAAACCATCA	CTAAGATGCT	CTGGAGTACC	60
CGCACCCTGT TG	AATATCAC CAAGGAGCA	G GTACCACTTG	TGGTGGAGGA	GTACCTGGAC	120
AATGTCAATG AGG	CATGACTG GAAGATGCT	A CGAAACCGTA	TGATGGACAT	AGTTCAAGAT	180
GCCACTTTCG TGT	TATGCCAC ACTGCAGAC	T GCTCACTACC	ACCGAGATGC	CGGCCTCCCT	240
GTCTACCTGT ATC	GAATTTGA GCACCACAC	G CTCGAG			276

- (2) INFORMATION FOR SEQ ID NO:1358:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 244 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1358:

GAATTCGGCC	TTCATGGCCT	AGGGGAGCAT	AAAAATACAA	AAAACATTTG	GCTTTATTCA	60
CAACGTATTT	TGTGAAAACT	CAGGAATAAC	TCTTTGAATT	TTGGGGAAAC	CAACAACATT	120
CTCAAAAACG	ATGATAATCA	ATTTTATTGT	GCACCTCTGC	ACCCTGCCTC	CATGGTCCCA	180
CCACCAGGTT	CCCTCTCCTC	CACAGTCAGA	AGTTCCTCCC	TGCATTCAAA	CACTGGGTCT	240
CGAG						244

- (2) INFORMATION FOR SEQ ID NO:1359:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 391 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1359:

GCGATTGAAT	TCTANACCTG	CCTCGAGGAC	CCAAATATTT	CTTTGAGATC	TTTCTTTCAA	60
TTCTTTTGGA	CATATACTCA	GAAGAGAGAT	CATTGGATTA	TTTTTTTTTTT	TTTCAGAAAC	120
TGCCTACCGT	ATTCCAAAGC	AGCTGCACCA	TTTCACATTC	CCACCAACAT	TGCATCAGGG	180
TTCCAATTTT	CCCACATCCT	TGTCAACATT	TGTTATGTTG	TTTTTTTGTT	TTTGTTTTTT	240
TTTGTTTCGC	TTTGTTTTGT	TTTGTTTTGT	TTTGTGCACA	CAGTCTCGCT	CTGTTGCACA	300
GGCTGGAGTG	CAGTGGTACA	GATCTCAGCT	CACTGCAGCC	TCTACCTCTC	CAGTTCAAGC	360
AATTCTCCTA	CCTCAGCCTC	CCCGGCTCGA	G .			391

- (2) INFORMATION FOR SEQ ID NO:1360:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 262 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1360:

GAATTCGGCC	TTCATGGCCT	ACATTTTTTT	CCTAGTATGG	ATATGCTTAT	TAATGCACTT	60
GTTTCAAAAT	CCCAAATTGC	ACAAATGTGT	TAATATTTTA	AGAAACAAAA	TGAATCCTAC	120
AAGGAGAATG	ATTTTTAGCC	ACACATAGGG	TTGGATCTTG	AGAGTGACCT	ACAGAATAAA	180
AGTACTTTTA	AAATAAAGTA	GTCAGAGGCT	ATTCAAAGGG	TAAAATAATC	ATAGTACCAC	240
ATTGGTCCAC	TTGACACTCG	AG				262

- (2) INFORMATION FOR SEQ ID NO:1361:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 252 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1361:

GAATTCGGCC TTCATGGCCT	' AGACAACCTG	AAACTGGATG	ACATGCTGAG	TGAACTCAGA	60
GACAAATGGG ATACCATATC	TGGAAAATCT	GTGGAAAGGT	AAAATGTTCT	TTAAGACAGT	120
TTGGTTACTC TGTAGACCTC	TTTCAAATAC	ACAGTAATGG	TGCTTTGCGG	GGACATTTCG	180
GGAACCTTAA ATATTTCCTT	TGCCTGAGGA	ACTTCTGCTT	GTCCTAAGTA	TCCCACACAC	240
ATAGCACTCG AG					252

- (2) INFORMATION FOR SEQ ID NO:1362:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 299 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1362:

GAATTCGGCC	TTCATGGCCT	ACATAGCAGT	ACACAGAAAC	TCATCTTTGG	TCTTAAAACT	60
GCATAGGTAC	TTTAGTCCTC	TGTTGACAAA	TGTTGGGTTG	TTTCAGTCTT	CTGCTATCAC	120
AAATAATGCT	GCAAAGAATA	CATTTGTTCA	TATGTCATTT	CATCCTTGGC	AATTTTGCCT	180
CTGGAAAGTT	CCTAGAAGTC	AGATTCCCAG	GTCAAAGGTT	AAATGCGCAT	GTAATTTTGC	240
TGGATATTGT	TAAATCCCCC	TACAGAGCAT	GCACCACTCA	GCATTCCCCT	CAGCTCGAG	299

- (2) INFORMATION FOR SEQ ID NO:1363:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 268 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1363:

GAATTCGGCC TTCATGGCCT AGCGAGATCT GCGTGAAAAA TACAGCAATT TTGGCAATAA CTCTTATCAC TCCTCAAGAC CCTCATCTGG ATCCAGTGTG CCCACCACCC CCACATCATC CGTCTCACCC CCACAGGAGG CCAGGTTGGA AAGGTCATCA CCGAGTGGTC TTCTCACATC ATCCTTCAGG CAGCACCAAG AGCTCACGG AGCAGAGAGA GAGAGGCGGC GGCAGGAGAG AGCACGAGG	60 120 180 240 268
(2) INFORMATION FOR SEQ ID NO:1364:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 273 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1364:	
GAATTCGGCT TCATGGCCTA CCAACCCCC CATTTCTCCC TTCCTCCAGC CACTGGCAAC CACCATTTCA TGTTCTTTT GTTTGTTTTT GTTTTTTTTTT	60 120 180 240 273
(2) INFORMATION FOR SEQ ID NO:1365:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 366 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1365:	
GAATTCGGCC TTCATGGCCT AATCGGTGTC TTTGGTAAAA ATTCTATGAG GATGACATAT TCCATCATGT TATTCGTTTC ACATTTCCTT TTGCTCAGTC TCCAATGCAA GCACAGCTTG TGGTATAACC TATTGTTTC CCATTCTAAT AACTTCTCAA TCGATCTTCG TGTTCTTTTA CTGAGGCAAA TAACTGGCCA CATACTGCAA CCTAATGTGC AGCAGCAACA AAGGCAGCCA CAAAGTAGCC AACGTACATT AACAGGAAGG TTCTTCTTAA GACAACTGTT AACTCTGTNG ATGCTGGCTT TAAATTCTTC AGGAGCTACT TTTTCAGTTA ATGAAGAAGG GAATTCAGAT TCAAAT	60 120 180 240 300 360 366
(2) INFORMATION FOR SEQ ID NO:1366:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 245 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1366:	
GTTGTTAGGC TGGTGTTGTT ATGTTGCTGT TGTTATGCTG GTCGTGCTGC TCCATGTTCT CCAGGTGTTC TTCCCTTTTA TCGTCACAGT TACCCCGTAC ACCTGACAAC TGGACATCTG CGCCTGGGGT CTTCAGCCTA AACACACCTA AACCCCTCCAC CAAACCCCTC TGCTTCCGCC	60 120 180

TCCCCGTGTC TGTGAGCGCC TCCACTGCCC ATCCCTCTGC TCAGGCCCCA TTTCCAGGGC

TCGAG	245
(2) INFORMATION FOR SEQ ID NO:1367:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 217 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1367:	
GTATTTTGT GACTGAAGTC ACCTTCTAAA TAATTTCTAG AATAAAATTT TTATATTGAA GAAGTTGGTC TTAACCATTT TTTTTTCAGG AGCATGCATT TTGAAATCAT TCTGTGGGAA GATGAAAACA AATTTAGTTC TATGTCTCCC CTTTTTAGAG ATGTTGACAC TTTCCTTAAA TGTACCATGC ATGATTTGTC TACCACCCAG ACTCGAG	60 120 180 217
(2) INFORMATION FOR SEQ ID NO:1368:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 289 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1368:	
GGCTAGAAGC AAGATGGCTG AACTCAATAC TCATGTGAAT GTCAAGGAAA AGATCTATGC AGTTAGATCA GTTGTTCCCA ACAAAAGCAA TAATGAAATA GTCCTGGTGC TCCAACAGTT TGATTTTAAT GTGGATAAAG CCGTGCAAGC CTTTGTGGAT GGCAGTGCAA TTCAAGTTCT AAAAGAATGG AATATGACAG GAAAAAAGAA GAACAATAAA AGAAAAAGAA GCAAGTCCAA GCAGCATCAA GGCAACAAAG ATGCTAAAGA CAAGGTAGGG AGTCTCGAG	60 120 180 240 289
(2) INFORMATION FOR SEQ ID NO:1369:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 230 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1369:	
GCGATTGAAT TCTAGACCTG CCTCGAGTGT TTTTTTAAAA CTCTCTCTCT TCACTGACAC CAGGTGTTGC TATTAATGTG CTCAAATCTC TCACTTATAA AAAAGAATAA AACCTCTCTC TTTTCTAGTT ACTGGTCTGT TTATTCTTTT GTAGAATGAT CTTTGGGAAG AGTGTTTTCA TTTATCCCAG TCTCTCATC TTTTATTCCT TAGTGCACTG TCATCTCGAG	60 120 180 230
(2) INFORMATION FOR SEQ ID NO:1370:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 254 base pairs	

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(a) 13.35501. Tilleat	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1370:	
GAATTCGGCC TTCATGGCCT AAACAAACAA AAAGAAGAAA ACACTCAACA AAACCAATCT ACATGTTTTG GACTAAAAAA AAAAATAGAG GTTGTATTCT CAGTGTCCGA CTCGGAATTA TGTTGCTGCC TCTCTGTGCT TTTGGCCTCT GTGTGGCCGT GTTTTGCCAG CATGAGATAC TGTCCCCTCT GGAGGATTT AGGGGAGGAA GAGCCACGTC CCCAGGGATT GGAGGAGGCT CCGGCACCCT CGAG	60 120 180 240 254
(2) INFORMATION FOR SEQ ID NO:1371:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 276 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1371:	
GAATTCAGCT ACACTTGAGT ATTAGGAAGC CATATAGAAT TCGCAGGGTC CAACTTCATA GACTCTATTC ACATTATTAG AGTAGTAGTG GGGACCGTTA CTTTTGGGAA AGGATCAGTG AGACAGTATA AACTTTTGAA ATAATACATT TTTGTATTCC AGAATTATTA GATAATACTA AAGCAAACTT TTTTAATGGA ACATTTTGAA GTCCTGTGTA TTTATTTTAT	60 120 180 240 276
(2) INFORMATION FOR SEQ ID NO:1372:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 249 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1372:	
GAATTCGGCC TTCATGGCCT ACTCGAATCA TAGTGATTAA AATAGTTGGG GTAAAGTTGT AGCTTATATG CAATACTACT TGGAGGAATT CTTCTACTAA TTTGTATTTA ATCTGGAAAT TGTATAGTTT CATTGATTTA ATCATAAATA ATGGAAATGG TCTCCAAGAA GTTTTATTTT TCATTTTTTTT GCTTATACAC TCTGATTCCT ATAATACAGT GCTATAAGCT ATGCACAGAA AATCTCGAG	60 120 180 240 249
(2) INFORMATION FOR SEQ ID NO:1373:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 218 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1373:

CCCGTTGTCA ATCTTTGGGT TTTATTCCTT TTTAAGAAAG AAAGAAGTTC TGCTGAATTT GGAAATAAAT TCTTTATTTA AACTTTCCTT CCCAGTTTTA TAGTTTCTGG TTCTGAGGAC TGATGAAAAT CATCTTCCAT CAGCAGATTT TCTTGCACTG TTTGCTGTGC CCCTCAAATA TAATGTCTTG GGTTTTAAGA TCGAGCAGAG AGCTCGAG	60 120 180 218
(2) INFORMATION FOR SEQ ID NO:1374:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 139 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1374:	
GAATTCGGCC TTCATGGCTT GGGTCTCTCT TTCCCATTTC TGCTTCTTGT TCTCCCAGAT CTTCCCCAAA ATAAGCTCAG TGCCCAGAAC TTGTGTGGCT TTGGGATATT CCACTGCCCG GGCAACAGGC AATCTCGAG	60 120 139
(2) INFORMATION FOR SEQ ID NO:1375:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 264 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1375:	
GAATTCGGCC TTCATGGCCT AGCAAGACGC AGCAAAAGTG GAACTTCCAA GATACTAATC TGAGAAGTTT TCAACAAGAA ACAGGTTTAG AATTAAAAAT CAAAACCTCT TTTAATTGTA TTAAGAGTAA ATCATATTT AAGACAACTT TCTTTTAAAA CAAGGGACCA AAATTTAGAA AGACTTTTAT AAATAATTTT AATTATAGCC AACTTAATCC CACACAAAAAT GCTTTTCATA AGTATTCTCT CACAAACACT CGAG	60 120 180 240 264
(2) INFORMATION FOR SEQ ID NO:1376:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 250 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1376:	
CTTAAACCCA GGAGTTAGAG ACCAGACTGG ACAATATAGC GAGACCTCAT TTCTAACCCC CAAAAAAATA TACACACGCA CACACACACA CACAAACACA CACACACA	60
AAAAAAATA TACACGCA CACACACAC CACAAACACA CACACACAC CACGCATGCA AACTATATTA AAAAAACGGT CATGCTGCAT GGTTTTTTAT TTGTGTTATT TTTATTGTTG	120 180
TAATGTTACT TTATTTTCTA ATATTTTCTG TTTGCGGTTG GTTGAATCCT CAGCTGTGGA	240

250

ACAGCTCGAG

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(2) INFORMATION FOR SEQ ID NO:1377:
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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 285 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1377:

GAATTCGGCC	TTCATGGCCT	AATTTCCCCT	TCTCTTTTTT	TTTTGGTTTT	GGTTAATTTG	60
TAATTTTGGT	TTCGTCCTGA	TGTATATGGA	CTGCCAGAAT	AGGGGGGGTG	GTGGTTTGTT	120
CGTGGTGTCT	GGGGGAGGAA	<b>GGAATCCTTA</b>	CCCTGGCTTC	CTTAATCGGG	GAAGGCTTCC	180
TGAAGGAGGT	GGGCTCAGAG	GTGAGTTGTG	AATGAAGCGG	GTAGGGAGTG	GGCTGGGTGG	240
ATGGTTTGGG	GATGTTTGGG	GGAGGTGAGT	AAAGGGTAAC	TCGAG		285

- (2) INFORMATION FOR SEQ ID NO:1378:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 384 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1378:

GAATTCGGCC	TTCATGGCCT	AGAAAGAGCA	AATATAATGA	AGACTTTGAA	AGAGCTTGGA	60
GAGAAGATCT	CACAATTAAA	AGATGAATTA	AAAACATCTT	CTGCAGTCTC	CACACCATCT	120
AAAGTGAAGA	CAAAAACGGA	GGCCCAGAAG	GAGTTATTAG	ATACTGAACT	GGACCTCCAC	180
AAGAGGCTGT	CCTCAGGAGA	AGACACCACA	GAATTACGGA	AAAAACTCAG	TCAGTTACAG	240
GTTGAGGCTG	CACGGTTAGG	TATTTTACCT	GTGGGTCGAG	GAAAGACCAT	GTCCTCTCAA	300
GGTCGAGGAA	GAGGCCGAGG	GCGTGGAGGA	AGAGGAAGGG	GCTCACTAAA	TCACATGGTG	360
GTGGACCATC	GTCCCAAACT	CGAG				384

- (2) INFORMATION FOR SEQ ID NO:1379:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 370 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1379:

GAATTCGGCC	TTCATGGCCT	AGTCAGGAAC	TCCAGTTTGC	TTTTCTGTTT	TGTGTCCTGG	60
TAGCAGCTGT	TGAGTAACTT	TCATTGGAGG	TTGGGAAGGA	AGTGAGGAGA	AAGTGTTCTT	120
GTTTAGTGTT	TTATTTCCTA	TAATAGGATG	CTGCCTAACC	CAGTTCATCT	CTATGTCCTG	180
TTCACTGAAT	ATTCCGGGTA	ATTGAAAGAA	AATATAATGG	ATGGGCTCCA	TTAAAACCAG	240
CTCAAAAATA	AATTCTTGTC	AGTAAAGATT	TCTTGTCAAG	ATGTCTTGGA	TTGCACTTTT	300
GTTGAGGAAA	GACAGTGTAA	ATAGTTAAAG	AATGTTGATA	AAATTGAAAC	ATTTGGGCCT	360
TCATGGCCTA						370

(2) INFORMATION FOR SEQ ID NO:1380:

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 366 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1380:	
GAATTCTAGA CCTGCCTCGA GTTGCTGAAC GGTTTAGATC CTCAAAAAAT AAAGCAATTG AACCTGGCCA TGATTAACTA TGTNTTGGTC GTCTATGGAC TTGCCATTTC TCTCCTTGGA ATAGGACAGC CTGAGGAATT ATCTGAAGCC GAAAACCAGT TTAAGAGGAT TATTGAACAC TACCCCAGTG AGGGCCTTGA TTGCTTGGCC TACTGTGGAA TTGGAAAAGT ATATTTGAAA AAAAACAGAT TTCTAGAAGC TCTCAATCAC TTNGAGAAAG CAAGAACCTT GATTTATCGT CTTCCTGGAG TGTTAACTTG GCCCACGAGT AATGTGATTA TTGAAGAGTC TCAGCCACCC CTCGAG	60 120 180 240 300 360
(2) INFORMATION FOR SEQ ID NO:1381:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 472 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1381:	
GAATTCGGCC TTCATGGCCT ACTTTAATGA GATAGGAACT AGTATATTCA CCGTCTATGA GGCCGCCTCA CAGGAAGGCT GGGTGTTCCT CATGTACAGA GCAATTGACA GCTTTCCCCG TTGGCGTTCC TACTTCTATT TCATCACTCT CATTTTCTTC CTCGCCTGGC TTGTGAAGAA CGTGTTTATT GCTGTTATCA TTGAAACATT TGCAGAAATC AGAGTACAGT TTCAACAAAT GTGGGGATCG AGAAGCAGCA CTACCTCAAC AGCCACCACC CAGATGTTTC ATGAAGATGC TGCTGGAGGT TGGCAGCTGG TAGCTGTGGA TGTCAACAAG CCCCAGGGAC GCGCCCCAGC CTGCCTCCAG AAAATGATGC GGTCATCCGT TTTCCACCATG TTCATCCTGA GCATGGTGAC CGTGGACGTG ATCGTGGCGG CTAGCAACTA CTACAAAGAA GAAAACCTCG AG	60 120 180 240 300 360 420 472
(2) INFORMATION FOR SEQ ID NO:1382:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 424 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1382:	
GAATTCGGCC TTCATGGCT AGAGTTTAAC CCAGAACTGG TGCTGGTCTC AGCTGGCTTT GATGCTGCAC GGGGGGATCC GCTGGGGGC TGCCAGGTGT CACCTGAGGG TTATGCCCAC CTCACCACCC TGCTGATGGG CCTTGCCAGT GGCCGCATTA TCCTTATCCT AGAGGTGGC TATAACCTGA CATCCATCTC AGAGTCCATG GCTGCCTGCA CTCGCTCCCT CCTTGGAGAC CCACCACCCC TGCTGACCCT GCCACGGCCC CCACTATCAG GGGCCCTGGC CTCAATCACT GAGACCATCC AAGTCCATCG CAGATACTGG CGCAGGCTTAC GGGTCATGAA GGTAGAAGAC AGAGAAGGAC CCTCCAGTTC TAAGTTGGTC ACCAAGAAGG CACCCCAACC ACCCAAACCT CGAG	60 120 180 240 300 360 420
551	

- (2) INFORMATION FOR SEQ ID NO:1383:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 494 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1383:

GAATTCGGCC	TTCATGGCCT	AGGCAGCGGC	CTCTGTCCCA	GGCCCCGGGG	TGCCAGCGTC	60
CTGCGAGCAC	CCAGCTGACC	AAAGATGTTT	CCCTCTGTAG	AAGACTCTGC	TAGACTGGGT	120
CTGAAGCTTG	AGTTTTCTAA	CAGGTGCTGC	TGCACAGGTG	GAAAGGAGCC	GTGGGAATGT	180
GTGTGTGGCA	CGGCCCAGAC	AAGGGCAGGG	CTGAGGGCCT	CCGACTCAGC	TGGGGGTAGA	240
CGGGCTCGAA	TGTGGCCTGG	GAGAGCCTAG	GGGGCCCCAG	GGGTCTGCTT	TTCTATGTGA	300
GCCTTTAAAC	TTCAGACAGG	CCACCACCCT	GCACCTGCAG	GGGCTTTGGC	ACAGGAGTGC	360
TGGCTTTGGA	GGGACTGTGG	CCTTCATCGT	GGTCCTCTGC	CCACACCTCC	ACGCACACAG	420
ACAGTGCCCT	AGGAGGGAAA	CAGAACTAAT	TACGAGGGG	AGGCAAGAGG	ACGCCAAGCA	480
AGGAGTGACT	CGAG					494

- (2) INFORMATION FOR SEQ ID NO:1384:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 460 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1384:

GCTCGAGAGT GGGG	CGTGGC AGTGTGTGCC	TGTAGTCCCA	GCCACCTGGG	AGGCTGAGGC	60
AGAAAAATTG CCTG	AACCCG GGGGTCGCAG	GTTACAGAGA	GAGACTCTGT	CTCCCCAAAA	120
AAAAAAAAAA AAAA	AAAAAA NNGTCTAAGG	GTTANACAAT	TCTTGTATAA	ATCTCTCCAC	180
AATACATTCA GAAA	TCTACT TTTGCTGTTG	GAGTTGTATC	TGAGAGCTGG	GGAATTTAAA	240
ATTGCTGAAA ACAG	ATATAA GGGGAAAGTG	AGATAAAAGC	AGAAGCTGCC	AAAAGGAGGT	300
ATTAGCATCA TCCT	CAATTT ACACAGAATC	ACATGCTAAG	AGAGGCTAAG	TATCTTTCCC	360
AAGATTACTC AGCC	AAGTTG TGAAGCCAAG	ATTTAACTGT	ATCTATTCAA	CTCTTATCTA	420
ATTATAAAAG CCTA	TGTTAT TTCCCACTGT	GCTACTCGAG			460

- (2) INFORMATION FOR SEQ ID NO:1385:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 501 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1385:

GCAGGAGTAT	CTGAGGATGG	AGAACTCAGC	ATAGAAAACC	CCTTTGGTGA	AACATTTGGA	60
AAAATACAAG	AAAGTGAAAA	AACTCTTATG	ATGAACACAT	TATATAAGCT	TCATGATCGA	120
TTGGCACAGC	TTGCAGGAGA	TCATGAATGT	GGCAGTTCTA	GTCAAAGAAC	GCTTTCTGTT	180
CAAGAGGCAG	CTGCGTATTT	AAAAGATTTA	GGTCCTGAAT	ATGAAGGTAT	ATTTAACACT	240

TCATTGCAGT	GGATCTTAGA	AAATGGAAAA	GATGTTGGAA	TAAGGTGTGT	TGGTTTTGGC	300
CCTGAGGAAG	AATTGACAAA	TATAACTGAT	GTGCAGTTTT	TACAGTCCAC	AAGACCACTG	360
ATGTCTTTTT	GGTGTCGTTT	TCGACGTGCT	TTTGTTACTG	TAACTCACAG	ATTATTGTTG	420
TTATGCTTAG	GTGTAGTGAT	GGTTTGTGTC	GTTCTGCGTT	ACATGAAATA	TCGATGGACA	480
	AGGATCTCGA					501

- (2) INFORMATION FOR SEQ ID NO:1386:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 377 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1386:

				ATCAAGATCT		60
GGTGTTTGGG	TATAGCCTGA	GGTTCAACGC	CGACCTCCTG	CGCAGTGCAG	TGCAGCAGGT	120
CAACCAGTCC	TACACACAGG	GCGGCCAGTT	CTATTCCTCT	TCGTCAGTGA	TGCTCCTCTT	180
GTTGGATATT	CGGGACCGAA	TTAATCGCCT	GGCCCCTCCT	GTGGCCCCGG	GGAAACCCCA	240
				CTGACCAACA		300
CAGGGTGAAC	CACGCCTTGG	ACCTGTACAA	CACGGAGATC	CTCAAACAGT	CGGACCAGAT	360
GACAGCCAAC	ACTCGAG					377

- (2) INFORMATION FOR SEQ ID NO:1387:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 538 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1387:

GAATTCGGCC	TTCATGGCCT	AGACGACGCC	TATGAAGCCC	TTAGTCCTTC	TAGTTGCGCT	60
TTTGCTATGG	CCTTCGTCTG	TGCCGGCTTA	TCCGACATCA	AAGGGATCAA	AATTTAAGGA	120
GCTAGTTACA	CATGGAGACG	CTTCAACTGA	GAATGATGTT	TTAACCAATC	CTATCAGTGA	180
AGAAACTACA	ACTTTCCCTA	CAGGAGGCTT	CACACCGGAA	ATAGGAAAGA	AAAAACACAC	240
GGAAAGTACC	CCATTCTGGT	CGATCAAACC	AAACAATGTT	TCCATTGTTT	TGCATGCAGA	300
GGAACCTTAT	ATTGAAAATG	AAGAGCCAGA	GCCAGAGCCG	GAGCCAGCTG	CAAAACAAAC	360
TGAGGCACCA	AGAATGTTGC	CAGTTGTTAC	TGAATCATCT	ACAAGTCCAT	ATGTTACCTC	420
ATACAAGTCA	CCTGTCACCA	CTTTAGATAA	GAGCACTGGC	ATTGAGATCT	CTACAGAATC	480
AGAAGATGTT	CCTCAGCTCT	CAGGTGAAAC	TGCGATAGAA	AAACCCGAAG	CACTCGAG	538

- (2) INFORMATION FOR SEQ ID NO:1388:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 406 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1388:

GAATTCGGCC	TTCATGGCCT	ACCTATTTTC	CATATTCCGT	<b>GTGACTCATA</b>	ATGTACTCCT	60
GCTGTTGCTG	ACGGGCAGTG	GTCGGTCAGA	GCAGAAGCTC	AGCTGTGATT	GCTGGGGGAG	120
TTCTGAGCTC	CATGAGCCAC	TCTGGCCACG	ACACCATCTT	TACTTGAAAG	AAAAACTTCC	180
				GCCCACCCAG		240
				TGGGGGATGC		300
				TTCCTCATCC		360
	CCCCAGCTCC				COGNIGNIGG	
		LITCOMCII	TOTIMATETE	CICONO		406

- (2) INFORMATION FOR SEQ ID NO:1389:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 369 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1389:

GAATTCGGCC	TTCATGGCCT	AAATTAACTC	TAATGGGCAA	TCATAAGAAT	AATTGAAAAT	60
AAGGAATTCA	GGGGAGCTTA	ATTCATTTGT	AGGTTTTAGG	TGATACCATT	GCTATTCAGA	120
TTGCTTTGGG	CAATTTATGT	AATTTTTTCC	AATGACATCC	AATTTCATAT	CACTGTAACT	180
GAAGAAACAG	AAAATTTAGT	TCAGATTTTA	AATCATCATT	CCCTGATGCC	ACCTCATCCA	240
ATGATGTTTC	ATAAACGATG	AAATCACGTA	AGAACCACCT	AAACCAGGAC	TGATAGTCTA	300
TTGCTAGAAA	CTTGGAATAA	TTTCCACTGA	TTTCTGTTTT	CACTGGAAAC	AGAACAGAGA	360
CTCCTCGAG						369

- (2) INFORMATION FOR SEQ ID NO:1390:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 548 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: CDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1390:

GAATTCGGCC TTCATGGCCT AAC	GACCAAAA CTAAACTGAA	ATTTAAAATG	TTCTTCGGGG	60
GAGAAGGGAG CTTGACTTAC ACT	TTTGGTAA TAATTTGCTT	CCTGACACTA	AGGCTGTCTG	120
CTAGTCAGAA TTGCCTCAAA AAG	SAGTCTAG AAGATGTTGT	CATTGACATC	CAGTCATCTC	180
TTTCTAAGGG AATCAGAGGC AAT	TGAGCCCG TATATACTTC	AACTCAAGAA	GACTGCATTA	240
ATTCTTGCTG TTCAACAAAA AAG	CATATCAG GGACAAAGCA	TGTAACTTGA	TGATCTTCGA	300
CACTCGAAAA ACAGCTAGAC AAG	CCCAACTG CTACCTATTT	TTCTGTCCCC	AACGAGGAAG	360
CCTGTCCATT GAAACCAGCA AAA	AGGACTTA TGAGTTACAG	GATAATTACA	GATTTTCCAT	420
CTTTGACCAG AAATTTGCCA AGG	CCAAGAGT TACCCCAGGA	AGATTCTCTC	TTACATGGCC	480
AATTTTCACA AGCAGTCACT CCC	CCTAGCCC ATCATCACAC	AGATTATTCA	AAGCCCACCG	540
AGCTCGAG				548

- (2) INFORMATION FOR SEQ ID NO:1391:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 178 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1391:

MIT, BEGOLDED DESCRIPTION: SEQ ID NO:1391:	
GTTTATTTTC ATCATCTACA GAACCAAACT CCCTTTCATG TGCACGAGTG AGAATCTCTT TGTACAGTGT TTCTGCTTGC TTGAACTTTC CTTGTTTCAA ATAGCAGGAT GCCAGGTTAT TTTTCGTCTT AGCCACGTTG GGGTCATCAG GTCCCAGTTT TGTCTGGTAG ATCTCGAG	60 120 178
(2) INFORMATION FOR SEQ ID NO:1392:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 329 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1392:	
GAATTCGGCC AAAGAGGCCT AGGGCCCTAT ACCTCCAGCC GTGAATGCCA GACTTTAAGA TTGCCCGGAG GAAGCAAACT CTTCGTATAA AAAAAGCAGG CCATCTGCTT AACCCTTGGC TCCACCATAA GGCACTGGGA CTCGGATTTC TCTATCTGAT AGAGGTATTT TCTGTGGCCC TGGGAGCTGT CTGTCTTTCC CCTACCCCCA AGGATGCCAG GAAGACGTCC ACCATTAGCC ATGTGGCAAC CTTTACTTCT ATGCCTCACA AGTGCCTTTC AGAGAGCCCC AATTCTGCTT TCCCACAAAA TAAACCCAAT GCACTCGAG	60 120 180 240 300 329
(2) INFORMATION FOR SEQ ID NO:1393:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 324 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1393:	
GAATTCGGCC AAAGAGGCCT ATTCCTTTCC TTTTCCCTTT GAGATTTTT TGTTGTTGTT CCTTTTTGT ATTTTACTGA TATCACCAGG ATAGTTTACT CTCCTTCTAG CTTTCTGCTT ACCGCACACT GGATAACACA CACATACACA CCCACAAAAA TGCTCATGAA CCCAATCCGG AGAAGGTTCC AGCAGGTCCC CCACCCTCCC CTCCTCCTCC TACTTCTCCT CTTGACAGCG AGGACAGGAG GGGACAAGG GGACACCTGG GCAGACCCGC CGGNTCTCCC CCCACCCCAC CCCGCCCCCC GCATCATACT CGAG	60 120 180 240 300 324
(2) INFORMATION FOR SEQ ID NO:1394:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 462 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	

120

GAATTCGGCC AAAGAGGCCT AACTGCAACG GAGAGACTCA AGATGATTCN CTTTTTACCC ATGTTTTCTC TACTATTGCT GCTTATTGTT AACCCTATAA ACGCCAACAA TCATTATGAC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1394:

AAGATCTTGG	CTCATAGTCG	TATCAGGGGT	CGGGACCAAG	GCCCAAATGT	CTGTGCCCTT	180
G11G1G1			0000	0000101	CIGIOCCCII	180
CAACAGATTT	TGGGCACCAA	AAAGAAATAC	TTCAGCACTT	GTAAGAACTG	GTATAAAAAG	240
TOCATORORO	G1.G1.G1.1.G				011111111111111111111111111111111111111	240
ICCAICIGIG	GACAGAAAAC	GACTGTGTTA	TATGAATGTT	GCCCTGGTTA	TATGAGAATG	300
CARCOLAMOA	*******				onoracio	300
GAAGGAATGA	AAGGCTGCCC	AGCAGTTTTG	CCCATTGACC	ATGTTTATGG	CACTCTGGGC	360
A TOCTOCOLA						300
AT CG TGGGAG	CCACCACAAC	GCAGCGCTAT	TCTGACGCCT	CAAAACTGAG	GGAGGAGATC	420
C100011100						720
GAGGGAAAGG	GATCCTTCAC	TTACTTTGCA	CCGAGGCTCG	AG		462

- (2) INFORMATION FOR SEQ ID NO:1395:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 515 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1395:

GAATTCGGCC	AAAGAGGCCT	AGAACTGCCA	TCATGAGGTC	TGACAAGTCA	GCTTTGGTAT	60
TTCTGCTCCT	GCAGCTCTTC	TGTGTTGGCT	GTGGATTCTG	TGGGAAAGTC	CTGGTGTGGC	120
	GAGCCATTGG					180
GCCATGAGGT	AACAGTATTG	ACTCACTCAA	AGCCTTCGTT	AATTGACTAC	AGGAAGCCTT	240
CTGCATTGAA	ATTTGAGGTG	GTCCATATGC	CACAGGACAG	AACAGAAGAA	AATGAAATAT	300
	AGCTCTGAAT					360
TAAATGATTT	TTTTGTTGAA	ATAAGAGGAA	CTTTAAAAAT	GATGTGTGAG	AGCTTTATCT	420
ACAATCAGAC	GCTTATGAAG	AAGCTACAGG	AAACCAACTA	CGATGTAATG	CTTATAGACC	480
CTGTGATTCC	CTGTGGAGAC	CTGATAGCTC	TCGAG			515

- (2) INFORMATION FOR SEQ ID NO:1396:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 406 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1396:

GAATTCGGCC	AAAGAGGCCT	AGTCCTTCAC	TAGACTATAT	GCATTTTATC	TTACCTTATT	60
CCTCATTTTA	GTGTCCAGTG	GCTGGCGTGT	ATAAACCCTG	AATGTTTTTA	AAGATAATAT	120
TTTAAAAGAT	CACTTTAGTT	ATAATACGGC	TTCAGTTGGT	GGAATAAAGA	AATTTTTTC	180
TTTTTTTTA	TTTTGAGTAA	AAATGATAAC	TTCTCTCCAC	CCTCTCTATA	GTTAAAGCCT	240
TCCATCTGAA	GTATGATGAA	GTTCGTCTGG	ATCCAAATGT	TCAGAAATGG	GATGTNACAG	300
TATTAGAACT	CAGCTATCAC	AAACGTCATT	TGGATAGACC	AGTGTTCTTA	CGGTTTTGGG	360
<b>AAACATTGGA</b>	CAGGTACATG	<b>GTAAAGCATA</b>	AATCGCACAT	CTCGAG		406

- (2) INFORMATION FOR SEQ ID NO:1397:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 299 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1397:

GAATTCGGCC AAAGGGGCCT AAGAATAGCA AATATCTTGT GCTTAGCAAA AAATAATCTT

60

GAAAAATTT TCTGAAATAA ATGTTATTGA AAAATGCAAA TAATTAGAAT TAAATACCAG CTGCAGTTCT ACATCCTCTT ATTGGCCAAT GTAAAGAGAA ATCAGGCATG TTAACTCCAA AAAAGGACAA TTCAACAACA TGGAAACCAT GACTAATATA TGGAGAATAC AAAGAAAGAC TAAAGATTTA GATCAGGCTA ATTTCTTTTT ATTCCCATCA AATCCAAGTA CCACTCGAG  (2) INFORMATION FOR SEQ ID NO:1398:	120 180 240 299
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 368 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1398:	
GAATTCGGAC AAAGAGGCCT AGGAGAGGCG GGAGCCTGGG AGAGCCTCTG CTAGACCTTT CCTGGCACTT CCCCAGGAAA GGCAAGGCAG GGCAGATGTG CGGCTGGCCA GCTGGAGTGA TTTCCATGGG CTCCAAGCTG TAGGAGTGGT CCCTGGCTGC CAGAGTGCTC TGGCCAGATA CAGGTGGGCT CTGGACTGGT GAGGCTGCAT TGCGGAGGCG CGCACACCCA GCTGGGCCCT TATCTGTAAG GACTGGCTGG CCTGGGAGGG GCAGTCTCCC ANCCAGAANG TGGAATTTTT TTTTTTTTTTT TGAGATATCA AAACATCCTA AGGTACAGGA AAGAAATTGT CNACACACAC GGCTCGAG	60 120 180 240 300 360 368
(2) INFORMATION FOR SEQ ID NO:1399:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 149 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1399:	
GAATTCGGCC AAAGAGGCCT ATTTTTTTGG AGATGTTGAT CAGATGTTCA CTGATAAACT TGAGCCCCCT TTTCTTCCTC TGGTCTACCC ATCTAGAATG CTATGACCCA TCTCAGACAC ACCCCTCTGG GAAGCTGCCT GAGCTCGAG	60 120 149
(2) INFORMATION FOR SEQ ID NO:1400:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 599 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1400:	
GAATTCGGCC AAAGAGGCCT AGTCGATGGA GATAAGTGTT TTAATTACTT TTTTAATGTC TGTGCTTTTG TATTTTTCTC CTCTCTTTCC TTTTATTTCC TGCTGTNGAG ATTACTGCCT CATCTCCACA GCAGGTGGCT GTTGCAAATT TGTTTTCTTT GTAAGCCTGG AAGATTTATT TTGTAATATA ACTGTTCCTT TTTAGTATTT TATTATTAAT GATTTCTTTA CTTTGGGATA	60 120 180 240
557	

TAGTGTACTT ACACAGTCCT AAACAGTAAT TTCCTAACAC TATCTAAGAA CTCCAATCAT TAAGAAAAAA AATCTTTGCC TGAGGCGTAT TGTTTGAGAT TTTTGCTTAC CCTTACTTCA CAATGCGGGG ATTAAAATTT AAGGAAATTG TTTTATAGCA AAAGCCAAAT GAGAAAAAGA AACAGAGAAA ATAGAAGGGA GGGAAATAAA GAAAAGGAGA AGAGAAAAGG CTCAAGAGAC AAAGTATACT TTAATAAATA ATACCATAAA GCAGAGTAAT GAGGATAAAT TTATGGCTGA AATATGAAAT TACATTAACA TCTTTTCTAG AAATGTTTCA ACTAAACCAA ATGCTCGAG	300 360 420 480 540 599
(2) INFORMATION FOR SEQ ID NO:1401:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 347 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1401:	
GAATTCGGCC AAAGAGGCCT ACAGTCACCC TATAAAATAG ATTAAGTGTT CCGAGTTCGG TTGGGTTTTC CGCAATTAAA AATTGTGTTA ACAGTTTAGT GTTTCTTACA GATAACACTG ATAACACTTT TTTGTTTTCA TTGGGTCTTA TCATTGGTAC AGACTGATCC AAAAATCCAA TTGGCTTGCT AGTAATTTTT TCCTGTGAAT TGCTAAGATT TATGGGTAAA TTAAATTTTC TTTTTCTTTT CTTTTTTTT TTTTTAAGCA TTTGCTCCTT AAATGCAAAT CGTACCACTA AGATCCTCTC ACAACAGATT AAGGTCGAAT TTGCAGAGAC ACTCGAG  (2) INFORMATION FOR SEQ ID NO:1402:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 357 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1402:	60 120 180 240 300 347
GAATTCGGCC AAAGAGGCCT ATATAAACTC AACTTTTCTT TGTCTCTTT GCCTGTGATG AGTAACAGAA ACCATCTTCC CAGAAACTAT CCCCACCCAC CCCCAGCCCA GCCCGAGCAG CCCAGACCCA GGAAGGAGGT CAGAGCCTGC GTGACTGTGT GGCAAAGGATC CCCCTCAAAG CAGGCAGTGA TCCCCCTCAA AGCAGGCAGT GATGACCAGG CTCCCCAGGG GAAGGAAAAA TGGTTGATTA CCCCACCTCA CTTTCTCAAG TTCCTGAAAG CCTCCCATCT TTTCAGGATG TTTTCCTTCT GCTTCCTTTC TGGGGTGATA TTGCAATGCA TGTGTCAGTC CCTCGAG  (2) INFORMATION FOR SEQ ID NO:1403:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 270 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	60 120 180 240 300 357
(ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1403:	
GAATTCGGCC AAAGAGGCCT AAGGATTGTC ATAGCCAGGA CCACACTATT GCTTTTTCAT AACATTTTCT TTTTGTTTCT TTCTTTTGAA TTTCTTACAG GGCTGCAAAG TATGCCAGGG	60 120

CCCCAGATGC CCCCCCATCC TGCTCAGCTG CGTCATGGGC CCCCCATGCA TACGTACATT CCTGGACACC CTCACCACCC AACTCTCGAG	180 240 270
(2) INFORMATION FOR SEQ ID NO:1404:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 129 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1404:	
GAATTCGGCC AAAGA~GCCT ACAGCCTTTC TTCCCACTTT TAACTATAGA ACTTGCTTTT AATTTCACTG ATATATGGAC ACAGTCAGAC GAGAACTCCT TCATGCTCCT ATTACCACAG CTACTCGAG	60 120 129
(2) INFORMATION FOR SEQ ID NO:1405:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 229 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1405:	
GAATTCGGCC AAAGAGGCCT AATTGCTTAA GCTCCTCAAG TTCTTTTAT TAAGAGTTGT AAGTAAAATT TAATAAACAA TAACATAGTC TCTGCTATTT TGATCCTTGC TCTTTGCCAT GCTGTTTTAC TTATTCTTTA TTGCATGTTT CACATCTATC AATTTTGGGA TATGCTTCTC ACCTTCCCTA CTAAAATGTG AGCTCCGTAA ACGCAACAGC TACCTCGAG	60 120 180 229
(2) INFORMATION FOR SEQ ID NO:1406:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 398 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1406:	
GAATTCGGCC AAAGAGGCCT AGTGGAGGTA TTTTGAAAAT ACAATTTAAC TACAACAACA TTTGCTTATT TTTAGAGTCT TTTATGACAT CAAGAGAAAT GATCCCAGAA AGAAAAAATC AAGAAAAAGA ATCTGATGAT GCCTTAACTG TGAATGAAGA GACTTCTGAG GAAAATAATC AAATGGAGGA ATCTGATGTG TCTCAAGCTG AGAAAGATTT GCTACATTCT GAAGGTAGTG AAAACGAAGG CCCTGTAAGT AGTAGTTCTT CTGACTGCCG TGAAACAGAA GAATTAGTAG GATCCAATTC CAGTAAAACT GGAGAGATTC TTTCAGAATC ATCCATGGAA AATGATGACG AAGCCACAGA AGTCACCGAT GAACCAATGG AACTCGAG	60 120 180 240 300 360 398
(2) INFORMATION FOR CEO ID NO. 1407.	

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(i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 131 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: CDNA
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1407:
60
CAATCCTGAT GTACCTTCTT CTAGTCTTGG TCTTTGGCAC CTTTTTTCA AGAAGAAACC
                                                                     120
ATACTCTCGA G
                                                                     131
(2) INFORMATION FOR SEQ ID NO:1408:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 622 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1408:
GAATTCGGCC AAAGAGGCCT AAGTCCAGGC TGTAGGGTCC CTGGTCACAG AGGACCCGGG
TCACCCGGGA CTCATCTTTC ACTTATTGTT TTTCAAGTCC AGGGCCCCAT GGATGCCACT
                                                                    120
GAGATGATTT CAGATGTTAC AGTCATCAAG AGGGATTGGG GCCGCATTCT GCCTCATTCC
                                                                    180
TTGGCTTTTG AAATCAGAGA CGACATTTTC ACTTTAAACA AACCCAAACC ATTCCTGCTG
                                                                    240
GTGGAGGATT TCTCCTGCAT CTCGGGGGTG GATTTTCACT GATTTATGTC TGCAGCGTGA
GCAGTCTCTG GGCTTTTCTG CAGCTCCAGA TGTTAGATGT TTTATCTCTC CGTCTTTTAT
                                                                    360
CNGCTTCAGT CCTTGCCCCA GTCTATCCTC GCATGCTCCN TCCTNNGGGA GGGCTTCCTG
                                                                    420
TCTTCACAGC CGCACCTTCC TCCCACTGCT ACCAGTGCCA TGGACCCACT GTATGTTTCC
                                                                    480
TGGGGGCCAT GCAGAAGGTC CCCAGACCAG TGCTGGCCTG CGACAAATAA GTACAGAAAT
                                                                    540
GGAGAATAAC CCCTTTCAAA CACATAATAG CATTTGATAG AATCAATCAG GAGACTCAAG
                                                                    600
TTTTTACTGC GTGCGTCTCG AG
                                                                    622
(2) INFORMATION FOR SEQ ID NO:1409:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 328 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1409:
GAATTCGGCC AAAGAGGCCT AGAACATGCA GATTTTTCCT CTAGAAAACC CCCTCCCCAC
                                                                     60
ATTCAGCTTA TTAGAAATCC TTAACAGCAG GTAACCACCA ATGCTCCTGC CTTCTAGCCA
CAGTCTGCTC CTGCCCCTAC AGGCTTTGAA CATGCAGATT TTTCCTCTAG AAAACCCCCT
CCCTGCATAT TCTCTCCTCT CCCCACTCAC ACAAACACCT GGCCTGCCAG GCCCCGTGGG
                                                                    240
GCTGCCGGGC TTCTGTGAAC CTGCCGCCTG CCTTGGAGCT TCGGCCTATG CCTCTGCCCG
                                                                    300
CCTTACAGAG CCTGGATCCA AACTCGAG
                                                                    328
(2) INFORMATION FOR SEQ ID NO:1410:
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(ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1410:  GAATTCGGCC AAAGAGGCCT NNAAAAAAAA AAACCAAAAA AAAAGAAAAA GCTGACACAG TTCTCTGAAA AAAGCCTAGA GAACACAAGG GTGACACAAA CTCCAGAGAG TATGCTGCTT GCAGCTTTGA TGATTGTATC AACAGTGGTA AGTCACCCCA TGTCTGCAGG AGCAGCTGCA GCTAATTATA CCTACTGGGC CTATGTGCCT TTCCCACCCT TAATTCGGGC AGTCACATGG ATGGATAATC CTATTGAAGT ATATGTTAAT AATAGTGCAT GGGTACCTGG CCCCATAGAG GATCGTTGCC CAGCCCAACT CGAG  (2) INFORMATION FOR SEQ ID NO:1411:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 323 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear
GAATTCGGCC AAAGAGGCCT NNAAAAAAAA AAACCAAAAA AAAAGAAAAA GCTGACACAG TTCTCTGAAA AAAGCCTAGA GAACACAAGG GTGACACAAA CTCCAGAGAG TATGCTGCTT 12 GCAGCTTTGA TGATTGTATC AACAGTGGTA AGTCACCCCA TGTCTGCAGG AGCAGCTGCA 18 GCTAATTATA CCTACTGGGC CTATGTGCCT TTCCCACCCT TAATTCGGGC AGTCACATGG ATGGATAATC CTATTGAAGT ATATGTTAAT AATAGTGCAT GGGTACCTGG CCCCATAGAG 30: GATCGTTGCC CAGCCCAACT CGAG 32:  (2) INFORMATION FOR SEQ ID NO:1411:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 323 base pairs  (B) TYPE: nucleic acid (C) STRANDEDNESS: double
TTCTCTGAAA AAAGCCTAGA GAACACAAGG GTGACACAAA CTCCAGAGAG TATGCTGCTT  GCAGCTTTGA TGATTGTATC AACAGTGGTA AGTCACCCCA TGTCTGCAGG AGCAGCTGCA  GCTAATTATA CCTACTGGGC CTATGTGCCT TTCCCACCCT TAATTCGGGC AGTCACATGG  ATGGATAATC CTATTGAAGT ATATGTTAAT AATAGTGCAT GGGTACCTGG CCCCATAGAG  GATCGTTGCC CAGCCCAACT CGAG  (2) INFORMATION FOR SEQ ID NO:1411:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 323 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double
(A) LENGTH: 323 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double
(B) TYPE: nucleic acid (C) STRANDEDNESS: double
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1411:
GAATTCGGCC AAAGAGGCCT AGAAGTTGAG TGAAGGAGAA AGAGAGGGAA GTAGAAAAGA 66 GGAGAAAAAT GTTAAGCAAA AAAGGTATTT TCCCTTGGAT ATTAACTTGC ATATCTGAAG 120 AAATGGCATT CCGGACAATT TGCGTGTTGG TTGGAGTATT TATTTGTTCT ATCTGTGTGA 180 AAGGATCTTC CCAGCCCCAA GCAAGAGTTT ATTTAACATT TGATGAACTT CGAGAAACCA 240 AGACCTCTGA ATACTTCAGC CTTTCCCACC ATCCTTTAGA CTACAGGATT TTATTAATGG 300 ATGAAGATCA GGAACAACTC GAG 322
(2) INFORMATION FOR SEQ ID NO:1412:
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 149 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1412:
GAATTCGGCC AAAGAGGCCT AGTTAGTTGC TCTCCTTTTT TCTTTTTTTT GTCGTGCATA TTTTATTTCT GTAGTTTCTG GTTAGCTACC CTAAAAGTGAT TTAAAAATTT AGAATGCTTT GTGTTTCCTA TTTGGTAATC ACACTCGAG  (2) INFORMATION FOR SEQ ID NO:1413:
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 308 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1413:

GAATTCGGCC	AAAGAGGCCT	AATAAGAATT	ACTTGTAACT	TTAGGGGGCA	TTTAGAATTA	60
TATTTGTCTT	ATTTGAGATT	TGGATTTAAA	TTTTATTTTA	GAGCATTTTT	TAAAAAATAA	120
ATAGAAGTGA	GGCTAATATT	GTTAATTATT	CTCTTTAAAA	AATACAGTAT	TTGCTTTGGG	180
					ATAAATTTAG	240
	GTGGCAGGCA	TTGTTCTATA	TACTTTATTC	GTTAAATTCA	CCAGCGAACA	300
CGCTCGAG						308

- (2) INFORMATION FOR SEQ ID NO:1414:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 252 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1414:

GAATTCGGCC AAAGAGGCC					60
TGGTTCATGT TTGCAGATA	AGACCTCACT	GTGTGGTGGA	CTTCCCCACT	TCCTGCTGCC	120
TTCATCCTGA TGGGTGGCT	CCTTCATCCT	GATGGGTGGC	AGCCTTGCCC	TGCAGTGGGA	180
GACCCAGGTA ATGTAGTTT	TTGTTTTGTA	TCCCTGATCT	CTTCTTGCAG	TTTTTGCCGG	240
GCAGGTCTCG AG					252

- (2) INFORMATION FOR SEQ ID NO:1415:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 332 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: CDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1415:

GAATTCGGCC	AAAGAGGCCT	AGTGATTCAG	AACCATTTGA	TAATAGCTTG	AAAGCCTAGA	60
TNGACTCTCT	GCATTGCCAC	CCCTCCCTAT	TCTCTTAAGC	CCACTCCATT	CACGCTGTCA	120
TCCACACCAC	TCGGCCACCA	ATTTCACACT	GCCAAATCCA	GTTCCCAGTT	CCTCATCGTG	180
TTTATTNGCA	ACATTTGAAA	CAAGTGATCA	ATCCCTTTTC	CATGAAAAAC	CTTCTTTGCA	240
CAGTTTCCAG	AATTCTAAAC	TTTCCTGGTT	TTCCTCCTAC	TTCAACTTTC	CAATTACCGT	300
CCCTCATTTT	TACCTCATCA	GCCCAACTCG	AG			332

- (2) INFORMATION FOR SEQ ID NO:1416:
  - (i) SEQUENCE CHARACTERISTICS:

(D) TOPOLOGY: linear

- (A) LENGTH: 346 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1416:

GAATTCGGGC CAAAGAAGCC TACAANAAAN TATATATATN TGGATCTTCT GAAAAGTTTT TTGAGGTGCA AGTTTTCTCT CTTTTTTTT TTTTTTTTT TTCTCATTGA TTAATGGACA TGATGCTGAG ATTCAATCAC TACATGAAAC ACCTGGCTGT GAAAACAAAA CAACCCAGAG GGCTGTGTTC CAAGCAGCCC TGGGGAAGCT ACGTAACAGT CGGATGCCAG TTTTGGAAGA TTCACCATGC GTTCTGACCC TCTGTTCGTC TCTTTCCTCT CCTCTTTCTT CAAGAAGGAA ATTGATCCTA GTGATTTCAG CCCATGCATT AAACAGGAAA CTCGAG	60 120 180 240 300 346
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 128 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1417:	
GAATTCGCCA AAGAGCCTAA GGGCAAGCAG CATTCATATA TCATATGACT TCTACAACTA AAATGAAGCT ATTAGCACTA GTATTTAGTA ATCTAGTAAC TCTCCTTCCA GCCCTCTTCA CCCTCGAG	60 120 128
(2) INFORMATION FOR SEQ ID NO:1418:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 385 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1418:	
GAATTCGGCC AAAGAGCCTA GGGAAGCGCT CTTCACGGCA CTGGGATCCG CATCTGCCTG GGATCATCAA GCCCTAGAAG CTGGGTTTCT TTAAATTAGG GCTGCCGTTT TCTGTTTCTC CCTGGGCTGC GGAAAGCCAG AAGATTTTAT CTAGCTTATA CAAGGCTGCT GGTGTTCCCT CTTTTTTTCC ACGAGGGTGT TTTTGGCTGC AATTGCATGA AATCCCAATG GTGTAGACCA GTGGCGATGG ATCTAGGAGT TTACCAACTG AGACATTTTT CAATTTCTTT CTTGTCATCC TTGCTGGGGA CTGAAAACGC TTCTGTGAGA CTTGATAATA GCTCCTCTGG TGCAAGTGTG	60 120 180 240 300 360
GTAGCTATTG ACAACATCAC TCGAG  (2) INFORMATION FOR SEQ ID NO:1419:	385
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 425 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1419:	
GAATTCGGCC AAAGAGCCCT AGTAGGTTTA TAAACAGAAG TTTAAACTTG TAAGCTTAAG CTTCCGTTTA TAAACAGAAG TTTAAAATTA TAGGTCCTGT TTAACATTCA GCTCTGTTAA CTCACTCATC TTTTTGTGT TTTACACTTT GTCAAGATTT CTTTACATAT TCATCAATGT	60 120 180

CTGAAGAAGT TACTTATGCA GATCTTCAAT TCCAGAACTC CAGTGAGATG GAAAAAAATCC CAGAAATTGG CAAATTTGGG GAAAAAAGCAC CTCCAGCTCC CTCTCATGTA TGGCGTCCAG CAGCCTTGTT TCTGACTCTT CTGTGCCTTC TGTTGCTCAT TGGATTGGGA GTCTTGGCAA GCATGTTTCA TGTAACTTTG AAGATAGAAA TGAAAAAAAAT GAACAAACTA CAAAACATCC TCGAG	240 300 360 420 425
(2) INFORMATION FOR SEQ ID NO:1420:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 264 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1420:	
GAATTCGGCC AAAGAGGCCT AAGACGCATG CCTGTAATCC CAGCAACTCG GGAAGCTGAG GCGGGAGAAT CGCTTGAACC CGGGAGCGGA GGTTGCGGTG AGTTGAGATG GCGCCACTGC ACTCCAGCCT TGGCAAAAAG AGCAAAACTT CATCTCAAAA AAAAAAAAAG AATGTGTGGA ATAATGGGGG TTTTTTCCTT ACTTTTGTGG CTTATTCTCA CTTACATGGG GATAGCCTTG GTCTTTGACT TGGATAGCCT CGAG	60 120 180 240 264
(2) INFORMATION FOR SEQ ID NO:1421:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 144 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1421:	
GAATTCGGCC AAAGAGGCCT AAGTGAATCG ATGTTCTGGC TTGGCTGTCT TTGGTGTTTT CATTCTTTCA TTTCTTTCTC CCTGTCCTCA TCTCTCTCTC CCCGTGCCCT GCTCCCTACA CCTATCCCTC CCCCTACCCT CGAG	60 120 144
(2) INFORMATION FOR SEQ ID NO:1422:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 286 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1422:	
GAATTCGGCC AAAGAGGCCT AGAGAGAATA AAATACATAT AGTTGATTAA AGGAAGGAAG TTTATTACTT AGGGAAAAGG AAGGTAAAAA AAGACCCTAA GCAATAAAGG CAATTCTTT TTAAGCAGAA TACTTTCATT TTATTTCATT TTTGTTTACC AGTGTTTAT CGAAAACTGC TGCTGGGGCT ACTTCAGCTG AGATGATTTG GCTCTTTTTT GTGGCTTTCT TCTTGTTCTG TACATCAGCA CTGTGGTTAT TACACCAGCT ACCAAGTCAT CTCGAG  (2) INFORMATION FOR SEQ ID NO:1423:	60 120 180 240 286

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(i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 157 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1423:
GCGATTGAAT TCTAGACCTG CCTCGAGACA GAGCAAGATT CCGTTCCCAA GAAAAAAAAA
                                                                      60
TTGTTCAACA ATAAGGGCAA AGGGAGAGAA TCATAACATC TGATTAAACA GAAAAAGCAA
                                                                      120
GATTTTTAAA ACTAACTATA TAAGGATGCA TCTCGAG
                                                                      157
(2) INFORMATION FOR SEQ ID NO:1424:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 408 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1424:
GAATTCGGCC AAAGAGGCCT ACTCAAAAGA CAAAAAAGAT ACATTAGGCA GTGTTCTGTA
AACATGGGAA AATTATTTA GGTTAAATGG GCTGAGAAGA AATTTGCTAA ATTTTGCTTT
                                                                      120
TGTTACCACG TTTCCTGAAA TGATGATAAT AAATAATATT TTAAAAGGGT GAATAGAAGG
                                                                      180
ATCTTTATTG TAGGTACTGG TGTTAAAATT TAGGTTCAGA AATAATACTG TAAAGCTACT
                                                                      240
TTCTTTACAC AGATTAACAC ATTTATCTTC TTGAATTATT TAATAATGAA TGTCAAAAAA
                                                                      300
TTCGAAATCT CATATAAGAT CTCACTTTGA AACAAAGTAT ATAAACTGTT GATTGCACAA
                                                                      360
TTTGGGTTTT GTGAAGCAGT CAGTTTTGAC TATAAGTGGC AGCTCGAG
                                                                      408
(2) INFORMATION FOR SEO ID NO:1425:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 468 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1425:
GAATTCGGCC AAAGAGGCCT ATTCTTGTCT CCTAAGAATA ACTGTGCTTG AAGAAGAAAA
                                                                       60
TTCCCAACAT GGACAACCA CGCAAAGAAA ATGAAGAAGA GCCGCAGAGC GCGCCCAAGA
                                                                      120
CCGATGAGGA GAGGCCTCCG GTGGAGCACT CTCCCGAAAA GCAGTCCCCC GAGGAGCAGT
                                                                      180
CTTCGGAGGA GCAGTCCTCG GAGGGAGGAG TTCTTTCCTG AGGAGCTCTT GCCTGAGCTC
                                                                      240
CTGCCTGAGA TGCTCCTCTC GGAGGAGCGC CCTCCGCAGG AGGGTCTTTC CAGGAAGGAC
                                                                      300
CTGTTTGAGG GGCGCCCTCC CATGGAGCAG CCTCCTTGTG GAGTAGGAAA ACATAAGCTT
                                                                      360
GAAGAAGGAA GCTTTAAAGA AAGGTTGGCT CGTTCTCGCC CGCAATTTAG AGGGGACATA
                                                                      420
CATGGCAGAA ATTTAAGCAA TGAGGAGATG ATACAGGCAA CTCTCGAG
                                                                      468
(2) INFORMATION FOR SEO ID NO:1426:
     (i) SEQUENCE CHARACTERISTICS:
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(A) LENGTH: 309 base pairs

(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1426:	
TTTGACCAGA TTATTCTTCT ATGCTTTTTT GCAATAAATC AAATCCCACA TATCTACAAG TGGTATGAAG TCCTGCACCC CCCAGGAGC CTGTCCAGGC ATGTCTTCAG AGGCAGGGTG GGTTACACTC ATTTACCTCC CCTCTCCCCA CCAAATTATG ACACAAACGA GTATGTTTCC TCTCTAGAAC CCTGTAATGC CTCCTCCCCC ATCCCCAGAG CTCCTTACTG TAGGTCTTAC CCTGGACAAG GATTTTTCA AGTTGGAGGC ACAGAACATG AGCAATCTGA CATTCCCACA GGCCTCGAG	60 120 180 240 300 309
(2) INFORMATION FOR SEQ ID NO:1427:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 501 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1427:	
GAATTCGGCC AAAGAGGCCT AAGTGAGGAC AGGGCAAAGA TTTTATAGTC TCCTGTAAAC AGGAAGTGTC CTAGTCTGAC GTAACTGCTA CGTTGTACCT GGATGGCCTC TTTCTTGATC CTGCTATTTT GCTGGCCCAC ACTGCTGGC CAAGGCTTGC GCCTTGGTAC TGGGCCTGAG AAGGGAGGAG TTATTCATCC CCTTAAGCTT TCAGGCCCCA GGGAGAATCT TACACTACTG GGCTGCATTT CCAGACAATT AGGGCATCT AAGGCACAGG ATGAGGTAGG AGGTCCGCAC AAGATACAGG TCATAAAGAC CTTGCAGATA AAACAGCTTG CAGTAAATAA GCTGGCCCAA ACCCACGAAA ATCAAGATTT TGACCAGAGT GACCCTCTGG TCATCCTCAC TGCTACACTC CCACCAGCAT CACGACTCGA G	60 120 180 240 300 360 420 480 501
(2) INFORMATION FOR SEQ ID NO:1428:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 135 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1428:	
GAATTCGGCC AAAGAGGCCT AGACCTTGTT TAGTGTTGTA AAGTTCTTCC AGTCTCGGAA TGGTAAGGAA TTTATGCATG CTTACTCCAT TTTCAATAAG AAGTTTTACA AATGCAACTC TATCCATTAC TCGAG	60 120 135
(2) INFORMATION FOR SEQ ID NO:1429:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 245 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	
566	

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1429:

GAATTCGGCC	AAAGAGGCCT	AGGGGCAGCG	AATGTTTTTA	GAAGCAGAAA	ACTTTCCAAA	60
TTTGGTGAAA	GACATAAATT	TACAGATTTC	AAGAAGCTCC	ACAAATTCCA	AATATGATAA	120
ATATGAAGAA	ACTCATAGCA	AGGATGCTAT	ACCACACACT	TCTGAATAAT	CCACAGGTCA	180
AAGAAGTCAG	ACTCTCCGGT	CTGACATGTA	AAGGGCCTGG	AAGTCGTCAC	TCCCATCCTC	240
TCGAG						245

- (2) INFORMATION FOR SEQ ID NO:1430:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 321 base pairs
    - (B) TYLE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1430:

GAATTCGGCC	ANNAGAGGCC	TAAGAAACTG	GAAGTGCCTT	TCATCTCCTC	CCCCACCTAA	60
CTCCCCAGAA	TTAATCACAA	ATACTTTTGT	GTGTATATTG	TTCTGGAAAT	TGTAAATGTT	120
TAAACAAATC	TACTAAGGTA	TACTCTTCTG	AAATTTTCCT	TTGAAAATTT	AGTTTATAAT	180
TTGGATTTAT	TTCTTGATGA	GCACATGCTA	AACTCATTCC	ACCCTTTTTT	GATGAAAATT	240
ATTACATGTT	TATTAATATA	TCACATTCCC	TCCCTCCCTG	TCCCTTTTTT	CCCCCATAAA	300
ACACAATACT	<b>GTCAACTCGA</b>	G				321

- (2) INFORMATION FOR SEQ ID NO:1431:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 316 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1431:

GAATTCGGCC	AAAGAGGCCT	AGTGTGAGAC	ATTTGTCATT	GCTCAGAATT	TTAAAATTGC	60
ATTCCAAGCT	GTTGGATTTG	AGTTTAAGTG	AGGCCAAACT	GGGGCGAGAT	CAAACACACC	120
ATCAAAGAAT	TACACACATA	TCCTTGTGGC	CACATCGCTT	TTGTTGTTTG	TTTCAAGGAT	180
GCTGTGTGTG	TTACTAGGGT	TAAGACTCTT	CTCCTTGGCT	GAGGGATCTC	CTCTGGAGAT	240
TTTGAAAACA	GGAAACAGAT	TTCTCTCTCC	CTTCTCTGGT	AGTCTTCCTA	TTCGTGTTAG	300
AAACAATCAA	CTCGAG					316

- (2) INFORMATION FOR SEQ ID NO:1432:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 515 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1432:

GAATTCGGCC	AAAGAGGCCT	ATAAAAATGC	AAAAAATCCA	GTCTAAATAT	TGTCTATAGT	60
TTTTTAGGAT	TATAGTGTAA	TCTGCTCTTT	TAACTTATGT	ATCTCTACAG	CCTGCCACCA	120
TATAAGCTTT	AAATTATAAA	ATTATGATGC	TTGACATTGG	GGAGAAAGGA	ACATAAGCAC	180
CCATAATGAG	TCATTTTTGT	TGACTGTATA	AATGAGTCAG	AGTTACATGT	AAGGATGAGA	240
ATATCCTCCT	ACAATTTTGG	TTTTTGATCT	TGATTTTTTC	CCATTGACTC	TCTTTTCTCC	300
CCGCCATTCT	CTCTCTTGCA	CGTAGCACAC	TTTTGCGCTC	TGTCTGCTAT	TACTGCTATT	360
ATAAACCTTT	TACTGGACTT	CAGTTGTAGT	GACCATTAGG	TCCTAAACAT	AGAACTAAGA	420
			AATTTŢAATA	ACTAGAGTTC	ATAATTTAGA	480
ATTAATATAT	GAGAATTTAC	TGTATAATCC	TCGAG			515

- (2) INFORMATION FOR SEQ ID NO:1433:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 304 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1433:

GAATTCGGCC	TTCATGGCCT	ACTGCTTTTT	TTTCTCTTTT	TTCTTTTTCC	CTTTTGACTT	60
TTGAGGCTCC	TGTTCTTTGG	CAGCACCAGC	TCCTTCTATT	TCTGCAGCCA	AGGCATCAAG	120
ATCAATGTCA	TCCTTGGTGC	TGTCTTCGCT	CTTGTTTTTC	TGTTTCTTCC	CCATTGCTTG	180
TCAATGGCGC	TCGTGGCCCC	AGCCCCTCTA	TTCGGTCTCT	CACAGACCCA	CTGTCTCCCG	240
GCTGACTTTG	GTCTCCGCTC	AGCTCTTTTC	CCCTCGTGCT	GCCGCCGCTC	GCACCCGGCT	300
CGAG						304

- (2) INFORMATION FOR SEQ ID NO:1434:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 291 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1434:

033MM000000	*****					
GAATTCGGCC	AAAGAGGCCT	AGAATTTATG	TAATCCCAGG	GTGGCTACCT	ATTTCAGTAG	60
TATTCCCCTC	GGCTCAGTTT	TAAATTTATT	TTAGAAGCTT	GGATTTCTCC	CTAAGAGTTC	120
AAATTTTCCC	AATTATATTT	GGCTTCCAGT	TGACTTTGAT	ACTGGAATTC	TCTGCCAGGA	180
AGGAGTGAGG	CCATCATGTT	TCCACTTATG	CCATCAGTGG	CATCTCTGAT	ATTTTGCCAC	240
GTGTTGCCCC	TGTACAGCCC	TGAGGTGTTG	GGCAGAGGAG	GCCAACTCGA	G	291

- (2) INFORMATION FOR SEQ ID NO:1435:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 422 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1435:

GAATTCGGCC AAAGAGGCCT AAGACCCCCC TCAGC GTGAGCCAAT GCATCCAGCT GACTTTTGGA CTCTA CATATGTCAA GCAAGGGATT GACATGATCA GATTA TCTACAGTGT GGAGAGTGGA TTGGGAGGCA GAATG. TCCAGGTTAC AGATGGGGGT AATGAGACCT AGGCAG GATAGATTCC AGAGACATTT GGAGGTGAAA TCAGGG TAAAGAGGTA GAAAGAAGAT TTGAGGATGA TGCTCG AG	ICTTG AGGTAGCTGG GAGCCACTGA 12 FTATG TAGAAAGGCC AGTCGCTCTG 18 ACCAG TCTGGAGGCT ATTATAGTAA 24 GGTAA TAGCGTGGCT AGAAGGAATG 30 GGTG GCGATTTAAC TCGGRAATG
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- (2) INFORMATION FOR SEQ ID NO:1436:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 142 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1436:

GAATTCGGCC AAAGAGGCCT AAGCTAGTT AGTTATTGCT ATCATGAAAA ATAAAATTT AACATTAACC CTGACACTCG AG	A TATGTTATTC I ATGTGTCCTA	TGGGAAAAA AATTTAATTA	TATTATTTGT TATTTTATGA	60 120 142
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- (2) INFORMATION FOR SEQ ID NO:1437:
  - (1) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 263 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1437:

GAATTCGGCC	AAAGAGGCCT	ACGTACATTT	ACTCTTTATA	СУЛСЛАТАТИ	TTGTATGTCA	
TACCTTTACA	CTCATTATTC			CALGITITI	TIGIATGTCA	60
	GICALIALLO	TICTIGATGT	TCATATCTCC	CCATCTTTGG	CCAGTTAGAG	120
CATTTCCAAG	TGAGCTCCTG	TGTCCTTTTG	ACAAGACCCC	<b>Δ</b> ርፓስ አጥርርምም	CTGCTTTTAG	
ATAGAATAAG	ስ ጥርጥጥጥር እ <i>ር</i> ርር	7 mm cmmmma =		MOIMMICGII	CIGCITITAG	180
	MIGILIANGG	ALTCITTTAT	ACAACTTTAC	CCTAGACCTG	AACTCAGACA	240
TCTCTCCAAG	GAGCGAACTC	GAG				•
						263

- (2) INFORMATION FOR SEQ ID NO:1438:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 467 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1438:

GAATTCGGCC AAAGAGGCCT AGCAGCCTCT GCCTCCCGGG TTCAAGTGAT TCTCCTGCCG

CAGCCTCCTG AGGATCTGGG ATTACAGAGG CTATTTGGAA GCTCCAGACT GTTTAGAAGA CCTGGACAGC CAGAAAGTCA TTAGTCCTAT CCAAAATGAA GCAATTTGTG CAGGAAAAAC AGATATTTTA TGGAAGAACT GTGAGTTTCT GGTAAATCGA ATGTGCCGTC TTGAAAGCCT CATGCAGTCC TTGAAGATGA ACATCTTTCG GCTGCAAACT GAAAAGGATT TGAATCCTCA GAAAACAGCT TTTCTGAAAG ATCGACTGAA TGCAATACAG GAAGAGCATT CTAAGGACCT GAAGCTGTTG CATCTCGAAG TTATGAATTT GCGCCAGCAA CTGAGAGCTG TAAAAGAGGA AGAAGACAAG GCACAAGATG AGGTGCAAAG GTTGACTGCC CCCTCGA	120 180 240 300 360 420 467
(2) INFORMATION FOR SEQ ID NO:1439:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 103 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1439:	•
GAATTCGGCC AAAGAGGCCT AGGCAGATCT GGCAACTTTC ATATCTGATA TTATGTTACT GAAACTAATT TTAGGTCGCT TTGCATCTCT CTGTGCCCTC GAG	60 103
(2) INFORMATION FOR SEQ ID NO:1440:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 465 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1440:	
GAATTCGGCC AAAGAGGCCT ACATNTTGA ATCTTAAACT GNNTTTTCT CTTAGTATTG CTAATGAGTA AAGAAAAGTC TCATAAGGTA GCCAAATGAA AAAGAATGAA AGGGAAAGTG AAAAATTAAG GGGACNAAAG ATGGGATGTG AAAAGAAGAA TTCTAGTTTG ATGGTGACTC ATATTCACGA TAGGATACAA AGTGTGATTT GTTGGAAACA TGTCCCAAAT TTCTAAAATT CTGCTTCTCT GCCAAAAGCA ATGTCTTTCT TGGTTGATAT TTGAGTTTTA AAAGGGTCAA ATCTTTCTAA TTTTTTGTAT CTNNAGAGGG CAGCACTAGA AGAAATCAGC AGGTCTAATC CCACCAGTAA GAAAACTACC ACTTCTTGAT TTTTACAGAT TTAAAAAAAAT CTTTTCAGTG ACCTTTCTTT TTAATGTAAA TACAAATTTA AACCTTAGGC TCGAG	60 120 180 240 300 360 420
(2) INFORMATION FOR SEQ ID NO:1441:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 336 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1441:	
GAATTCGGCC AANGAGGCCT AGAATTATAC AGGTAGAGAT GTATGCAGAT GTGTCCATAT ATGTCCATAT TTACATTTTG ATAGCCATTG ATGTATGCAT CTCTTGGCTG TACTATAAGA ACACATTAAT TCAATGGAAA TACACTTTGC TAATATTTTA ATGGTATAGA TCTGCTAATG	60 120 180

AATTCTCTTA AAAACATACT GTATTCTGTT GCTGTGTGTT TCATTTTAAA TTGAGCATTA AGGGAATGCA GCATTTAAAT CAGAACTCTG CCAATGCTTT TATCTAGAGG CGTGTTGCCA TTTTTGTCTT ATATGAAATT TCTAATCCCT CTCGAG	240 300 336
(2) INFORMATION FOR SEQ ID NO:1442:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 119 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1442:	
GAATTCGGCC AAAGAGGCCT ATGATTTTTA GACATCCAGA AAGCAAACTT TAACTGTCTG TGAGGTACAG AGACTGGATG ATGTTAAAGA AAACCATAGT TGGACACAAG ATACTCGAG	60 119
(2) INFORMATION FOR SEQ ID NO:1443:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 214 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEO ID NO:1443:	
GAATTCGGCC AAAGAGGCCT AGAGAAATTT TAAAAAGCAT AGTTGAGGCA TATTTTTCA TAATTATATA CTTATCTGTT TATTGCCCAT GGAAAATATA TGTGTAGAAG TATTTCTTCT GTTATTTGTT ACTATCTTCT TAATTTGTTC CAAAGAAAAT GCTGCCATAC TGCATTCCCT CTGGAAGGAA ACAAAACAAA ACAAAACTCT CGAG	60 120 180 214
(2) INFORMATION FOR SEQ ID NO:1444:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 499 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1444:	
GAATTCGGCC AAAGAGGCCT AGGAAAGGAA AAATTAAAAA CCCTAGATCT CTGGTACACA TAAGTCTGGG TTTGCGATTG CTATTTGTGC TGGGGCAGTG TGATTGAGAC TGACATTGAG GAAAGAAGCA GCTATGAAGA CCAGGGGGTT CAGCTTTCCA AGACAAAGGC AAGTCCTGTT TCTTTTTCTT TTCTGGGGAG TGTCCTTGGC AGGTTCTGGG TTTGGACGTT ATTCGGTGAC TGAGGAAACA GAGAAAGGAT CCTTTGTGGT CAATCTGGCA AAGGATCTGG GACTAGCAGA GGGGGAGCTG GCTGCAAGGG GAACCAGGGT GGTTTCCGAT GATAACAAAC AATACCTGCT CCTGGATTCA CATACCGGGA ATTTGCTCAC AAATGAGAAA CTGGACCGAG AGAAGCTGTG TGGCCCTAAA GAGCCCTGTA TGCTGTATTT CCAAATTTTA ATGGATGATC CCTTTCAGAT TTACAGGGCC GAGCTCGAG	60 120 180 240 300 360 420 480 499
(2) INFORMATION FOR SEC ID NO.1445.	

> (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 329 base pairs

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(B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1445:
GAATTCGGCC AAAGAGGCCT AAAATTTGAT TAGAAATGCA AGACTGGATG CCAAGATTGA
                                                                       50
TTCTAAATTA GGTCATGTGG TTATGGGTAA CAATGCAGTC TCACCCTATC AGCAAGTGAT
                                                                      120
TGAAAAGACC AAAAGCCTTT CCTTTAGAAG CCAGATGTTG GCCATGAATA TTGAGAAGAA
                                                                      180
ACTTAATCAG AATAGCAGGT CAGAGGCTCC TAACTGGGCA ACTCAAGATT CTGGCTTCTA
                                                                      240
CTGAAGAACC ATAAAGAAAA GATGAAAAAA AAAACTATCA AAGAAAGATG AAATAATAAA
                                                                      300
ACTATTATAT AAAGGGTGAC TTACTCGAG
                                                                      329
(2) INFORMATION FOR SEQ ID NO:1446:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 607 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1446:
GAATTCGGCC AAAGAGGCCT AACAGAGGAA ACCACCCTTC AACTGGAAGA TATCATTAAA
                                                                      60
CAGAGGATAA GAGATCAGGC TTGGGATGAT GTAGTACGTA AAGAAAAACC TAAAGAGGAT
                                                                      120
GCATATGAAT ATAAAAAGCG TTTAACCTTA GACCATGAGA AGAGTAAATT GAGCCTTGCT
                                                                      180
GAAATTTATG AACAGGAGTA CATCAAACTC AACCAGCAAA AAACAGCAGA AGAAGAAAAT
                                                                      240
CCAGAACATG TAGAAATTCA GAAGATGATG GATTCCCTCT TCTTAAAATT GGATGCCNTC
                                                                      300
TCAAACTTCC ACTTTATCCC TAAACCGCCT GTACCAGAGA TTAAAGTTGT GTCAAATCTG
                                                                      360
CCAGCCATAA CCATGGAGGA AGTAGCCCCA GTGAGTGTTA GTGATGCAGC TCTCCTGGCC
                                                                      420
CCAGAGGAGA TCAAGGAGAA AAATAAAGCT GGACATATAA AAACAGCTGC TGAAAAAACA
                                                                      480
GCTACAGAAC AACTCGAGGT GTGGGGAAAA GAAAGAGAGA TCAGATTGTT ACTGTGTCTG
                                                                      540
TATAGAAAGA AGTAGACATA GGAGACTCCA TTTTGTTCTG TACTAAGAAA AATTCTTCTG
                                                                      600
CCTCGAG
                                                                      607
(2) INFORMATION FOR SEQ ID NO:1447:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 467 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1447:
CTGCTGCAGC AATATTCAGA TTGAAAAAAA TAGGTTTGGG TTCACTGAGT TTAAAGGGAT
GATGATAAAA AGGAGGTTCT TCTTCCTCTT CATCCGAAAC ATGAGGTTTA TTCACTATTA
CATCATCATC TTCTTTACTC TGTGCGATCT GTTTACATTT CTCAGTTAGT TCTTCTATAG
                                                                      180
TAGCTCCTCC TGACTTTTTA GCAACTTTCT CTTCTATAGT AGGTGGAGGT GCAGGCTTTA
                                                                      240
GGTTTGGTGG TAAAGGGACA CCAGCCTTAG CACACATGGC AGCTGCATTA GCTTTGGCTA
                                                                      300
TTTCAAGTAA TTGAGCCTTA TCCAAATCTG TCAGACGTTT GGGTGATCTG CCTCGTTCAG
                                                                      360
                                   572
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TTGATCGCCT TAATCTGACT GGTGAGTAGG CCTCTTTAGC CGAATTC	420 467
(2) INFORMATION FOR SEQ ID NO:1448:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 128 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1448:	
GAATTCGGCC AAAGAGGCCT AGACACTTAT AGGCTTTTTA AGAAGCATTG ATCAATTTGC AAACTTAGTG CTACATCAGA CTGTGGAGCG TATTCATGTG GGCAAAAAAT ACGGTGATAT TCCTCGAG	60 120 128
(2) INFORMATION FOR SEQ ID NO:1449:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 314 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1449:	
GAATTCGGCC ACNGAGGCCT ATTTAAATGA AAATNATTTG AATGTTTAAT ACTCTTCCCT TCTTCAATTG TAGAAACATT ACCCTTTTGC ACTATCTCAT CACTATTGTG GAAAATAAGT ACCCCAGTGT TCTCAATCTA AATGAAGAAT TGCGAGATAT TCCTCAAGCT GCGAAAGTAA ACATGACTGA GCTGGACAAA GAAATAAGTA CCTTGAGAAG TGGCTTGAAA GCAGTAGAGA CAGAGCTGGA ATATCAGAAG TCTCAGCCCC CACAGCCCGG AGATAAGTTT GTGTCTGTTG TCAGCCATCT CGAG	60 120 180 240 300 314
(2) INFORMATION FOR SEQ ID NO:1450:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 432 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1450:	
GGAATTCGGC CAAAGAGGCC TAGTGGTTTT CCCAGGAGGA AAGAGAGCTG CAGGGATACA GATGCCTTCC TGAGCAGAA AAATAGAATA CTTGAGCCAA TTTTCATGTA AAATGGATTA TTTTCCTGGC GTTTCCTGTC CTTCAAGTAA AAGGTTCTGG AATGAGTACT TCACTGCTGT AATGGAGACA CTAATATTTT ATGAATGCAG TTTTACAGTT TGCAGTAATG CCAGGCCTTT GGCTGTTTTC CATTAGATGG TGCACTTGGC TGGAAGCATA TACTCTTGTA GCTTTGATTT	60 120 180 240
TAAATTTAAC TTTCAAGTTG AAAGAGCAGT GACTCATCCA AAGGACAGGT GATATTTATT	300 360
TATTTTTTCT TGAAAATGCA GCACGGGTAT GTTGTTATCA CACGTTTAGG GGAATTGCCA	420

- (2) INFORMATION FOR SEQ ID NO:1451:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 463 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1451:

GAATTCGGCC	AAAGAGGCCT	AGGATTGAAC	GCTTTCACCC	TGTGCCCCGC	GCCTGGCGTA	60
ACGCGTGGCC	CCAGACCACA	CGCTGTAACC	CGGGGTGAGA	GGGAGTGAGG	TGGGACTTCG	120
TACCGGACCC	GGAGCGCCGG	CCTCGCCCGC	GCGGGCAGCG	TTCACTGTGG	GGAGTGCTCA	180
CTCAGCCTAG	GGCGGCCCGG	GAGGACTGCC	GGGAGGAGGG	AGTCGGCCTT	GAATTGAGGC	240
CTCAGCCTTG	AATAGGGTAG	GGAGGCAAGC	CTAGCCGAGA	GTTTAGCACT	AGCAAAAGCC	300
TGGAGGCACC	AGGGTCTGCC	CTAAGAACTG	CAGCGCCTCT	GCTCTGGCTG	GGATTTAACG	360
CATTACGTCT	CTGCTGTTTA	TAGGTGTTGT	GTTTGGTCTT	ACGACTTCGT	ATTCTATAGT	420
TTTTATTTAT	TCCTGTTTTC	TGAATTTTCC	CACTTTGCTC	GAG		463

- (2) INFORMATION FOR SEQ ID NO:1452:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 407 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1452:

GAATTCGGCC	AAAGAGGCCT	AATGCAAGTC	TGGACCGTTT	AAAAGCTGGT	AATTAAACAC	60
TTTATTCCAT	ATCAGAATAA	AAGTCAACTA	GTTGAATATT	TCTAGGTGAG	ATGTGGTACT	120
ACTTTTTTT	TNGCTGTTAT	TTTATGTCTG	TATCTAAAAT	ATCTTACTGC	ACTCTTTTTT	180
CAGGTTGCAG	CAGATCCTTG	AGTTTTGAAC	CTGACGGGCA	AATCAGAGCT	TCTTCCTCAT	240
GGCAGTCGGT	CAATGAGAGT	GGAGACCAAG	TTCACTGGTC	TCCTGGCCAA	GCCCGACTTC	300
AGGACCAAGG	CCCATCATGG	GCTTCGGGCG	ACAGTAGCAA	CAACCACAAA	CCACGAGAGT	360
GGCTGGAGAT	CGATTTGGGG	GAGAAAAAGA	AAATAACAGG	ACTCGAG		407

- (2) INFORMATION FOR SEQ ID NO:1453:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 368 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1453:

GAATTCGGCC	AAAGAGGCCT	ACGGCCAAAG	AGGCCTATAG	GCCTCTTTGG	CCGGAAATCA	60
TGGTGTTATA	GATCAAAAGA	TAAAAGTTTC	ACAGAAGAGG	TGGGATTTGA	ACTAAGCTGT	120
TCATGCTCAG	TAAGATTAGA	GGAGGTGAAG	CAAATGGGGG	AATGTGTGCC	AGAAGAGGAC	180
AGGTGCAAAG	ATAAGCACTG	GTGCTTGATC	TTGACTGAAT	TTTCAACCAA	ACCAGCTGAC	240
TCTCAGGATA	GTTGAAGGTC	ACTTTCTGCT	GTTTAAAGAA	AGATTCTAAA	GTTACTTAAG	300
AAATATTTGG	CAAAAGACTC	AAAAGGAAGG	ATTCCAATTA	CAATATAAAT	AAAGTAAGAA	360

А	ACCTCGAG	368
(	(2) INFORMATION FOR SEQ ID NO:1454:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 618 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1454:	
T G G C C T A G G	CAAATCCGCC TTCATGGCCT ACCGTGCTCT ATGCTGATCC TTTTTCTCGT GAGAAAACGC GCCCTGTTA TTATTAGCTA AGGTCACACC CGCTGGGCAG CTCCTGGGAT TTTTGGATTC TCCCCCACTC CAGAGGGAAG GCTATTTCTA GTGGCTTCT TTCTTTGAGT CCTCCCTTCT CTCTGTGTCT CTCCTGTTCC TCCTCTTTAC CAGTAGGGCT TCCTCAATGC TGACAGCCCT GTGAAAAAAAG GGAGACATG CCGAGCTCCG GCAGGAAACT GCTGGCCCAG GACCTGGCTT GTGAGAACACA AAGGAGAAT TCTGTGTTTG GAAAAGTACA GACTGAGCAG GTGACCCCCG CACAGCCCCT TGGGGGAAAC ACTTGTGCCC TTTGAGTCTG ACTGATATAA ACACAGACTC CCTTGACTGT CCCATAAAAGG CCAAAAGCCAG AGAACCTCAG AAAGGGACTT GCAAATTGTG GTGAGGCAT ATCAGCTGGT GCTTTCTTTT CTCTGTGGGC TGCCATTTAT GAATCCTTG CTTCTCTCT GTCTCTCTCT CTCCCTTTT CTCTCTTTG CTGGTGTGT CATTCCCTCT CACGCGCTGG CTCTCCAGT	60 120 180 240 300 360 420 480 540 600 618
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 312 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1455:	
C A T	AATTCGGCC TTCATGGCCT AGCCTTTTTG AAACTCAGGA AAGACAAAGG TTCAATTACA CACTTTTGT CAATAAGCAA ACCAGGTATT TTTTTTTTCT CCTGTTGTCT GGATATGGCA TAAATTTTT TAAATTGCTG TGAGAACCCA TATATGAAAA GAGAGGAGTT GAATTGTGTG GCCTTTTAT GTCTTGAGAT TTATATGTGG AAAAGACGAC ATCTACTTCA AACTGTATTT TTTCGTTTT TTTTTTTTTT TGGGGAAGGG GGGAGAACGG GGTCTTGCTC TGTCGCCCAG	60 120 180 240 300
	CTGAACTCG AG	312
(	2) INFORMATION FOR SEQ ID NO:1456:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 415 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: CDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1456:	
	AATTCGCCT TCATGGCCTA GCTTAATCTT ACAGTCATTT AAAATAATTT CAGAAATGTT	60

TTCAGTCCTT CCTCTTCCTC TCCCCTGCTC CCAGACAAGG GTGTGTACTC AATACTGTAT TCAGAAGTTA CTTGGGTTAG TTCTTTTTTT CCGATCTTC AGTGTGATTA TTTTATTCAT TTGAAATACA ATTGGATTCA TTCGTTTCCG TATGCTTTCA GTTTTAGCTT TTTTCCACTA TCTTTGTTGA TATAATTGCA TTTTTTGATA GGGGGATATT AATATACTTC ACAAAGTCAG AATAACATAA GGGTTTACTC AGATGTAACC TGTTATCTTA GCCCGTGATC TCGAG	180 240 300 360 415
(2) INFORMATION FOR SEQ ID NO:1457:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 231 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1457:	
GAATTCGGCC TTCATGGCCT ACATTTTCT ATTGATATAA AAATTGTTAG AGAAATATAC AGTTGTATAT TTCCCCCCTT TATACAGAAA TTTTACAATA ATTTCAGATT TTTCTGAGTT TTTTCAGATT TTTGATTCTA TAATATGAGA TTATTCTTTC TTCCTCTTAT TTTTTTAGGT TATTTATTTT TTCTTTTCTT TTTAATTTGC TCATACAGGT TTACTCTCGA G	60 120 180 231
(2) INFORMATION FOR SEQ ID NO:1458:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 155 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1458:	
GAATTCTGTT CATATTTTA AATGTTCCTT TTTTTCAACA TTCAGCAAAA TATTATGTGC TAGGAACTCT CCCAGACGCT TGTTAACATC TATGAATACA ACAAAGATTC TGCCCTCCTG GGCCTCTTTT CTGATGGGGA AGCAAAAATC TCGAG	60 120 155
	133
(2) INFORMATION FOR SEQ ID NO:1459:	133
(2) INFORMATION FOR SEQ ID NO:1459:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 312 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	133
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 312 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double	133
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 312 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 312 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA	60

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 459 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     1xi) SEQUENCE DESCRIPTION: SEQ ID NO:1460:
GAATTCGGCC TTCATGGCCT AGTCTCCCTC GGCCTGTGCC GCCGCCGACG CCGCTTGTGG
GCCCGACTCC GCTCTGTCTG CTTCGCCACC TTCTCCCCGA GCACTGCCCG GCCGGCCGCC
                                                                     120
ATGGCTAACG TGGCTGACAC GAAGCTGTAC GACATCCTGG CGTCCCGCCC GGCGCCAGCG
AGAACGAGCT GAAGAAGGCA TACAGAAAGT TAGCCAAGGA ATATCATCCT GATAAGAATC
CAAATGCAGG AGACAAATTT AAAGAAATAA GTTTTGCATA TGAAGTACTA TCAAATCCTG
                                                                     300
AGAAGCGTGA GTTATATGAC AGATACGGAG AGCAAGGTCT TCGGGAAGGC AGCGGCGGAG
GTGGTGGCAT GGATGATATT TTCTCTCACA TTTTTGGTGG GGGATTGTTC GGCTTCATGG
                                                                      420
GCAATCAGAG TAGAAGTCGA AATGGCAGAA GAACTCGAG
                                                                     459
(2) INFORMATION FOR SEQ ID NO:1461:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 511 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (11) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO.1461:
GAATTCGGCC TTCATGGCCT ACGAGATCAA GGACAAGAGG CAGCTTATAG ACAACCGCAA
GCTCATTGAG ACGCAAATGG AACGGTTCAA AGTTGTGGAA CGAGAGACCA AAACCAAAGC
                                                                      120
TTACAGCAAA GAGGGCCTGG GCCTGGCCCA GAAGGTAGAT CCTGCCCAGA AGGAGAAGGA
AGAGGTTGGC CAGTGGCTCA CGAATACCAT CGACACGCTC AACATGCAGG TGGACCAGTT
TGAGAGTGAA GTGGAGTCAC TGTCAGTGCA GACACGCAAG AAGAAGGGCG ACAAGGATAA
                                                                      300
GCAGGACCGG ATTGAGGGCT TGAAGCGGCA CATCGAGAAG CACCGCTACC ACGTGCGCAT
                                                                      360
GCTAGAGACC ATCCTGCGCA TGCTGGACAA TGACTCCATC CTCGTTGACG CCATCCGCAA
                                                                      420
GATCAAGGAC GACGTTGAGT ACTATGTTGA CTCATCCCAG GACCCCGACT TCGAGGAGAA
                                                                      480
CGAGTTTCTC TACGATGACC TGGACCTCGA G
                                                                      511
(2) INFORMATION FOR SEQ ID NO:1462:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 130 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1462:
GAATTCGGCC AAAGAGGCCT ATTTGTTTTG TGGTTTTAAA ATTTTTCTT CGCATAAAGG
                                                                      60
GTAACATCTT GCAACTTGAT TCTTTCACTT CATGATATGC CTTAGATTTC TTTCCTTCCC
                                                                     120
                                                                      130
(2) INFORMATION FOR SEQ ID NO:1463:
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(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 379 base pairs

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(B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1463:
GAATTCGGCC AAAGAGGCCT ACTTGTNAAG TGCTTTTGAA TTAATAAAAT ATTAGCATAA
TTGTGTNTAG TCAGTTGAAC CCACTGTTAC CATTGTTCTT ATCCCATGGG AAGCAGTTGG
                                                                    120
TTACACGATT CTTATTTTAT AAGAAACAGC TGAGAGGCAC TATGGATTAG TCTTCTGAAG
                                                                    180
240
AGAAGCCAGT TCAGGGTCCA TAATATTTAG TGACCAACAT TTTAAAGTAT AGCAGCAACC
                                                                    300
TGGTTCTTAA ACACAAAGTA AGTTGCCCAT TAACAAATGG CTTTTATCTT TAGCATGAAA
                                                                    360
ACTTTCCACA CGTCTCGAG
                                                                    379
(2) INFORMATION FOR SEQ ID NO: 1464:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 354 base pairs
         (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: cDNA
    (xi) SEQUENCE DESCRIPTION: SEO ID NO:1464:
GAATTCGGCC AAAGAGGCCT ANAANAAACT TTTTCTTGGG AGCAAGGTAG TTATTTCAAA
                                                                     60
GCACAGAAAA AGGCGGCGG GGGCACAGAG AAGCACAGAG AAGCGGGGGC AGTTGCACAG
                                                                    120
GTAAAACATT CATCTTGGCT TTTCTTTTTA AAAGATAAAC TTTGTCCCAC GTAAAGAGGA
                                                                    180
ANACTGCATA GATATTCATT GAGATTATCT GATTTGTCAC TGTTGCCAAA GAAAAACAA
                                                                    240
AGGTAAAATA CACGAGTTTC NNCATTCAGA AGAAAGTATT TCAGGTAAAA ATTAACTATT
                                                                    300
AAGCAACTTT TCTCAGCAGA AGAAATGCCC AAATTCTTAA GGACAGTACT CGAG
(2) INFORMATION FOR SEQ ID NO:1465:
    (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 229 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: cDNA
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1465:
GAATTCGGCC AAAGAGGCCT ACACTGCTCC AGCTCTGACT CCCTCATCCC TTGCCTGGAC
                                                                    60
CATGGTAATT GACCCTAGCT GGTCTCCTTT TCTCCTCTCA TCAGTCCTCC ACATTGCTGC
                                                                    120
TGTTTTCATC TTTGTGACAT ACAAATGTGT TGCTTTCCCG TCTAAAACCC TGCTTGTCCC
                                                                    180
TCCCCATTTT GACTGCCTGC CCCCAGCACG CACACACACA ACACTCGAG
(2) INFORMATION FOR SEQ ID NO:1466:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 327 base pairs
          (B) TYPE: nucleic acid
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- (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1466: GAATTCGGCC AAAGAGGCCT ATTTTTTTT TTTTTTTTT TTTTTTTTT TTTAATTTAT AAGGAATAGA AATTTATTGG CTCACAGTTC TGGGGGCTGG GAAGTCCCAG AGTAAGGTGC CAGCGTCTGG TGCAATCCTT CTTGTTGTGT CACTGTGGAA GGTGGAAGGG CAAGAGAGGG 180 CCAAGCTCAT CTTATTATAC CAGCACCCAT TCCAACATCA TCCTCGAAGG ATCCCAATTT 240 TGAAAGAAAA AGCATGTGAG ACACAGAACA GGCGAGAGAG TGAGGGCCCG GCATGCCCCC 300 AAGTCCCCAC CACCGCACCT GCTCGAG 327 (2) INFORMATION FOR SEO ID NO:1467: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 403 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1467: GAATTCGGCC TTCATGGCCT AGAGAGAGAG AGAGAAAAGG AGGGGGTGGT GGAGAAGCGG 60 GAGCGAAGGA AAGGAGGCAA AAGGCAAAGT GAAGGAAAGC TGGATAGCTC GGCCTCTCCA 120 AACTGATTGA TTAGTCATGA TCCCCGCAGT TTTAACAGGG ACTCATTCAA TTGGGAAGGT 180 GGAGCGCTGG GGAGCAGATT AGCATACGCT TGTTTACTCA TCTTCTGAGG GATTTTTTCC 240 300 AGGGGGCTGT GGCTTGTGTT ATAAAGGACG CAAAAAATAA ATAAATTAGA GCATCTTTTG 360 GGGGGAGGGA ATTCAGCGGA TCAGTCTTAA GATGGAGCTC GAG 403 (2) INFORMATION FOR SEQ ID NO:1468: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 329 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468: GAATTCGGCC TTCATGGCCT ACACGAGGTC AGACGTCACA CATTGTTTTT TGGCTTGTTC TTTTGAAGTT TTTACGACTT GTCATGAGTC TCGGCCTGGC TTCTGTTTTT CACTGTCCGG 120 AAGAGTGTGG TCCTTCTGCA TTTGACCTTC CTTCACCCTC ATCCAGTCCT CCCAGTGTGG 180 CCGGTCTCAT TTCGTGTCGT CAGCTGGGTC AGCTGGCTCG GTGTGGAGTT TGGATTTTCC 240
  - GTGATCCATC CCATGCTTTT TTTTTCTTTC TTTCTTTTTT CCTTTTCTTT TCTTTTTCTT
    TTTTTTCAGT TTTCTCCCCA ACTCTCGAG
  - (2) INFORMATION FOR SEQ ID NO:1469:
    - (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 352 base pairs
      - (B) TYPE: nucleic acid
      - (C) STRANDEDNESS: double

300

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1469:

GAATTCGGCC	TTCATGGCCT	ACAGGAAAAT	TCTTCTCCCC	TATTTCATTC	TGATGTTTAT	60
						60
AGTATATGCC	TTTGAAGTGG	CATCTTGTAT	CACAGCAGCA	ACACAACGAG	ACTTTATGCT	120
AGAGAGGTAC	CAAAACAACA	GCCCTCCAAA	CGATGATGAC	CACTCCAAAA	ACAATGGAGT	180
						190
					ATGGTCCATC	240
AGACTGGCAA	AAATACACAT	CTGCCTTCCG	GACTGAGAAT	AATGATGCTG	ACTATCCCTG	300
						300
GCCTCGTCAA	TGCTGTGTTA	TGAACAATCT	TAAAGAATCT	CTCACCCTCG	AG	352

- (2) INFORMATION FOR SEQ ID NO:1470:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 609 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1470:

GAATTCGGCC	TTCATGGCCT	AGAGCCGTCC	TATCAGATTA	TCTTAACAAG	AAAACCAACT	60
GGAAAAAAA	ATGAAATTCC	TTATCTTCGC	ATTTTTCGGT	GGTGTTCACC	TTTTATCCCT	120
GTGCTCTGGG	AAAGCTATAT	GCAAGAATGG	CATCTCTAAG	AGGACTTTTG	AAGAAATAAA	180
AGAAGAAATA	GCCAGCTGTG	GAGATGTTGC	TAAAGCAATC	ATCAACCTAG	CTGTTTATGG	240
TAAAGCCCAG	AACAGATCCT	ATGAGCGATT	GGCACTTCTG	GTTGATACTG	TTGGACCCAG	300
ACTGAGTGGC	TCCAAGAACT	AGAAAAAGCC	ATCCAAATTA	TGTACCAAAA	CCTGCAGCAA	360
GATGGGCTGG	AGAAAGTTCA	CCTGGAGCCA	GTGAGAATAC	CCCACTGGGA	GAGGGGAGAA	420
GAATCAGCTG	TGATGCTGGA	GCCAAGAATT	CATAAGATAG	CCATCCTGGG	TCTTGGCAGC	480
AGCATTGGGA	CTCCTCCAGA	AGGCATTACA	GCAGAAGTTC	TGGTGGTGAC	CTCTTTCGAT	540
GAACTGCAGA	GAAGGGCCTC	AGAAGCAAGA	GGGAAGATTG	TTGTTTATAA	CCAACCTTAC	600
AACCTCGAG						609

- (2) INFORMATION FOR SEQ ID NO:1471:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 399 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1471:

GAATTCGGCC	TTCATGGCCT	AATTGAATTC	TAGACCTGCC	TCGAGCCTGG	GCAATAGAAT	60
GAGGCTCCAT	CTCATAATAA	TAATAAGCAG	CAGCGGCAGC	TCTGGTAGAT	TTTTTTGTGT	120
GCTTGTCCTC	ATGAAGACTT	AAGCCTGCTC	TTTCAATTTG	AAACCTAGGC	ACTTGGACTA	180
ACTTAAAAGA	TCATGTAAAA	AATTTAATTT	TTGTTTGGTA	TAGATTTAAT	TGTGGTTTTT	240
TTTTTCTCTT	TTAGATATAA	TTGATCCTGT	TGCTTTAGAA	ATTCCATTAT	CCAAAAACCT	300
TCTGGCACAG	ATTAGTGCTC	TTGCTCTTCA	GCTGGATTCA	GAAGATCTTC	ATAATTATTC	360
AGGAAGCCAA	CTATTTGAAA	TGCACGAGAA	AACCTCGAG			399

(2) INFORMATION FOR SEQ ID NO:1472:

- (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 306 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1472:

GAATTCGGCC	TTCATGGCCT	ACAGGTTTTA	AACTGGTTTT	TTGCATACTG	CTATATAATT	60
CTCTGTCTCT	CTCTGTTTAT	CTCTCCCCTC	CCTCCCCTCC	CCTTCTTCTC	CATCTCCATT	120
CTTTTGAATT	TCCTCATCCC	TCCATCTCAA	TCCCGTATCT	ACGCACCCC	CCCCCAGGC	180
AAAGCAGTGC	TCTGAGTATC	ACATCACACA	AAAGGAACAA	AAGCGAAACA	CACAAACCAG	240
CCTCAACTTA	CACTTGGTTA	CTCAAAAGAA	CAAGAGTCAA	TGGTACTTGT	CCTAGCGTTT	300
CTCGAG		•				306

- (2) INFORMATION FOR SEQ ID NO:1473:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 385 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1473:

GAATTCGGCC	TCATGGCCTA	CAACTCCGCA	GCAAACAACT	CCGCAAACGG	AAAAAGAACG	60
ACATGATGCA	ATCTTCAGGA	AAGTAAGAGG	CATACTAAAT	AAGCTTACTC	CTGAAAAGTT	120
TGACAAGCTA	TGCCTTGAGC	TCCTCAATGT	GGGTGTAGAG	TCTAAACTCA	TCCTTAAAGG	180
GGTCATACTG	CTGATTGTGG	ACAAAGCCCT	AGAAGAGCCA	AAGTATAGCT	CACTGTATGC	240
TCAGCTATGT	CTGCGATTGG	CAGAAGATGC	ACCAAACTTT	GATGGCCCAG	CAGCAGAGGG	300
TCAACCAGGA	CAGAAGCAAA	GCACCACATT	CAGACGCCTC	CTAATTTCCA	AATTACAAGA	360
TGAATTTGAA	AACCGAACGC	TCGAG				385

- (2) INFORMATION FOR SEQ ID NO:1474:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 428 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1474:

GAATTCGGCC	TTCATGGCCT	AGATCCCCTT	ATTTTGCCAA	AAAGTGTCAT	CAATTCATTT	60
GGATAACTTT	TATGTTTTAG	GAACGTGGCC	TCTCTTTTAA	TTACTGAGAA	CTTACAAAAT	120
GGTTCAGAAA	GTTTATATTT	TTAAAGCTTT	CATTCATTGA	TATATTGAAC	ATCTAAGGCT	180
TAACTATCTT	TCCACTGGGA	CAAAAACAGA	ATTCTTAAAA	ATGAGGAGGA	GGGCCCAGTG	240
TGGTGGCTTA	CACCTGGAAT	TCCAGTGCTT	TGGGAGTCCA	AGGTAGGAGA	ACTGCTTGAG	300
GCCAGGGGTT	TGAGACCAGC	CTGGGCAACA	CAGCAAGACA	ACTCTACAAA	AAATTAAAA	360
AACAATCCAG	GGCCGAGCAT	AGTGGTTCAC	ACCTGTAATC	CCAGCACTTT	AGGAGGCCAA	420
GCCTCGAG						428

(2) INFORMATION FOR SEQ ID NO:1475:

(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 338 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1475:	
GAATTCGGCC TTCATGGCCT ACTGGGATGT ATATGAGAGA CAGTGCTTTC AATTAAATCC TTGGGTATAT TTTTATTAAT TTCCTCCAGA TTTTTCTTTT AAGGCCTTTT CTAAGTTATA CTGCATATCA AACTTCCCTG TTATTGAAGG ATATAAGGTA GAAGGTAAAA GCCATTTTCC TATAAGTAAC TTGGGCATTT GCAAAGATTT TTCTCAAGTG CAGTTGTAAC TATACTAAAA TATACTAATA TTGTGTTATG ATATACCTTG CTTTTTTTCT TTTATTTTTT CTTTTGAGAC AGAGTTTTGC TCTTGTTTCC CAGGCTGAAG CGCTCGAG	60 120 180 240 300 338
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 346 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1476:	
GAATTCGGCC TTCATGGCCT ACAAAGAGCT AGAAGCCATT GAAAGTCGGC TAGAAAAGAC AGAATTCACT CTAAAAGAGG ATTTAACTAA ACTGAAAACA TTAACTGTGA TGTTTGTAGA TGAACGGAAA ACAATGAGTG AAAAATTAAA GAAAACTGAA GATAAATTAC AAGCTGCTTC TTCTCAGCTT CAAGTGGAGC AAAATAAAGT AACAACAGTT ACTGAGAAGT TAATTGAGGA AACTAAAAGG GCGCTCAAGT CCAAAACCGA TGTAGAAGAA AAGATGTACA GCGTAACCAA GGAGAGAGAT GATTTAAAAA ACAAATTGAA AGCGGCAGAA CTCGAG	60 120 180 240 300 346
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 298 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1477:	
GAATTCGGCC TTCATGGCCT ACAGGTTTC ATTTTATATT ATTTTCCTTT AGCCTGAAAA ATTTATTTAT TTTTTCTCTT AGTACAAGTC TGCTGGTGGT AAATTCTCTT AGTTTTTGTT TATTGAAAGA TATTTTTATT TTGCCTTCAT TCCAGAAGGT TGCTTTTGCT GGATATAGGA TTCTACAACT TTTGCCTTTA ACATGTTATG GATGCCATTC CTCTGTCTTT TAGCTTCCAT TGTTTCTGAT GCTAAATCTT CAGTCATTT ATCATTGATC CTCTGTAATG TACTCGAG	60 120 180 240 298
(2) INFORMATION FOR SEQ ID NO:1478:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 107 base pairs  (B) TYPE: nucleic acid	

(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1478:	
MCG1 COMCOMM - COMC1 COMCC - 1 - 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2	60 07
(2) INFORMATION FOR SEQ ID NO:1479:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 340 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1479:	
CCAGTAGATA TCCACAAGCA ATATTAGCAG GGCTTCTGTT TCTAAGTGAC CACAGACTAA 1 CCCTTTCTAG GCTTTAACAT TGTAAATAAT CCTATAAACA GTTTGATTTT TTAAGATGAT 1 TTTTGATTTG AAGAGACAGG CTTTACATAA GCCTTCATTC CTTCAAAAGG TCCTGACAAA 2 ATACTTGGGT TTTTTTCTCT TTTTTTCATT CTGGTATGCT TTGCAGCATT TCAGCTGCTT 3	60 20 80 40 00
(2) INFORMATION FOR SEQ ID NO:1480:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 233 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1480:	
ATAGCTTAAG AATACAGTAT GGTATGATTA AATCAAGTTA TTAACCTATC CTTCACGTTA AATGCTTAAA TTTTTTGATG AGAACATTTG AAATTTACTC TTGGAAGGTA AAAAAAAATC  1	60 20 80 33
(2) INFORMATION FOR SEQ ID NO:1481:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 266 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1481:	

GAATTCGGCC TTCATGGCCT AGATAACTAT TGCTCCCAGT ACCCTTTCAG CTATCTCACA

60

120

TAACTTTGAT ATATATTATT TITATTATCG TITATTAAGT GCCTAATTTC CATTGTGAAG TCTCCTTGGA CCTATAAGGC TGAAATAAAA TAATTTAAAA TITATTTTCT TATTGTTTCT AATTCAATTT CATTATAGTT AATGCAAGTG GTCATTGTGC TATTGAGTTT GGTACTTTGG AGGTTTCTTT TTCTGGCTAT CTCGAG	120 180 240 266
(2) INFORMATION FOR SEQ ID NO:1482:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 267 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1482:	
GAATTCGGCC TTCATGGCCT AAGAAATGTT CACTTTTCCA ACTTAAAAGG ATTTTTAAAA ATACAAACAT AATTGACCTA CCTGGTTCAA AGAACAGAAG TGAGGAGAAC TTGCTTAAAG GTATTGATGT TATATTTTCT CTTGACTGAG TGCTTGAAAA AAAATTTTAT TGAACATATG TTCTCCTTCC GTGGCTTTTT TGTCTTTGCT TTTTTGTTTT GTTTTTGTTTT GAGGATGGAGT CTCACTCTCT GCTCGAG	60 120 180 240 267
(2) INFORMATION FOR SEQ ID NO:1483:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 242 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1483:	
GAATTCGGCC TTCATGGCCT AAATTAGCAT CTAGTGTCAC AGGTAAAAGA ATTTCAGGAC CAGGTTTAAA CTTTATTTTA AATATTTTTA TACTTAGGTC TCTTTTTCCT GCCTCTCCCC AAAGAAGAAGAC CACTGGCCTT AGTTGTTTGA GCTTACTGCT TATATTATAG AGTGTAAATA GGTAAACTAGA GACTAAAAATT TTATTAACCA GCATGTTTGG TATATTTAAA GCAGTTCTCG AG	60 120 180 240 242
(2) INFORMATION FOR SEQ ID NO:1484:	
(1) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 291 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1484:	
GAATTCGGCC TTCATGGCCT ACAGAGTGTG GTTTCTGTAG CAACACTTCT CATGACCATC TGTTTTGTGT TTATGATGAT TTTTTCAGGT CTGTTGGTCA ATCTCACAAC CATTGCATCT TGGCTGTCAT GGCTTCAGTA CTTCAGCATT CCACGATATG GATTTACGGC TTTGCAGCAT AATGAATTTT TGGGACAAAA CTTCTGCCCA GGACTCAATG CAACAGGAAA CAATCCTTGT AACTATGCAA CATGTACTGG CGAAGAATAT TTGGTAAAGC AAGGGCTCGA G	60 120 180 240 291

(2) INFORMATION FOR SEQ ID NO:1485:	
(i) CECHENCE CUADACTERICA	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 264 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
157 15152551. 141622	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1485:	
GAATTCGGCC TTCATGGCCT AGTAATTTTT GATAGTAAGG GCTTTTTATT GTCATTTTTT	60
GTTAATCGTT TCCTGTCTGT TTTGTATTTC TTTTGTTCCT CTCTTCCTCG CTTGGTATCA	120
TCTTTGCAAT TTGATAATTT TTGTTGTGAT ATACTTTGAT TCTTTCTATT TATCTCTTCT	180
GAATCTAATA TTAGTTTTTT TTATCTTTTC TGTATCTATT ATTAGTTTTT TTTCTTTGTG	240
GTTATCATGA GGCTTCCACT CGAG	264
(2) INFORMATION FOR SEQ ID NO:1486:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 292 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1486:	
GAATTCGGCC TTCATGGCCT ACCAGTGCCT TCCTCTTCCC TATATTCTGT GTGTCTTAAC	
GGAATTATTT TTCCAAATCA TTGTGTGCAA AGAAACTAAT GACATCATAA GTATGATTTC	60
TGTACACATT TTAGTTGTAA TTGCTAGGTT TTCCAAGATT TCACAGTCAT CAAGTCATCT	120 180
GTTCCCAGAC ATCCCAACAA GTACTTATCA AGTGTCTCCA TCTGCTGCCT TCATCTCTCT	240
CAGGTGCCAT TCCAGTGACA TTGCTATAGC CTCTTGCTGT ACCCCCCTCG AG	292
(2) INFORMATION FOR SEQ ID NO:1487:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 261 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1487:	
GAATTCGGCC TTCATGGCCT AATGGATATA GAATTCCAGG TTGATAAACA TTTTCTGTCA	60
CAACTTTACA ACTGAAGGCA TTGCCCTTTT GTCTTTTACC GTTCATTTGA TAAAAAGTCT	120
GGTGGTAATC TAATTCTTAC ACCTTTGTAG GTGAGCATTT TTTCCTTTCC	180
TTGTGATTAT CTGATCCTTA GAGATCTGAA GTTTTATCAT TTGTATCTAT GAGATCTTTT	240
CCCATCCTCC TGGTGCTCGA G	261

- (2) INFORMATION FOR SEQ ID NO:1488:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 488 base pairs
      (B) TYPE: nucleic acid

	1 01/05/0/00/54
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1488:	
GAATTCGGCC TTCATGGCCT AATTTTCTGT ATATTTTTAC ATGAATTTCA	GTACTATATT 60
GAACAGCTAT GTTTAAGGAT AATCAAAAGA TGACTGTGAC AGGGAGAATT	TGGAAATATT 120
AGCCCAAGTC TAGTCAATTG TGATTGTTGT TGCGTTGGTA CTAGTTTAAA	TTGGGGCTAA 180
ATTTAGAGCC ACTGGGACTG AGTACCTCGG TTGATCTCCA ATGATTCCAA	TTGCTAAAAA 240
GTAAAGGGCA ACCACACATA CGTACCAATT CTGAAGTCCT AGGAAATTTT	TAAAAGAATG 300
TAAGAGAATA AGAAAATGTA AAAGGGAGAA GAGTTTATAT GTCATGACGT	AAGTTTTAGA 360
GTTATTTACT TTGTAACTGG ACCTTCTCTG CTTCTTCCAA TGTGTTCATT	AAGACCCTGC 420
TGAAAAATGA CCTTCCAACT CCCCTGAGTA ATTATTTAAG ACCCTTTCAT	CTTACCAACC 480
CTCTCGAG	488
(2) INFORMATION FOR SEQ ID NO:1489:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 238 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(b) Toronogi: Timear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1489:	
GAATTCGGCC TTCATGGCCT AGTCTCAAAA AAAAAATCAA AATAAAAGTA	AAAGTAAGAA 60
GATGGAAATT TGCTTAGCTG TGAAAGGAAA GGCGATCTGT CTGATGTCCT (	
CCTAGGTGGG CTTGGTGCTT GCATTTCCTG CGTTGCAGTG TCAGGATTTT	
GCCTTGGCAC TGGAGACCTT CACATTTTCC ATCTGGTTAC TATGGCACAC	
(2) INFORMATION FOR SEQ ID NO:1490:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 263 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1490:	
GAATTACTCT GGAAGATATG CTCTATGCTG CTTCATCCAT AAAGAGTAAT	TATTTGGTGT 60
TCATGGCGGA ACTGTTCTGG TGGTTTGAAG TGGTGAAGCC GTCTTTTGTA	
TTGTTCGTCC ACAAGGAGCT GAACCTGTAA AAGATATGCC TTCAATTCCT (	
CTGCCAAAAG AAATGTCTTA GATAGTAGTT CTGACTTCCC TTCAAGTGGG (	
CATTTACACA GTCTCATCTC GAG	263
(2) INFORMATION FOR SEQ ID NO:1491:	
(1) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 257 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1491:

					GTTTCCCAAC	60
TGGTTTCCTT	GTTTCCATTC	TTGCCTCCTT	CTGTCTACTC	TCAATATAAC	AGCTAGAACA	120
ATCCTTTTAC	AATGGAATTC	AGATCATGTT	TACCCCTCTG	TTCAAATTCT	CCAGTGACTT	180
TCCAGTTTTT	ACATGATCTG	GCTCCTACTA	CCTGTCTCAC	TGTGTTTCCT	ACTACTCTCC	240
TGCCCTTTCT	CCTCGAG					257

- (2) INFORMATION FOR SEQ ID NO:1492:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 297 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1492:

GAATTAAAGA	GGGCGATATC	ATCACACTCA	CTAACCAAAT	TGATGAGAAC	TGGTATGAGG	60
GGATGCTGCA	TGGCCATTCA	GGCTTCTTCC	CCATCAATTA	TGTGGAAATT	CTGGTTGCCC	120
TGCCCCATTA	GGATGTTATG	CTGGCTGGCT	CGCCTCCTCT	TGACCCAGAT	AGTTACGGTT	180
AACCACTGCT	TTGGCAATGC	TGCTTATAAC	ACATCCCAAG	TGCAGGCCGC	AGTGGTCCAC	240
GTCATCCAGC	CCCACCAAGT	GACTTTGGTT	GACTTGTGGG	CTCCCACAGG	ACTCGAG	297

- (2) INFORMATION FOR SEQ ID NO:1493:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 229 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1493:

GAATTCGGCC	TTCATGGCCT	AAAAAGAAAG	AAAAAGAAAA	GAAAAAACCT	TGGAGAAGTA	60
AGGGATTCTG	TAAAAAATTT	CCCCAATTTC	ACTAGAGAGA	TTGACATATA	AATTTAGAAA	120
ATTCAGATAA	CCTATGTAAG	ATGCTATGTA	AGACAACCAT	TGCAGAGACA	CAAAGTAATC	180
AGATTCTTGA	AGGTCAATGC	AAAAGAAAAA	AATATTAAAG	GCACTCGAG		229

- (2) INFORMATION FOR SEQ ID NO:1494:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 264 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1494:

GAATTCGGCC TTCATCTGAC AATTAAAAAC ACTACCTTAG TTTGTTTTTC TGTAATTGAA

TTTGCACAGT TCTATTTTAC TTGAATTAGT CTTTTTATAT ATATATAGGC AGAAGTACTT

AAATAAATCT TCCCTTAAGT ATCAAAAGCA AAAGAATAAC ATTCATAGAA GTCTAACATG

120

180

TTCAAACTGT TAAATATACT ACAATTGTTC ATTCACATTA TAAATGCAGC TAAAATGACT AACCTTTCAG ATCAACCCCT CGAG	240 264
(2) INFORMATION FOR SEQ ID NO:1495:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 190 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA	,
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1495:	
GAATTCGGCC TTCATGGCCT ACCTTCCTTC CTTCCTTCCT TCCTTTCCTT	60 120 180 190
(2) INFORMATION FOR SEQ ID NO:1496:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 232 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1496:	
GGCCTTCATG GCCTACTAAG CTATTTGATT CTAAGTGAAT ATGTTATCTC TTATTAGAGG ATATGTTAAT TTTCCTGCAT TTTATTCATT TATTAACTTA ACATCTCTGA TTGCCTACCA TGTGTCAGGC TCTGTACTAA GGATTGAGGA CCCAAAGATG AACAAAACAT GGGGCCTAAT TCAAAGATTT CACAAACTGG AGAGAAAGTC AGCCACATAC AAAAGCCTCG AG	60 120 180 232
(2) INFORMATION FOR SEQ ID NO:1497:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 152 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1497:	
GTAGAATTGT ACAGTGCTTA TGAGTTATGC ATGTGTTCCT GGTCTTTGTT CTAGGATTTT TTTTTTTTTT TGATTGCTGC TCCAGTTGCC TTACTTACTT TGACATTGGA GTTGACCACA TGATGGTGTT CCACACTTCC CCTAGGCTCG AG	60 120 152
(2) INFORMATION FOR SEQ ID NO:1498:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 254 base pairs	

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1498:	
GCGATTGAAT TCTAGACCTG CCTCGATCTC TTGTATTCAG TATTTTGTGG GGGAGGTACT	60
TTGAAACTGT GTAAATATAC CATTTCTCAT TAAACTTTTC AATTTATTCC CTTATTTAGA	120
TGCGTATGAA CTCATGGCTT CTTGTTTTAT TTGATGGATC CAAATCTGTT AATATCCTTA	180
CTGATTTGGA TGCTCAGACT GCCCCAGATT TGGCCAGTGG AAGCCCTTTC AGGCTTGCTC	240
CCATGTCCCT CGAG	254
(2) INFORMATION FOR SEQ ID NO:1499:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 658 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1499:	
GAATTCGGCC TTTCATGGCC TAGAGAGCGC GGTTGGCTGC CATTTAAACG CGGCCATCGG	60
TCCGGCCATC ATCCCCTTCA CGGTACTAGA CTCCGGGATG GTGAGATCCT TCTCATCCTT	120
TGGGGGCCGA CCCCGCTTCC GGGGACTTTG CTCTTGGGCT CTTTTCAGAG GGGATTTGGA	180
GCCTCTCTCT GAAGAGCCTG AAGACACCCT CTTCTTTCCT TCTCCCATGT TCTTCTTCAC	240
CTTCCCTTCA GACAGGCTAA GTTTGCGCTT CTCATCACCT GAGTTTGGCC TACTTCTCTC	300 360
CTCACTGGAA TTACGTCGAT TCTTGTCATC AGAAGAATTG TGGGATGACG TCTGGTCTTT CCCTTTGGCT CTCCTGTAGG CCATGAAGGC CCGGCCTTCA TGGCCTACCA TTTCTTACAC	420
ACACTGCCAG AGATACTCTA GGCATGTAAA GCACAAACAT ACATATAAAA TCTGCGGGCT	480
TCAAAAAATA TAAGTAGGAT GTCATCTATA CTGTCATACA CTTTGTTTTT TATCACTTAC	540
TTAATGTTAT ATCTTGGATA TTGTATTACC CTGGGTATTA AAAAGAACTC CTTTCACATT	600
TTAAAATAAC AATCTGAGCA CTTCATAAAT CCAAATGCGT ATCTCCAGTC TGCTCGAG	658
(2) INFORMATION FOR SEQ ID NO:1500:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 113 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1500:	

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GAATTCTAGA CCTGTCTCGA GAAACCAGAG GACTTTTCTG CTTTTGTTTT TCTTTTAGGA

GGTAATAAAA CCGTGAATTT ATTTAAATGC TAATGTGTAG GATCTCACTC GAG

What is claimed is:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145,

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2. An isolated polynucleotide consisting of a nucleotide sequence selected from the group consisting of:

or a complement of said sequence.

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or a complement of said sequence.

1

3. An isolated polynucleotide consisting essentially of a nucleotide sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ

ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEO ID NO:155, SEO ID NO:156, SEO ID NO:157, SEO ID NO:158, SEO ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEO ID NO:173, SEO ID NO:174, SEO ID NO:175, SEO ID NO:176, SEO ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEO ID NO:182, SEO ID NO:183, SEO ID NO:184, SEO ID NO:185, SEO ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,

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NO:1489, SEQ ID NO:1490, SEQ ID NO:1491, SEQ ID NO:1492, SEQ ID
NO:1493, SEQ ID NO:1494, SEQ ID NO:1495, SEQ ID NO:1496, SEQ ID
NO:1497, SEQ ID NO:1498, SEQ ID NO:1499, and SEQ ID NO:1500;
```

or a complement of said sequence.

4. An isolated polynucleotide comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ

ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEO ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID

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NO:1493, SEQ ID NO:1494, SEQ ID NO:1495, SEQ ID NO:1496, SEQ ID NO:1497, SEQ ID NO:1498, SEQ ID NO:1499, and SEQ ID NO:1500; or to a complement of said sequence.

- 5. An isolated protein encoded by an isolated polynucleotide of claim 1.
- 6. An isolated protein encoded by an isolated polynucleotide of claim 2.
- 7. An isolated protein encoded by an isolated polynucleotide of claim 3.
- 8. An isolated protein encoded by an isolated polynucleotide of claim 4.

